

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 161 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..161  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1576112  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3229:

Met Ala Arg Ser Pro Ala Ala Ser Ser Ser Tyr Thr Asp Ser Thr  
1                    5                    10                    15  
Gly Ser Ser Ser Asp Ser Gly Ser Thr Ser Ser Gly Ile Asp Arg Arg  
                    20                    25                    30  
Arg His Glu Arg Glu Arg Arg Arg Ser Ala Ser Asp Asp Asp Ser Tyr  
                    35                    40                    45  
Ser Thr Ser Ser Tyr Asp Ser Asp Arg Glu Val Ser Gly Arg Ser Arg  
50                    55                    60  
Lys His Lys Lys Ser Ser Arg Ser Arg Lys Ser Arg Glu Arg Glu Arg  
65                    70                    75                    80  
Ser Lys Asp Arg His His Lys Arg Asp Lys Ser Lys His Lys Glu Lys  
                    85                    90                    95  
Lys Glu Ser Glu His Ala Asp Gly Pro Val Gln Leu Ser Lys Phe Leu  
                    100                    105                    110  
Gly Arg Asp Lys Glu Lys Glu Glu Gly Thr Gln Arg Ser Ala Ile Ser  
                    115                    120                    125  
Gly Lys Lys Ile Met Met Lys Leu Glu Lys Thr Lys Glu Asp Lys Ala  
130                    135                    140  
Ala Glu Ser Lys Arg Asn Glu Leu Leu Lys Phe Leu Asn Ala Ser Tyr  
145                    150                    155                    160  
Asp

- (2) INFORMATION FOR SEQ ID NO:3230:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 921 base pairs  
        (B) TYPE: nucleic acid  
        (C) STRANDEDNESS: single  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: DNA (genomic)  
    (ix) FEATURE:  
        (A) NAME/KEY: -  
        (B) LOCATION: 1..921  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1576129  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3230:

atcttttagac gacaccccta cccgacccga tcggcgggag agcacgagac gccagcgcca 60  
tccatcgcg caaaaagccga gacgacccag gaatctcggc accgtcgccc ccctttctct 120  
ctcgctcaaa agttgctgct ggagccctct cccctctctc cgaccaccaa ccatggatga 180  
ggcgcaagtt gtggagtcaa aggatggaac catctcggtt gcttctgcat ttgctggtta 240  
tcaggaagct gtgcaagaca gggatcacaa attcttgaca maagcagtgg aagaagcata 300  
tcgaggagtc gattgcggtg acggaggtcc attcggagca gttgtcgtct gtaatgacga 360  
agTagtagtc agctgccata acatggttct gaagcacact gaccctactg cgcattgctga 420  
agtaactgca attagagagg cttgcaaaaa gcttgggaaa attgagctct cagactgcga 480  
aatttacgcg tcctgcgagc catgcccatt gtgctttagt gcagttcctc tctcccgaat 540  
caagaggctg gtttatgggg ccaaggcaga ggctgccatc gccattggat ttgatgactt 600  
cattgcagat gctctgagag gcaactgggt ctaccagaag gccaaacttg agatcaagaa 660  
agctgacggc aatggtgcat tgatcgctga gcaagtcttt gaaaagacta aagagaagtt 720  
ccagatgtac tgatgctgag cagaagagag atctcagatt tgtacaatgc ttactcataa 780  
ggacaagaaa taatacagtg cccaaatgtc cattgtttcg ggaaaaaaat ctcaattcca 840  
ctgttcaaca ttttgatgat gcctgaattt cttgttaaca gacacaagat tgttatttgc 900  
tgtaaaatgt gcagttgatg g

(2) INFORMATION FOR SEQ ID NO:3231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..243
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3231:

Phe Leu Asp Asp Thr Pro Thr Arg Pro Asp Arg Arg Glu Ser Thr Arg  
1 5 10 15  
Arg Gln Arg His Pro Ser Arg Gln Lys Pro Arg Arg Pro Arg Asn Leu  
20 25 30  
Gly Thr Val Ala Pro Leu Ser Leu Ser Leu Lys Ser Cys Cys Trp Ser  
35 40 45  
Pro Leu Pro Ser Leu Arg Pro Pro Thr Met Asp Glu Ala Gln Val Val  
50 55 60  
Glu Ser Lys Asp Gly Thr Ile Ser Val Ala Ser Ala Phe Ala Gly Tyr  
65 70 75 80  
Gln Glu Ala Val Gln Asp Arg Asp His Lys Phe Leu Thr Xaa Ala Val  
85 90 95  
Glu Glu Ala Tyr Arg Gly Val Asp Cys Gly Asp Gly Gly Pro Phe Gly  
100 105 110  
Ala Val Val Val Cys Asn Asp Glu Val Val Val Ser Cys His Asn Met  
115 120 125  
Val Leu Lys His Thr Asp Pro Thr Ala His Ala Glu Val Thr Ala Ile  
130 135 140  
Arg Glu Ala Cys Lys Lys Leu Gly Lys Ile Glu Leu Ser Asp Cys Glu  
145 150 155 160  
Ile Tyr Ala Ser Cys Glu Pro Cys Pro Met Cys Phe Ser Ala Val His  
165 170 175  
Leu Ser Arg Ile Lys Arg Leu Val Tyr Gly Ala Lys Ala Glu Ala Ala  
180 185 190  
Ile Ala Ile Gly Phe Asp Asp Phe Ile Ala Asp Ala Leu Arg Gly Thr  
195 200 205  
Gly Phe Tyr Gln Lys Ala Asn Leu Glu Ile Lys Lys Ala Asp Gly Asn  
210 215 220  
Gly Ala Leu Ile Ala Glu Gln Val Phe Glu Lys Thr Lys Glu Lys Phe  
225 230 235 240  
Gln Met Tyr

(2) INFORMATION FOR SEQ ID NO:3232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..186
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3232:

Met Asp Glu Ala Gln Val Val Glu Ser Lys Asp Gly Thr Ile Ser Val  
1 5 10 15  
Ala Ser Ala Phe Ala Gly Tyr Gln Glu Ala Val Gln Asp Arg Asp His  
20 25 30  
Lys Phe Leu Thr Xaa Ala Val Glu Glu Ala Tyr Arg Gly Val Asp Cys

35 40 45  
Gly Asp Gly Gly Pro Phe Gly Ala Val Val Val Cys Asn Asp Glu Val  
50 55 60  
Val Val Ser Cys His Asn Met Val Leu Lys His Thr Asp Pro Thr Ala  
65 70 75 80  
His Ala Glu Val Thr Ala Ile Arg Glu Ala Cys Lys Lys Leu Gly Lys  
85 90 95  
Ile Glu Leu Ser Asp Cys Glu Ile Tyr Ala Ser Cys Glu Pro Cys Pro  
100 105 110  
Met Cys Phe Ser Ala Val His Leu Ser Arg Ile Lys Arg Leu Val Tyr  
115 120 125  
Gly Ala Lys Ala Glu Ala Ala Ile Ala Ile Gly Phe Asp Asp Phe Ile  
130 135 140  
Ala Asp Ala Leu Arg Gly Thr Gly Phe Tyr Gln Lys Ala Asn Leu Glu  
145 150 155 160  
Ile Lys Lys Ala Asp Gly Asn Gly Ala Leu Ile Ala Glu Gln Val Phe  
165 170 175  
Glu Lys Thr Lys Glu Lys Phe Gln Met Tyr  
180 185

(2) INFORMATION FOR SEQ ID NO:3233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 455 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..455
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3233:

aaatggatgg cattatgaac acggcctccg caagcatgtc catgtacgct taccttgctc	60
tectcaagcc ccagggaag atgacccctgc ttggcctgcc tgagaagcct ctgcagatct	120
ccgccttctc ttgtgttact gggggcaaga ctctggcccg gagctgcatg gggagcatca	180
gggacacgca ggagatgatg gacttcgcag ccaagcacgg gttgacagcg gacatcgaac	240
tgatcggcac cgaagaagtt aatgaggcca tggaacNgyc tcgccaaagg cgaggNtcag	300
gtaccgcttc gtcacgcaca tcggcaacac catcagcgcg gcatcactag ggagctcgcc	360
ggtcccagct ctgtagctgc gacacttggt cctgcttgga tatatcgtgc gataagcaag	420
tatatattgga ataaaaagga actcaatttta aacgc	

(2) INFORMATION FOR SEQ ID NO:3234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..115
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3234:

Met Asp Gly Ile Met Asn Thr Ala Ser Ala Ser Met Ser Met Tyr Ala  
1 5 10 15  
Tyr Leu Ala Leu Leu Lys Pro Gln Gly Lys Met Ile Leu Leu Gly Leu  
20 25 30  
Pro Glu Lys Pro Leu Gln Ile Ser Ala Phe Ser Leu Val Thr Gly Gly  
35 40 45  
Lys Thr Leu Ala Gly Ser Cys Met Gly Ser Ile Arg Asp Thr Gln Glu  
50 55 60  
Met Met Asp Phe Ala Ala Lys His Gly Leu Thr Ala Asp Ile Glu Leu  
65 70 75 80

Ile Gly Thr Glu Glu Val Asn Glu Ala Met Glu Xaa Xaa Arg Gln Gly  
85 90 95  
Arg Xaa Ser Gly Thr Ala Ser Ser Ser Thr Ser Ala Thr Pro Ser Ala  
100 105 110  
Arg His His  
115

(2) INFORMATION FOR SEQ ID NO:3235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..111
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576137

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3235:

Met Asn Thr Ala Ser Ala Ser Met Ser Met Tyr Ala Tyr Leu Ala Leu  
1 5 10 15  
Leu Lys Pro Gln Gly Lys Met Ile Leu Gly Leu Pro Glu Lys Pro  
20 25 30  
Leu Gln Ile Ser Ala Phe Ser Leu Val Thr Gly Gly Lys Thr Leu Ala  
35 40 45  
Gly Ser Cys Met Gly Ser Ile Arg Asp Thr Gln Glu Met Met Asp Phe  
50 55 60  
Ala Ala Lys His Gly Leu Thr Ala Asp Ile Glu Leu Ile Gly Thr Glu  
65 70 75 80  
Glu Val Asn Glu Ala Met Glu Xaa Xaa Arg Gln Gly Arg Xaa Ser Gly  
85 90 95  
Thr Ala Ser Ser Thr Ser Ala Thr Pro Ser Ala Arg His His  
100 105 110

(2) INFORMATION FOR SEQ ID NO:3236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 518 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..518
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576138

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3236:

aaacgcactc tcctatatcc gccgccatcg tctcgggctc tcctctctaa tcttcgggtt 60  
cgcgctcgag tgtcttccgc ccgggctacc accatgccga agcagatcca cgagatcaag 120  
gacttcctgc tgactgcgcg gcggaaggac gcacggtcgg tgcggatcaa gcgggccaag 180  
gacgccgtca agttcaaggt gcgctgctcc aggtacctct acaccctctg cgtccacgac 240  
gccgacaagg ccaacaagct caagcagtcg ctcccgccag gtctgactgt ccaggagatt 300  
taaggtatca agccacaaac tgtgcttttt ttgcgggtgtc agggacgttt gctccagtgt 360  
tactttagtt tgtaggtggg ctccattgct gtgtttgaat gaattatgaa gtttgagttt 420  
gggatgcgaa tgatgtgtcg aacctatgag Gcctgtgttg taatggttac cccagaccgc 480  
aaaggatggc aatctatcat aagttaaact gatttccg

(2) INFORMATION FOR SEQ ID NO:3237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:



(A) NAME/KEY: peptide  
(B) LOCATION: 1..100  
(D) OTHER INFORMATION: / Ceres Seq. ID 1576139

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3237:

Lys Arg Thr Leu Tyr Pro Pro Pro Ser Ser Arg Ala Leu Ile Ser  
1 5 10 15  
Asn Leu Arg Val Arg Val Ala Val Ser Ser Ala Arg Ala Thr Thr Met  
20 25 30  
Pro Lys Gln Ile His Glu Ile Lys Asp Phe Leu Leu Thr Ala Arg Arg  
35 40 45  
Lys Asp Ala Arg Ser Val Arg Ile Lys Arg Ala Lys Asp Ala Val Lys  
50 55 60  
Phe Lys Val Arg Cys Ser Arg Tyr Leu Tyr Thr Leu Cys Val His Asp  
65 70 75 80  
Ala Asp Lys Ala Asn Lys Leu Lys Gln Ser Leu Pro Pro Gly Leu Thr  
85 90 95  
Val Gln Glu Ile  
100

(2) INFORMATION FOR SEQ ID NO:3238:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 69 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..69  
(D) OTHER INFORMATION: / Ceres Seq. ID 1576140

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3238:

Met Pro Lys Gln Ile His Glu Ile Lys Asp Phe Leu Leu Thr Ala Arg  
1 5 10 15  
Arg Lys Asp Ala Arg Ser Val Arg Ile Lys Arg Ala Lys Asp Ala Val  
20 25 30  
Lys Phe Lys Val Arg Cys Ser Arg Tyr Leu Tyr Thr Leu Cys Val His  
35 40 45  
Asp Ala Asp Lys Ala Asn Lys Leu Lys Gln Ser Leu Pro Pro Gly Leu  
50 55 60  
Thr Val Gln Glu Ile  
65

(2) INFORMATION FOR SEQ ID NO:3239:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1034 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..1034  
(D) OTHER INFORMATION: / Ceres Seq. ID 1576144

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3239:

accaaagatg	ttgccgtggc	ctcgccgcac	aagaaaaatca	cagcagtaca	gcaccagaaa	60
cagaaaggta	gtagatcaag	gaacgccagt	gcggcgacaa	tgaccggcag	tggaagcacg	120
ggcgccaatg	gcaagagcca	gagatccagg	gccaaggcaa	tgctgttcgc	cttgggcaag	180
agcttttctg	accaagtctt	gcctcaggag	aaggttgttg	agagctacct	ccaagaaagc	240
agctgcgacg	atcccgccac	cagggccaag	cttcagcgcc	tttgacgac	tacaacagtg	300
aagacaaggt	acactgttat	gtccaaggag	ctattggata	agcaccaga	gctgaagatg	360
gaGggtactc	cgacactgac	acctcgccct	gacatctgca	atgccgcggt	gatcgacctt	420
ggtgctgccc	cagCtcgcgc	tgcccttgac	gaatggggtc	gccctgcagc	tgatattacc	480
cacctcatct	acatctcatc	cagtgcacct	cgtctcccag	ggggcgacct	tcacctggct	540

gctcgccttg gccttagccc aaacacocgtg cgcacttccc ttctcttccct tggctgctcc 600  
ggtggtgctg ctgcctcccg cactgccaag gacattgctg agaacaatcc agggagccgt 660  
gtcctagtaa cagctgctga gaccactgtg ctaggcttcc ggccaccaag ttatgaccgt 720  
ccttatgacc ttgttggtst gcgctgtttg gtgatgggtgc atcagccgtg attataggag 780  
caggtcccat gacaccagca gaaaatcctt tcttgagct tgagttctcc acgcaggagt 840  
tcctacctgg gactgataag gtaattgatg gcaaaatctc agaggaagga attaatttta 900  
aactagggcg tgatttgcct gagaagattg aaagccgcac agaaggtttc tgcaggactc 960  
tcatgaacca ggtagggata aaggatttca acgatatatt ttgggctgtg catcctgggtg 1020  
gaccagcaat attg

(2) INFORMATION FOR SEQ ID NO:3240:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 256 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..256

(D) OTHER INFORMATION: / Ceres Seq. ID 1576145

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3240:

Thr Lys Asp Val Ala Val Ala Ser Pro His Lys Lys Ile Thr Ala Val  
1 5 10 15  
Gln His Gln Lys Gln Lys Gly Ser Arg Ser Arg Asn Ala Ser Ala Ala  
20 25 30  
Thr Met Thr Gly Ser Gly Ser Thr Gly Ala Asn Gly Lys Ser Gln Arg  
35 40 45  
Ser Arg Ala Lys Ala Met Leu Phe Ala Leu Gly Lys Ser Phe Pro Asp  
50 55 60  
Gln Val Leu Pro Gln Glu Lys Val Val Glu Ser Tyr Leu Gln Glu Ser  
65 70 75 80  
Ser Cys Asp Asp Pro Ala Thr Arg Ala Lys Leu Gln Arg Leu Cys Thr  
85 90 95  
Thr Thr Thr Val Lys Thr Arg Tyr Thr Val Met Ser Lys Glu Leu Leu  
100 105 110  
Asp Lys His Pro Glu Leu Lys Met Glu Gly Thr Pro Thr Leu Thr Pro  
115 120 125  
Arg Leu Asp Ile Cys Asn Ala Ala Val Ile Asp Leu Gly Ala Ala Ala  
130 135 140  
Ala Arg Ala Ala Leu Asp Glu Trp Gly Arg Pro Ala Ala Asp Ile Thr  
145 150 155 160  
His Leu Ile Tyr Ile Ser Ser Ser Asp Leu Arg Leu Pro Gly Gly Asp  
165 170 175  
Leu His Leu Ala Ala Arg Leu Gly Leu Ser Pro Asn Thr Val Arg Thr  
180 185 190  
Ser Leu Leu Phe Leu Gly Cys Ser Gly Gly Ala Ala Ala Leu Arg Thr  
195 200 205  
Ala Lys Asp Ile Ala Glu Asn Asn Pro Gly Ser Arg Val Leu Val Thr  
210 215 220  
Ala Ala Glu Thr Thr Val Leu Gly Phe Arg Pro Pro Ser Tyr Asp Arg  
225 230 235 240  
Pro Tyr Asp Leu Val Gly Xaa Arg Cys Leu Val Met Val His Gln Pro  
245 250 255

(2) INFORMATION FOR SEQ ID NO:3241:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 223 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

SEQUENCE - 1576145

(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..223

(D) OTHER INFORMATION: / Ceres Seq. ID 1576146

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3241:

Met Thr Gly Ser Gly Ser Thr Gly Ala Asn Gly Lys Ser Gln Arg Ser  
1 5 10 15  
Arg Ala Lys Ala Met Leu Phe Ala Leu Gly Lys Ser Phe Pro Asp Gln  
20 25 30  
Val Leu Pro Gln Glu Lys Val Val Glu Ser Tyr Leu Gln Glu Ser Ser  
35 40 45  
Cys Asp Asp Pro Ala Thr Arg Ala Lys Leu Gln Arg Leu Cys Thr Thr  
50 55 60  
Thr Thr Val Lys Thr Arg Tyr Thr Val Met Ser Lys Glu Leu Leu Asp  
65 70 75 80  
Lys His Pro Glu Leu Lys Met Glu Gly Thr Pro Thr Leu Thr Pro Arg  
85 90 95  
Leu Asp Ile Cys Asn Ala Ala Val Ile Asp Leu Gly Ala Ala Ala Ala  
100 105 110  
Arg Ala Ala Leu Asp Glu Trp Gly Arg Pro Ala Ala Asp Ile Thr His  
115 120 125  
Leu Ile Tyr Ile Ser Ser Ser Asp Leu Arg Leu Pro Gly Gly Asp Leu  
130 135 140  
His Leu Ala Ala Arg Leu Gly Leu Ser Pro Asn Thr Val Arg Thr Ser  
145 150 155 160  
Leu Leu Phe Leu Gly Cys Ser Gly Gly Ala Ala Ala Leu Arg Thr Ala  
165 170 175  
Lys Asp Ile Ala Glu Asn Asn Pro Gly Ser Arg Val Leu Val Thr Ala  
180 185 190  
Ala Glu Thr Thr Val Leu Gly Phe Arg Pro Pro Ser Tyr Asp Arg Pro  
195 200 205  
Tyr Asp Leu Val Gly Xaa Arg Cys Leu Val Met Val His Gln Pro  
210 215 220

(2) INFORMATION FOR SEQ ID NO:3242:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 203 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..203

(D) OTHER INFORMATION: / Ceres Seq. ID 1576147

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3242:

Met Leu Phe Ala Leu Gly Lys Ser Phe Pro Asp Gln Val Leu Pro Gln  
1 5 10 15  
Glu Lys Val Val Glu Ser Tyr Leu Gln Glu Ser Ser Cys Asp Asp Pro  
20 25 30  
Ala Thr Arg Ala Lys Leu Gln Arg Leu Cys Thr Thr Thr Thr Val Lys  
35 40 45  
Thr Arg Tyr Thr Val Met Ser Lys Glu Leu Leu Asp Lys His Pro Glu  
50 55 60  
Leu Lys Met Glu Gly Thr Pro Thr Leu Thr Pro Arg Leu Asp Ile Cys  
65 70 75 80  
Asn Ala Ala Val Ile Asp Leu Gly Ala Ala Ala Ala Arg Ala Ala Leu  
85 90 95  
Asp Glu Trp Gly Arg Pro Ala Ala Asp Ile Thr His Leu Ile Tyr Ile  
100 105 110  
Ser Ser Ser Asp Leu Arg Leu Pro Gly Gly Asp Leu His Leu Ala Ala

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      115              120              125
Arg Leu Gly Leu Ser Pro Asn Thr Val Arg Thr Ser Leu Leu Phe Leu
      130              135              140
Gly Cys Ser Gly Gly Ala Ala Leu Arg Thr Ala Lys Asp Ile Ala
145              150              155              160
Glu Asn Asn Pro Gly Ser Arg Val Leu Val Thr Ala Ala Glu Thr Thr
      165              170              175
Val Leu Gly Phe Arg Pro Pro Ser Tyr Asp Arg Pro Tyr Asp Leu Val
      180              185              190
Gly Xaa Arg Cys Leu Val Met Val His Gln Pro
      195              200
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(2) INFORMATION FOR SEQ ID NO:3243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1107 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1107
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3243:

```

gagaganana ngcgargaar gavggagaga gcacgggggc ttgatcgaag atgggatgccg      60
gagcaaaggt ggtgaagaag gccgcggcgg ggcgtcgcgg cgggggcaag tacttcttcc      120
acgagcagat ttcaaggcat cgcaccatca tgaatatctt tgacaaaacc cctcatgtgc      180
ataaagacgc atttgttgct ccaagtgcac cccttattgg tgatgttcaa gtcgggtcag      240
gagcttccat ttggtatggg tgcgtcttaa gaggggatgc aaacatcata caaattggat      300
ctgggaccaa tatacaagac aattctctta tacatgtggc taaatctaata ctaagtggga      360
aggtctttcc aacaaccatt ggtaataacg tcacagtagg tcatagtgtc gtgttacaag      420
gatgcacggt tgaggatgag gctttgtgtg gcattggggc aaccctatta gatggtgttg      480
ttgttgaaaa gcacggaatg gtggccttgc ggagccctcg tacggcagaa tactaggatc      540
ccttggtggg aggtatgggg agggaaccCt gccaaatttc tgaggaagct cacagatgac      600
gagatcagtt tcattgcgga atcagctgcc aactattcca atctgtccaa ggtccatgct      660
gctgagaatg ccaaacctct tgaaaagatt gagtttgaga aggtgttggg caagaagttt      720
gctcaccagg atgagtatga ttctctgatt ggcgtcactg aaggggcacc accagagctc      780
acgtccccaa atccagccca atgaacctct gtttctgttt tctctttggc gccttaatca      840
ttttctggtg gacagtgtg gatcgttgat cgggtgactg ttccatgaca ctggtggtt      900
atgtttactt ttctcccca ataactcttg atcgagcgat gttataaagc tggccatgca      960
cttcttccag attctgtatt cggtatgttt aagatgtgct ccctttcata acctcaagag      1020
tagttttagc accgtccata ttctgtcatg gttctgtact atgctttctg gcccggcgtg      1080
tatgaacat ctttataaaa atctctt
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(2) INFORMATION FOR SEQ ID NO:3244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..161
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3244:

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Met Asp Ala Gly Ala Lys Val Val Lys Lys Ala Ala Ala Gly Arg Arg
1              5              10              15
Gly Gly Gly Lys Tyr Phe Phe His Glu Gln Ile Ser Arg His Arg Thr
      20              25              30
Ile Met Asn Ile Phe Asp Lys Thr Pro His Val His Lys Asp Ala Phe
      35              40              45
Val Ala Pro Ser Ala Ser Leu Ile Gly Asp Val Gln Val Gly Ser Gly
```

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50	55	60
Ala Ser Ile Trp Tyr Gly Cys Val Leu Arg Gly Asp Ala Asn Ile Ile		
65	70	75
Gln Ile Gly Ser Gly Thr Asn Ile Gln Asp Asn Ser Leu Ile His Val		80
	85	90
Ala Lys Ser Asn Leu Ser Gly Lys Val Phe Pro Thr Thr Ile Gly Asn		95
	100	105
Asn Val Thr Val Gly His Ser Ala Val Leu Gln Gly Cys Thr Val Glu		110
	115	120
Asp Glu Ala Phe Val Gly Ile Gly Ala Thr Leu Leu Asp Gly Val Val		125
130	135	140
Val Glu Lys His Gly Met Val Ala Cys Trp Ser Pro Arg Thr Ala Glu		
145	150	155
Tyr		160

(2) INFORMATION FOR SEQ ID NO:3245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..170
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576157

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3245:

Met Thr Arg Ser Val Ser Leu Arg Asn Gln Leu Pro Thr Ile Pro Ile	
1	5 10 15
Cys Pro Arg Ser Met Leu Leu Arg Met Pro Asn Leu Leu Lys Arg Leu	
	20 25 30
Ser Leu Arg Arg Cys Trp Ala Arg Ser Leu Leu Thr Arg Met Ser Met	
	35 40 45
Ile Pro Arg Leu Ala Ser Leu Lys Gly His His Gln Ser Ser Arg Pro	
	50 55 60
Gln Ile Gln Pro Asn Glu Pro Leu Phe Leu Phe Ser Leu Trp Arg Leu	
65	70 75 80
Asn His Phe Leu Leu Asp Ser Ala Gly Ser Leu Ile Gly Val Leu Phe	
	85 90 95
His Asp Thr Gly Gly Leu Cys Leu Leu Phe Leu Pro Asn Asn Leu Gly	
	100 105 110
Ser Ser Asp Val Ile Lys Leu Ala Met His Phe Phe Gln Ile Leu Tyr	
	115 120 125
Ser Val Cys Leu Arg Cys Ala Pro Phe His Asn Leu Lys Ser Ser Phe	
130	135 140
Ser Thr Val His Ile Arg His Glu Phe Cys Thr Met Leu Ser Gly Pro	
145	150 155 160
Ala Cys Met Asn His Leu Tyr Lys Asn Leu	
	165 170

(2) INFORMATION FOR SEQ ID NO:3246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..150
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576158

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3246:

116-117-118-119-120-121-122-123-124-125-126-127-128-129-130-131-132-133-134-135-136-137-138-139-140-141-142-143-144-145-146-147-148-149-150-151-152-153-154-155-156-157-158-159-160-161-162-163-164-165-166-167-168-169-170-171-172-173-174-175-176-177-178-179-180-181-182-183-184-185-186-187-188-189-190-191-192-193-194-195-196-197-198-199-200-201-202-203-204-205-206-207-208-209-210-211-212-213-214-215-216-217-218-219-220-221-222-223-224-225-226-227-228-229-230-231-232-233-234-235-236-237-238-239-240-241-242-243-244-245-246-247-248-249-250-251-252-253-254-255-256-257-258-259-260-261-262-263-264-265-266-267-268-269-270-271-272-273-274-275-276-277-278-279-280-281-282-283-284-285-286-287-288-289-290-291-292-293-294-295-296-297-298-299-300-301-302-303-304-305-306-307-308-309-310-311-312-313-314-315-316-317-318-319-320-321-322-323-324-325-326-327-328-329-330-331-332-333-334-335-336-337-338-339-340-341-342-343-344-345-346-347-348-349-350-351-352-353-354-355-356-357-358-359-360-361-362-363-364-365-366-367-368-369-370-371-372-373-374-375-376-377-378-379-380-381-382-383-384-385-386-387-388-389-390-391-392-393-394-395-396-397-398-399-400-401-402-403-404-405-406-407-408-409-410-411-412-413-414-415-416-417-418-419-420-421-422-423-424-425-426-427-428-429-430-431-432-433-434-435-436-437-438-439-440-441-442-443-444-445-446-447-448-449-450-451-452-453-454-455-456-457-458-459-460-461-462-463-464-465-466-467-468-469-470-471-472-473-474-475-476-477-478-479-480-481-482-483-484-485-486-487-488-489-490-491-492-493-494-495-496-497-498-499-500-501-502-503-504-505-506-507-508-509-510-511-512-513-514-515-516-517-518-519-520-521-522-523-524-525-526-527-528-529-530-531-532-533-534-535-536-537-538-539-540-541-542-543-544-545-546-547-548-549-550-551-552-553-554-555-556-557-558-559-560-561-562-563-564-565-566-567-568-569-570-571-572-573-574-575-576-577-578-579-580-581-582-583-584-585-586-587-588-589-590-591-592-593-594-595-596-597-598-599-600-601-602-603-604-605-606-607-608-609-610-611-612-613-614-615-616-617-618-619-620-621-622-623-624-625-626-627-628-629-630-631-632-633-634-635-636-637-638-639-640-641-642-643-644-645-646-647-648-649-650-651-652-653-654-655-656-657-658-659-660-661-662-663-664-665-666-667-668-669-670-671-672-673-674-675-676-677-678-679-680-681-682-683-684-685-686-687-688-689-690-691-692-693-694-695-696-697-698-699-700-701-702-703-704-705-706-707-708-709-710-711-712-713-714-715-716-717-718-719-720-721-722-723-724-725-726-727-728-729-730-731-732-733-734-735-736-737-738-739-740-741-742-743-744-745-746-747-748-749-750-751-752-753-754-755-756-757-758-759-760-761-762-763-764-765-766-767-768-769-770-771-772-773-774-775-776-777-778-779-780-781-782-783-784-785-786-787-788-789-790-791-792-793-794-795-796-797-798-799-800-801-802-803-804-805-806-807-808-809-810-811-812-813-814-815-816-817-818-819-820-821-822-823-824-825-826-827-828-829-830-831-832-833-834-835-836-837-838-839-840-841-842-843-844-845-846-847-848-849-850-851-852-853-854-855-856-857-858-859-860-861-862-863-864-865-866-867-868-869-870-871-872-873-874-875-876-877-878-879-880-881-882-883-884-885-886-887-888-889-890-891-892-893-894-895-896-897-898-899-900-901-902-903-904-905-906-907-908-909-910-911-912-913-914-915-916-917-918-919-920-921-922-923-924-925-926-927-928-929-930-931-932-933-934-935-936-937-938-939-940-941-942-943-944-945-946-947-948-949-950-951-952-953-954-955-956-957-958-959-960-961-962-963-964-965-966-967-968-969-970-971-972-973-974-975-976-977-978-979-980-981-982-983-984-985-986-987-988-989-990-991-992-993-994-995-996-997-998-999-1000

Met Leu Leu Arg Met Pro Asn Leu Leu Lys Arg Leu Ser Leu Arg Arg  
1 5 10 15  
Cys Trp Ala Arg Ser Leu Leu Thr Arg Met Ser Met Ile Pro Arg Leu  
20 25 30  
Ala Ser Leu Lys Gly His His Gln Ser Ser Arg Pro Gln Ile Gln Pro  
35 40 45  
Asn Glu Pro Leu Phe Leu Phe Ser Leu Trp Arg Leu Asn His Phe Leu  
50 55 60  
Leu Asp Ser Ala Gly Ser Leu Ile Gly Val Leu Phe His Asp Thr Gly  
65 70 75 80  
Gly Leu Cys Leu Leu Phe Leu Pro Asn Asn Leu Gly Ser Ser Asp Val  
85 90 95  
Ile Lys Leu Ala Met His Phe Phe Gln Ile Leu Tyr Ser Val Cys Leu  
100 105 110  
Arg Cys Ala Pro Phe His Asn Leu Lys Ser Ser Phe Ser Thr Val His  
115 120 125  
Ile Arg His Glu Phe Cys Thr Met Leu Ser Gly Pro Ala Cys Met Asn  
130 135 140  
His Leu Tyr Lys Asn Leu  
145 150

(2) INFORMATION FOR SEQ ID NO:3247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 922 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..922
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576159

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3247:

aaaactgttc	tgcttcgctc	gcrggcgctc	atctccactc	ctccgatggc	gccgccaccc	60
accagcccct	cattcctcgc	cccgccgcgc	ctgccacacc	acccgcaccc	tcgcctcctt	120
ttgcgacctc	cctccgcctc	ttccgcgcgc	gccgaaatac	tcggcggtcg	gggcctctgc	180
aatggtgagg	tcggcggtcc	caaagaactc	gcacccgggt	ccaccacctc	ctcgcccgcg	240
ccctctcctc	ctccttcgac	agattctcct	ccgcccgcgc	ttgatccgga	cgcgttcgag	300
aaggagatga	tgggcctcac	aggcggcttc	cctggcggtg	aggtcggcct	caaggacttc	360
gtagccaaga	acccgcctcc	tcccaagaaa	tcagaatccc	agccccaagc	cacgctctcc	420
gcgcgcgcgc	ggccgcgcga	gctgcgcgct	ttcttgcccg	gcattggtgt	gctggtcaag	480
aaccccaaca	acgcctacca	catgtactgc	ggtatcgtgc	agcgcgtcag	CGacggcaag	540
gNtcgcggtg	ctcttcgagg	gaggagtgtg	ggacaggctc	atcaccttca	acctcgacga	600
gctcgagggc	agggagaagg	gaccccttat	ggccaacccc	aagtccgttg	tgctagagga	660
tcttgtcgcg	gagctcgagg	atgacgatga	tgataaggag	gacgaagcgg	ccaagaagaa	720
ggaaccggag	ggcgcgccgc	cgcgcgccgc	atgaccaggc	ttcttggttc	tggtatacac	780
atcctctgta	tgtatgcatt	tatacagctc	aaataaaaata	tttgagagta	attaaaaagg	840
aacgataata	taactcttat	tatgaagtat	atagtttgaa	tgttagtgtg	aattggggca	900
tggaagaatt	gccatacggt	tg				

(2) INFORMATION FOR SEQ ID NO:3248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..227
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576160

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3248:

Lys Thr Val Leu Leu Arg Ser Xaa Ala Leu Ile Ser Thr Pro Pro Met

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1 5 10 15  
Ala Pro Pro Pro Thr Ser Pro Ser Phe Leu Arg Pro Pro Pro Leu Pro  
20 25 30  
His His Pro His Pro Arg Leu Leu Leu Arg Pro Pro Ser Ala Ser Phe  
35 40 45  
Arg Val Ala Glu Ile Leu Gly Gly Arg Gly Leu Cys Asn Gly Glu Val  
50 55 60  
Gly Val Arg Lys Glu Leu Ala Ser Gly Ser Thr Thr Ser Ser Pro Ala  
65 70 75 80  
Pro Ser Pro Pro Pro Ser Thr Asp Ser Pro Pro Pro Ala Val Asp Pro  
85 90 95  
Asp Ala Phe Glu Lys Glu Met Met Gly Leu Thr Gly Gly Phe Pro Gly  
100 105 110  
Gly Glu Val Gly Leu Lys Asp Phe Val Ala Lys Asn Pro Pro Pro Pro  
115 120 125  
Lys Lys Ser Glu Ser Gln Pro Gln Ala Thr Leu Ser Ala Pro Pro Arg  
130 135 140  
Pro Pro Glu Leu Pro Leu Phe Leu Pro Gly Met Val Val Leu Val Lys  
145 150 155 160  
Asn Pro Asn Asn Ala Tyr His Met Tyr Cys Gly Ile Val Gln Arg Val  
165 170 175  
Ser Asp Gly Lys Xaa Arg Gly Ala Leu Arg Gly Arg Ser Val Gly Gln  
180 185 190  
Ala His His Leu Gln Pro Arg Arg Ala Arg Gly Gln Gly Glu Gly Thr  
195 200 205  
Pro Tyr Gly Gln Pro Gln Val Arg Gly Ala Arg Gly Ser Cys Arg Gly  
210 215 220  
Ala Arg Gly  
225

(2) INFORMATION FOR SEQ ID NO:3249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..212

(D) OTHER INFORMATION: / Ceres Seq. ID 1576161

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3249:

Met Ala Pro Pro Pro Thr Ser Pro Ser Phe Leu Arg Pro Pro Pro Leu  
1 5 10 15  
Pro His His Pro His Pro Arg Leu Leu Leu Arg Pro Pro Ser Ala Ser  
20 25 30  
Phe Arg Val Ala Glu Ile Leu Gly Gly Arg Gly Leu Cys Asn Gly Glu  
35 40 45  
Val Gly Val Arg Lys Glu Leu Ala Ser Gly Ser Thr Thr Ser Ser Pro  
50 55 60  
Ala Pro Ser Pro Pro Pro Ser Thr Asp Ser Pro Pro Pro Ala Val Asp  
65 70 75 80  
Pro Asp Ala Phe Glu Lys Glu Met Met Gly Leu Thr Gly Gly Phe Pro  
85 90 95  
Gly Gly Glu Val Gly Leu Lys Asp Phe Val Ala Lys Asn Pro Pro Pro  
100 105 110  
Pro Lys Lys Ser Glu Ser Gln Pro Gln Ala Thr Leu Ser Ala Pro Pro  
115 120 125  
Arg Pro Pro Glu Leu Pro Leu Phe Leu Pro Gly Met Val Val Leu Val  
130 135 140  
Lys Asn Pro Asn Asn Ala Tyr His Met Tyr Cys Gly Ile Val Gln Arg  
145 150 155 160

Val Ser Asp Gly Lys Xaa Arg Gly Ala Leu Arg Gly Arg Ser Val Gly  
165 170 175  
Gln Ala His His Leu Gln Pro Arg Arg Ala Arg Gly Gln Gly Glu Gly  
180 185 190  
Thr Pro Tyr Gly Gln Pro Gln Val Arg Gly Ala Arg Gly Ser Cys Arg  
195 200 205  
Gly Ala Arg Gly  
210

(2) INFORMATION FOR SEQ ID NO:3250:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..125

(D) OTHER INFORMATION: / Ceres Seq. ID 1576162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3250:

Met Met Gly Leu Thr Gly Gly Phe Pro Gly Gly Glu Val Gly Leu Lys  
1 5 10 15  
Asp Phe Val Ala Lys Asn Pro Pro Pro Pro Lys Lys Ser Glu Ser Gln  
20 25 30  
Pro Gln Ala Thr Leu Ser Ala Pro Pro Arg Pro Pro Glu Leu Pro Leu  
35 40 45  
Phe Leu Pro Gly Met Val Val Leu Val Lys Asn Pro Asn Asn Ala Tyr  
50 55 60  
His Met Tyr Cys Gly Ile Val Gln Arg Val Ser Asp Gly Lys Xaa Arg  
65 70 75 80  
Gly Ala Leu Arg Gly Arg Ser Val Gly Gln Ala His His Leu Gln Pro  
85 90 95  
Arg Arg Ala Arg Gly Gln Gly Glu Gly Thr Pro Tyr Gly Gln Pro Gln  
100 105 110  
Val Arg Gly Ala Arg Gly Ser Cys Arg Gly Ala Arg Gly  
115 120 125

(2) INFORMATION FOR SEQ ID NO:3251:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 627 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..627

(D) OTHER INFORMATION: / Ceres Seq. ID 1576221

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3251:

aaggtgtttt gccctcttct tcgcgarcnc ccccgccgca acccgagcc gcatcgagg 60  
acccgagcc gccgatggcg aagaagcaca gggaccagc ctctgargcc gcgagcggcg 120  
actccccggc cgcgtccatc cgctccctct tctccgcgga caaMcccgtt ccgcccgaag 180  
gcctctacgg aggagcccc cgcgactcct gcacccgcca cgacgcccct ccccatgcaa 240  
cccagccgtg acgccaggga tgccgagccg tcctcgaaga agaataagaa gagcaaggag 300  
gagggccccg gcgcgaagcg gaagcgrgac gagttggagg ccggccggga gcggcgcgga 360  
ggcgcgaggaga atccgtcgag agttggggag aagaggaagg ctcccgaaga cgcgccacag 420  
ggggccgggg aggacgagga ggaggctttc gacgacgaga gcaagctgct caggaccgtg 480  
ttcgtgggga acctgccgct gcggwccaag cgcaaggtgc tcatcaagga gttcgtcaa 540  
aaaggacagg caggcagctg cctcccccca tgttatgatg acaaaactct agtagctagg 600  
aaaggaatca cggtgacctt ttgtttc

(2) INFORMATION FOR SEQ ID NO:3252:

(i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 209 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..209
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1576222
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3252:

Lys Val Phe Cys Pro Leu Leu Arg Xaa Xaa Pro Arg Arg Asn Pro Gln  
1 5 10 15  
Pro His Arg Glu Thr Arg Ser Arg Arg Trp Arg Arg Ser Thr Gly Thr  
20 25 30  
Gln Pro Leu Xaa Pro Arg Ala Ala Thr Pro Arg Pro Arg Pro Ser Ala  
35 40 45  
Pro Ser Ser Pro Arg Thr Xaa Pro Phe Arg Arg Lys Ala Ser Thr Glu  
50 55 60  
Glu Pro Pro Ala Thr Pro Ala Pro Ala Thr Thr Pro Leu Pro Met Gln  
65 70 75 80  
Pro Ser Arg Asp Ala Arg Asp Ala Glu Pro Ser Ser Lys Lys Asn Lys  
85 90 95  
Lys Ser Lys Glu Glu Gly Pro Arg Arg Lys Arg Lys Xaa Asp Glu Leu  
100 105 110  
Glu Ala Gly Arg Glu Arg Arg Arg Gly Ala Glu Asn Pro Ser Arg Val  
115 120 125  
Gly Glu Lys Arg Lys Ala Pro Asp Asp Ala Ala Gln Gly Ala Gly Glu  
130 135 140  
Asp Glu Glu Glu Ala Phe Asp Asp Glu Ser Lys Leu Leu Arg Thr Val  
145 150 155 160  
Phe Val Gly Asn Leu Pro Leu Arg Xaa Lys Arg Lys Val Leu Ile Lys  
165 170 175  
Glu Phe Ala Gln Lys Gly Gln Ala Gly Ser Cys Leu Pro Pro Cys Tyr  
180 185 190  
Asp Asp Lys Thr Leu Val Ala Arg Lys Gly Ile Thr Val Thr Phe Cys  
195 200 205  
Phe

- (2) INFORMATION FOR SEQ ID NO:3253:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 131 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..131
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1576223
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3253:

Met Gln Pro Ser Arg Asp Ala Arg Asp Ala Glu Pro Ser Ser Lys Lys  
1 5 10 15  
Asn Lys Lys Ser Lys Glu Glu Gly Pro Arg Arg Lys Arg Lys Xaa Asp  
20 25 30  
Glu Leu Glu Ala Gly Arg Glu Arg Arg Arg Gly Ala Glu Asn Pro Ser  
35 40 45  
Arg Val Gly Glu Lys Arg Lys Ala Pro Asp Asp Ala Ala Gln Gly Ala  
50 55 60  
Gly Glu Asp Glu Glu Glu Ala Phe Asp Asp Glu Ser Lys Leu Leu Arg  
65 70 75 80  
Thr Val Phe Val Gly Asn Leu Pro Leu Arg Xaa Lys Arg Lys Val Leu

85 90 95  
Ile Lys Glu Phe Ala Gln Lys Gly Gln Ala Gly Ser Cys Leu Pro Pro  
100 105 110  
Cys Tyr Asp Asp Lys Thr Leu Val Ala Arg Lys Gly Ile Thr Val Thr  
115 120 125  
Phe Cys Phe  
130

(2) INFORMATION FOR SEQ ID NO:3254:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 110 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..110

(D) OTHER INFORMATION: / Ceres Seq. ID 1576224

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3254:

Met Pro Ser Arg Pro Arg Arg Arg Ile Arg Arg Ala Arg Arg Arg Ala  
1 5 10 15  
Arg Gly Ala Ser Gly Ser Xaa Thr Ser Trp Arg Pro Ala Gly Ser Gly  
20 25 30  
Gly Glu Ala Arg Arg Ile Arg Arg Glu Leu Gly Arg Arg Gly Arg Leu  
35 40 45  
Pro Thr Thr Arg His Arg Gly Pro Gly Arg Thr Arg Arg Arg Leu Ser  
50 55 60  
Thr Thr Arg Ala Ser Cys Ser Gly Pro Cys Ser Trp Gly Thr Cys Arg  
65 70 75 80  
Cys Xaa Pro Ser Ala Arg Cys Ser Ser Arg Ser Ser Leu Lys Lys Asp  
85 90 95  
Arg Gln Ala Ala Ala Ser Pro His Val Met Met Thr Lys Leu  
100 105 110

(2) INFORMATION FOR SEQ ID NO:3255:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 750 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..750

(D) OTHER INFORMATION: / Ceres Seq. ID 1576229

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3255:

gcttccacca tcgcacccac ccggagcgcc tcctcttctc cagcgtcgga tccccattcc 60  
ccacctctcc tccctccgcc gccagctccc gcmcccttct ctcccctcct cgccctcccg 120  
cgcgcgcggtt tttataaggg tttaagcgga ggcgcccggt cgctggcgat ggccgamgac 180  
ggcgggagcc acgagggcag cggcgggcggc ggaggcgctc gggagcagga ccggttcctg 240  
cccatcgcca acatcagccg gatcatgaag aargCcgccc cggccaacgg caagatcgcc 300  
aaggacgcta aggagaccgc tgcaaaaccg aggggtgctga aacagagatg attctggttt 360  
ggcccgtaga agcgatgcaa aaggtcgtct cccaaggtaa cgacgaatga tggAcagcgg 420  
gggtgctctt gctctctaca agttgatgac aactagctgg ttgccttttg aaagcaccog 480  
tgcatgtgat ctgacgaatg aaaacaaagt gatgggtgta aacgtgtaaa gactttaaac 540  
tggtgccaat aaatattacg tatttatgta aatgcacgga tctgatggaa tgcacatatg 600  
gtgcccacat atctgggcat tgcgcgctgc cgaatgtctg gttaaagcgcg ctattttcatg 660  
gttggtgtgcg tccgagaaaa ggcaatggcc gtgcaaaagt ttcttcgacg gatggttgca 720  
gatgttagca gtacaggatg ttttcttgt

(2) INFORMATION FOR SEQ ID NO:3256:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 amino acids

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

```
(A) NAME/KEY: peptide
(B) LOCATION: 1..60
```

(D) OTHER INFORMATION: / Ceres Seq. ID 1576231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1															
Met	Ala	Xaa	Asp	Gly	Gly	Ser	His	Glu	Gly	Ser	Gly	Gly	Gly	Gly	Gly
1				5				10						15	
Val	Arg	Glu	Gln	Asp	Arg	Phe	Leu	Pro	Ile	Ala	Asn	Ile	Ser	Arg	Ile
			20					25					30		
Met	Lys	Xaa	Ala	Val	Pro	Ala	Asn	Gly	Lys	Ile	Ala	Lys	Asp	Ala	Lys
		35					40					45			
Glu	Thr	Ala	Ala	Lys	Pro	Arg	Val	Leu	Lys	Gln	Arg				
	50					55				60					

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 59 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

```
(A) NAME/KEY: peptide
(B) LOCATION: 1..59
```

(D) OTHER INFORMATION: / Ceres Seq. ID 1576232

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1

Met	His	Gly	Ser	Asp	Gly	Met	His	Ile	Trp	Cys	Pro	Ser	Ile	Trp	Ala
1			5					10						15	
Leu	Arg	Ala	Ala	Glu	Cys	Leu	Val	Lys	Arg	Ala	Ile	Ser	Trp	Leu	Cys
			20					25					30		

Ala Ser Glu Lys Arg Gln Trp Pro Cys Lys Ser Phe Phe Asp Gly Trp  
35 40 45  
Leu Gln Met Leu Ala Val Gln Asp Val Phe Leu  
50 55

(2) INFORMATION FOR SEQ ID NO:3259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 934 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..934
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576241

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3259:

aaaaattgca	aaaatctctg	ccgtgcctct	cgtctctctt	ctcargcgcc	acgcaaaacg	60
gtctccgttt	tccctctccg	gatccggccc	gcgggagcca	ggagccatcg	atgatccgga	120
ccgcaacggt	gcgagcgcg	ctcctcctat	cgcgcctcta	cgtagcacag	gcaaaggcag	180
cttctcgctg	gcctctcgtc	cgtcggaagg	cttcgcctct	tggatctgta	cgctctttct	240
atcagatgga	cattacaagg	caatacaaaa	ataaaaattt	gactgcaaga	gggtgccata	300
gctccccctg	gagtcagaaa	ttagcaatga	aaagctgtgt	tccatgcaac	totaaggatt	360
taggtcccat	gtcagaagat	tctgctaaaa	agttgcttga	acaggtgaat	ggttggaac	420
tgatcactga	aggtggtgtt	ctgaaattac	atagaacatg	gaaggtgaag	aactttgtta	480
aaggacttga	gttctttcag	cttggtgctg	ctatcgctga	ggaagaagg	caccatccag	540
atcttcatct	tgttggttgg	aataatgtga	aaattgatgt	ttggactcat	tctgtcagag	600
gtttaacaag	taatgatttc	atccttgctg	cgaagatcaa	tcattctact	ttagacggca	660
ttataaggaa	gaaagctaaa	tagccaatgt	ctcagaagca	actcaaatat	gcagctcgta	720
tttgtttgga	attttgtatg	cgcagcgatg	gagaagccaa	atgttgagga	cacctcgccc	780
tgtgtgagat	taacttgctg	aaatgtagt	ccttattcag	tagctcattt	taccttgcta	840
tttaattagta	atttgcata	gtagacgttg	aatccatcat	tgtacttggt	tacctactta	900
cottacctgt	cagttttgaa	aagacacatg	gtcg			

(2) INFORMATION FOR SEQ ID NO:3260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..226
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576242

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3260:

Lys	Leu	Gln	Lys	Ser	Leu	Pro	Cys	Leu	Ser	Ser	Leu	Phe	Ser	Xaa	Ala
1			5					10						15	
Thr	Gln	Asn	Gly	Leu	Arg	Phe	Pro	Ser	Pro	Asp	Pro	Ala	Arg	Gly	Ser
		20					25					30			
Gln	Glu	Pro	Ser	Met	Ile	Arg	Thr	Ala	Thr	Val	Arg	Ala	Arg	Leu	Leu
		35					40					45			
Leu	Ser	Arg	Ser	Tyr	Val	Ala	Gln	Ala	Lys	Ala	Ala	Ser	Arg	Trp	Pro
		50				55					60				
Leu	Val	Arg	Trp	Lys	Ala	Ser	His	Leu	Gly	Ser	Val	Arg	Ser	Phe	Tyr
		65			70				75					80	
Gln	Met	Asp	Ile	Thr	Arg	Gln	Tyr	Lys	Asn	Lys	Ile	Leu	Thr	Ala	Arg
			85				90							95	
Gly	Cys	His	Ser	Ser	Pro	Glu	Ser	Gln	Glu	Leu	Ala	Met	Lys	Ser	Cys
			100				105						110		
Val	Pro	Cys	Asn	Ser	Lys	Asp	Leu	Gly	Pro	Met	Ser	Glu	Asp	Ser	Ala
			115				120						125		
Lys	Lys	Leu	Leu	Glu	Gln	Val	Asn	Gly	Trp	Glu	Leu	Ile	Thr	Glu	Gly

130		135		140																
Gly	Val	Leu	Lys	Leu	His	Arg	Thr	Trp	Lys	Val	Lys	Asn	Phe	Val	Lys					
145					150					155									160	
Gly	Leu	Glu	Phe	Phe	Gln	Leu	Val	Ala	Ala	Ile	Ala	Glu	Glu	Glu	Gly					
				165					170						175					
His	His	Pro	Asp	Leu	His	Leu	Val	Gly	Trp	Asn	Asn	Val	Lys	Ile	Asp					
			180					185					190							
Val	Trp	Thr	His	Ser	Val	Arg	Gly	Leu	Thr	Ser	Asn	Asp	Phe	Ile	Leu					
		195					200					205								
Ala	Ala	Lys	Ile	Asn	His	Leu	Thr	Leu	Asp	Gly	Ile	Ile	Arg	Lys	Lys					
	210					215					220									
Ala	Lys																			
225																				

(2) INFORMATION FOR SEQ ID NO:3261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 190 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..190
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3261:

Met	Ile	Arg	Thr	Ala	Thr	Val	Arg	Ala	Arg	Leu	Leu	Leu	Ser	Arg	Ser					
1				5				10						15						
Tyr	Val	Ala	Gln	Ala	Lys	Ala	Ala	Ser	Arg	Trp	Pro	Leu	Val	Arg	Trp					
		20					25					30								
Lys	Ala	Ser	His	Leu	Gly	Ser	Val	Arg	Ser	Phe	Tyr	Gln	Met	Asp	Ile					
		35				40						45								
Thr	Arg	Gln	Tyr	Lys	Asn	Lys	Ile	Leu	Thr	Ala	Arg	Gly	Cys	His	Ser					
	50				55					60										
Ser	Pro	Glu	Ser	Gln	Glu	Leu	Ala	Met	Lys	Ser	Cys	Val	Pro	Cys	Asn					
	65			70					75					80						
Ser	Lys	Asp	Leu	Gly	Pro	Met	Ser	Glu	Asp	Ser	Ala	Lys	Lys	Leu	Leu					
			85					90						95						
Glu	Gln	Val	Asn	Gly	Trp	Glu	Leu	Ile	Thr	Glu	Gly	Gly	Val	Leu	Lys					
		100					105						110							
Leu	His	Arg	Thr	Trp	Lys	Val	Lys	Asn	Phe	Val	Lys	Gly	Leu	Glu	Phe					
		115				120						125								
Phe	Gln	Leu	Val	Ala	Ala	Ile	Ala	Glu	Glu	Glu	Gly	His	His	Pro	Asp					
	130				135					140										
Leu	His	Leu	Val	Gly	Trp	Asn	Asn	Val	Lys	Ile	Asp	Val	Trp	Thr	His					
	145			150					155					160						
Ser	Val	Arg	Gly	Leu	Thr	Ser	Asn	Asp	Phe	Ile	Leu	Ala	Ala	Lys	Ile					
			165					170						175						
Asn	His	Leu	Thr	Leu	Asp	Gly	Ile	Ile	Arg	Lys	Lys	Ala	Lys							
		180				185							190							

(2) INFORMATION FOR SEQ ID NO:3262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..145
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576244

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3262:

SEQUENCE LISTING

Met Asp Ile Thr Arg Gln Tyr Lys Asn Lys Ile Leu Thr Ala Arg Gly  
1 5 10 15  
Cys His Ser Ser Pro Glu Ser Gln Glu Leu Ala Met Lys Ser Cys Val  
20 25 30  
Pro Cys Asn Ser Lys Asp Leu Gly Pro Met Ser Glu Asp Ser Ala Lys  
35 40 45  
Lys Leu Leu Glu Gln Val Asn Gly Trp Glu Leu Ile Thr Glu Gly Gly  
50 55 60  
Val Leu Lys Leu His Arg Thr Trp Lys Val Lys Asn Phe Val Lys Gly  
65 70 75 80  
Leu Glu Phe Phe Gln Leu Val Ala Ala Ile Ala Glu Glu Glu Gly His  
85 90 95  
His Pro Asp Leu His Leu Val Gly Trp Asn Asn Val Lys Ile Asp Val  
100 105 110  
Trp Thr His Ser Val Arg Gly Leu Thr Ser Asn Asp Phe Ile Leu Ala  
115 120 125  
Ala Lys Ile Asn His Leu Thr Leu Asp Gly Ile Ile Arg Lys Lys Ala  
130 135 140  
Lys  
145

(2) INFORMATION FOR SEQ ID NO:3263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 698 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..698
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576245

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3263:

aaagaaaagg aaggaagaag ggcctcctgt atcctctcac ttccctcagt cctcgctccgt	60
ctgctccctc ctctckctas ctagctctag ctagccttcc tgtagcgcgg cagagatggc	120
tgccctgcc tccaccacgg cggcgccggc ggcagcgcgt ctgctgctgc tcctcctgtc	180
gctcgccgcg gcggcggnac atgtcgatcg tgtcctacgg ggagcgcagc brcraggagg	240
cgcggcggat gtacgcggag tggatggcgg cgcacggccg gacctacaam gccgtcggcK	300
aggaggagcg gcggtaccag gtgttccggg acaacctccg ctacatcgac gcgcacaacg	360
ccgccgccga cgcgggcgtc cactccttcc gcctcgAgcc tcaaccgCtt cgccgacctc	420
accaacgacg agtaccgcgc cacctacctc ggcgccagga ccaggccgca gaggggagagg	480
aagctcggcg ccaggtacca cgccgccgac aacgaggacc tgccggagtc cgtcgactgg	540
agggccaagg gcgcgcgtcg cgaggtcaag gaccagggca gctgcgggag ctgttgggct	600
ttctcaacaa tagcagctgt ggaaggcatc aaccagattg ttacaggcga cttgatctcc	660
ttgtctgaac aagagcttgt cgactgtgac mytcgtac	

(2) INFORMATION FOR SEQ ID NO:3264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..221
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576246

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3264:

Arg Lys Gly Arg Lys Lys Gly Leu Leu Tyr Pro Leu Thr Ser Leu Ser  
1 5 10 15  
Pro Arg Pro Ser Ala Pro Ser Ser Xaa Xaa Leu Ala Leu Ala Ser Leu  
20 25 30  
Pro Val Ala Arg Gln Arg Trp Leu Pro Leu Pro Pro Pro Arg Arg Arg

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(D) TOPOLOGY: linear

MOLECULE TYPE: peptid

(A) NAME/KEY: peptide

(B) LOCATION: 1..165

(D) OTHER INFORMATION: / Ceres Seq. ID 157624 /  
 - NAME DESCRIPTION SEQ ID NO: 3265:

(2) INFORMATION FOR SEQ ID NO:3266:

(A) LENGTH: 155 amino acids

(B) TYPE: amino acid

- (C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..155  
(D) OTHER INFORMATION: / Ceres Seq. ID 1576248  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3266:

Met Ser Ile Val Ser Tyr Gly Glu Arg Ser Xaa Xaa Glu Ala Arg Arg  
1 5 10 15  
Met Tyr Ala Glu Trp Met Ala Ala His Gly Arg Thr Tyr Xaa Ala Val  
20 25 30  
Gly Xaa Glu Glu Arg Arg Tyr Gln Val Phe Arg Asp Asn Leu Arg Tyr  
35 40 45  
Ile Asp Ala His Asn Ala Ala Ala Asp Ala Gly Val His Ser Phe Arg  
50 55 60  
Leu Glu Pro Gln Pro Leu Arg Arg Pro His Gln Arg Arg Val Pro Arg  
65 70 75 80  
His Leu Pro Arg Arg Gln Asp Gln Ala Ala Glu Gly Glu Glu Ala Arg  
85 90 95  
Arg Gln Val Pro Arg Arg Arg Gln Arg Gly Pro Ala Gly Val Arg Arg  
100 105 110  
Leu Glu Gly Gln Gly Arg Arg Arg Arg Gly Gln Gly Pro Gly Gln Leu  
115 120 125  
Arg Glu Leu Leu Gly Phe Leu Asn Asn Ser Ser Cys Gly Arg His Gln  
130 135 140  
Pro Asp Cys Tyr Arg Arg Leu Asp Leu Leu Val  
145 150 155

(2) INFORMATION FOR SEQ ID NO:3267:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 988 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..988  
(D) OTHER INFORMATION: / Ceres Seq. ID 1576267

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3267:

cgatagtatg ctaggaagga gagaaaatcc aggggagcat gaagcgatgc gcaagatgaa 60  
gaatgaattt atggtaaaatt gggatgggtt ggcactaaa gataaggagc gtgtgcttgt 120  
tcttggtgct acaaataggc cttttgacct cgacgaggct gtgattagga gggtcccccg 180  
cagggttaatg gtaaaacttgc ccgatgcacg aaatagggag aaaatttctaa aagtaatttt 240  
ggcaaaaagaa gagctgggat ctgatgttga tatggactcg cttgccaata tgactgatgg 300  
ttattcagga agcgacctga agaactctgtg tgtvaccgcg gcgcattacc ccatccgaga 360  
aattctggag aaggaaaaga aggagaagag tttggctaaa acagaaggta ggccggagcc 420  
tgcattatat ggaagcgagG acatccgccc ccttagcata gatgacttca aaAtctgccm 480  
atgagcaggt gtgtgcgasc gtttcgtccg actcggcgaa catgaacgag ctcccttcaat 540  
ggaacgacyt gtacgktgaa ggcgggtcaa ggaagaagaa agcgtgagc tacttcatgt 600  
gatgtggtga gagcatagaa tccagaagga tcacagccgt ggcataagat cagaaggaac 660  
acagagcggc catagtacca caccacacc cactatggcc ctaaattccag tcagggttttc 720  
gctccttccc cctccctcag tagccgcccgc cgccccaccg ccgcctggtg taattagaac 780  
tgtgtaccga gtcgagttgg tttgccagct gtttcgaggt tacagagttg agatttgaa 840  
ttacaatggc gccattgccc tctccaacc ccccttttt cttcctctca taagttgcgg 900  
tcactgtcct tcttgactc tctggccttt gttcttgtaa atgcgaaatg aagggatgtg 960  
aaataagaac atcttcgtcc tgttgttg

(2) INFORMATION FOR SEQ ID NO:3268:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 160 amino acids  
(B) TYPE: amino acid



(X1) SEQUENCE DESCRIPTION: SEQ ID NO:3200:															
Asp 1	Ser	Met	Leu	Gly 5	Arg	Arg	Glu	Asn 10	Pro	Gly	Glu	His	Glu 15	Ala	Met
Arg	Lys	Met	Lys 20	Asn	Glu	Phe	Met	Val 25	Asn	Trp	Asp	Gly	Leu 30	Arg	Thr
Lys	Asp	Lys 35	Glu	Arg	Val	Leu	Val 40	Leu	Gly	Ala	Thr	Asn 45	Arg	Pro	Phe
Asp 50	Leu	Asp	Glu	Ala	Val	Ile 55	Arg	Arg	Phe	Pro	Arg 60	Arg	Leu	Met	Val
Asn 65	Leu	Pro	Asp	Ala	Ser 70	Asn	Arg	Glu	Lys 75	Ile	Leu	Lys	Val	Ile 80	Leu
Ala	Lys	Glu	Glu 85	Leu	Gly	Ser	Asp	Val 90	Asp	Met	Asp	Ser	Leu 95	Ala	Asn
Met	Thr	Asp 100	Gly	Tyr	Ser	Gly	Ser 105	Asp	Leu	Lys	Asn 110	Leu	Cys 115	Xaa	Thr
Ala	Ala	His 115	Tyr	Pro	Ile	Arg	Glu 120	Ile	Leu	Glu	Lys 125	Glu	Lys	Lys	Glu
Lys	Ser 130	Leu	Ala	Lys	Thr	Glu 135	Gly	Arg	Pro	Glu	Pro 140	Ala	Leu	Tyr	Gly
Ser 145	Glu	Asp	Ile	Arg 150	Pro	Leu	Ser	Ile	Asp 155	Asp	Phe	Lys	Ile	Cys 160	Xaa

(i) SEQUENCE CHARACTERISTICS:

```
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
```

(D) OTHER INFORMATION: / Ceres Seq. ID 1576269

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:3209:																
Met	Leu	Gly	Arg	Arg	Glu	Asn	Pro	Gly	Glu	His	Glu	Ala	Met	Arg	Lys	
1				5					10					15		
Met	Lys	Asn	Glu	Phe	Met	Val	Asn	Trp	Asp	Gly	Leu	Arg	Thr	Lys	Asp	
			20					25					30			
Lys	Glu	Arg	Val	Leu	Val	Leu	Gly	Ala	Thr	Asn	Arg	Pro	Phe	Asp	Leu	
		35					40					45				
Asp	Glu	Ala	Val	Ile	Arg	Arg	Phe	Pro	Arg	Arg	Leu	Met	Val	Asn	Leu	
	50					55					60					
Pro	Asp	Ala	Ser	Asn	Arg	Glu	Lys	Ile	Leu	Lys	Val	Ile	Leu	Ala	Lys	
65					70					75					80	
Glu	Glu	Leu	Gly	Ser	Asp	Val	Asp	Met	Asp	Ser	Leu	Ala	Asn	Met	Thr	
			85						90					95		
Asp	Gly	Tyr	Ser	Gly	Ser	Asp	Leu	Lys	Asn	Leu	Cys	Xaa	Thr	Ala	Ala	
			100					105					110			
His	Tyr	Pro	Ile	Arg	Glu	Ile	Leu	Glu	Lys	Glu	Lys	Lys	Glu	Lys	Ser	
		115					120					125				
Leu	Ala	Lys	Thr	Glu	Gly	Arg	Pro	Glu	Pro	Ala	Leu	Tyr	Gly	Ser	Glu	
	130					135					140					
Asp	Ile	Arg	Pro	Leu	Ser	Ile	Asp	Asp	Phe	Lys	Ile	Cys	Xaa			

145

150

155

(2) INFORMATION FOR SEQ ID NO:3270:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 145 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..145

(D) OTHER INFORMATION: / Ceres Seq. ID 1576270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3270:

Met	Arg	Lys	Met	Lys	Asn	Glu	Phe	Met	Val	Asn	Trp	Asp	Gly	Leu	Arg
1			5						10					15	
Thr	Lys	Asp	Lys	Glu	Arg	Val	Leu	Val	Leu	Gly	Ala	Thr	Asn	Arg	Pro
			20					25					30		
Phe	Asp	Leu	Asp	Glu	Ala	Val	Ile	Arg	Arg	Phe	Pro	Arg	Arg	Leu	Met
			35				40					45			
Val	Asn	Leu	Pro	Asp	Ala	Ser	Asn	Arg	Glu	Lys	Ile	Leu	Lys	Val	Ile
	50					55				60					
Leu	Ala	Lys	Glu	Glu	Leu	Gly	Ser	Asp	Val	Asp	Met	Asp	Ser	Leu	Ala
65					70				75					80	
Asn	Met	Thr	Asp	Gly	Tyr	Ser	Gly	Ser	Asp	Leu	Lys	Asn	Leu	Cys	Xaa
			85					90					95		
Thr	Ala	Ala	His	Tyr	Pro	Ile	Arg	Glu	Ile	Leu	Glu	Lys	Glu	Lys	Lys
			100					105					110		
Glu	Lys	Ser	Leu	Ala	Lys	Thr	Glu	Gly	Arg	Pro	Glu	Pro	Ala	Leu	Tyr
		115					120					125			
Gly	Ser	Glu	Asp	Ile	Arg	Pro	Leu	Ser	Ile	Asp	Asp	Phe	Lys	Ile	Cys
	130					135					140				

Xaa

145

(2) INFORMATION FOR SEQ ID NO:3271:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 824 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..824

(D) OTHER INFORMATION: / Ceres Seq. ID 1576273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3271:

accagccacc	gccaaagccgc	attacaaaga	acgcgaaccg	ctgccagtcc	aaaccctacg	60
gccgccgcca	gcatcaagct	ccccgaccaa	accctactcg	taccccgccg	cgcgcgcagc	120
cgcagccgcg	gccacaccag	caagcagaac	tagcagccat	gccgcccaaa	ttggaccctt	180
ctcaggtggt	ggaggtcttc	gtccgcgtga	cgggaggcga	ggtcggcgcg	gcgtcgtcgc	240
tggcccccaa	gatcggcccg	ctcggctctt	ccccgaagaa	gatcggcgag	gacatcgcca	300
aggagaccgc	caaggactgg	aagggcctcc	gcgtcaccgt	caagctcacc	gtgcagaacc	360
ggcaggccaa	ggtctccgtc	gtcccctccg	ccgcggcgct	cgatcatcaag	gcgctcaagg	420
aacccgagag	ggacaggaag	aaggtcaaga	acatcaagca	cagcGggcaa	catcagcctc	480
gacgacgtca	tcgagatcgc	caagaCccat	gcggaacagg	tccatggcca	aggagttggc	540
cgggaccgtc	aaggagatcc	tggggacctg	cgtcaGcgtc	gggtgcaccg	tcgatgggaa	600
ggaccccaag	gacttgcagc	aggagatcga	tgatggtgag	gtcgagatcc	cctcagctta	660
aaggctatac	aactagaaat	catcggacac	tattaaagtg	tggtgttttg	ttccaakksa	720
gttcctgcac	ctcaatcgcc	tattattgtc	tgctttagtt	ccttcaagtc	ttgtgagaga	780
cctaatacgt	accttgtgcc	ttataaaatt	acatcttccg	attc		

(2) INFORMATION FOR SEQ ID NO:3272:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 219 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..219  
(D) OTHER INFORMATION: / Ceres Seq. ID 1576274  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3272:

Pro	Ala	Thr	Ala	Lys	Pro	His	Tyr	Lys	Glu	Arg	Glu	Pro	Leu	Pro	Val
1				5					10					15	
Gln	Thr	Leu	Arg	Pro	Pro	Pro	Ala	Ser	Ser	Ser	Pro	Thr	Lys	Pro	Tyr
			20					25					30		
Ser	Tyr	Pro	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Thr	Pro	Ala	Ser
			35				40						45		
Arg	Thr	Ser	Ser	His	Ala	Ala	Gln	Ile	Gly	Pro	Leu	Ser	Gly	Gly	Gly
					55						60				
Gly	Leu	Arg	Pro	Arg	Asp	Gly	Arg	Arg	Gly	Arg	Arg	Gly	Val	Val	Ala
65					70					75					80
Gly	Pro	Gln	Asp	Arg	Pro	Ala	Arg	Ser	Leu	Pro	Glu	Glu	Asp	Arg	Arg
			85						90					95	
Gly	His	Arg	Gln	Gly	Asp	Arg	Gln	Gly	Leu	Glu	Gly	Pro	Pro	Arg	His
			100					105					110		
Arg	Gln	Ala	His	Arg	Ala	Glu	Pro	Ala	Gly	Gln	Gly	Leu	Arg	Arg	Pro
			115				120					125			
Leu	Arg	Arg	Gly	Ala	Arg	His	Gln	Gly	Ala	Gln	Gly	Thr	Arg	Glu	Gly
			130			135					140				
Gln	Glu	Glu	Gly	Gln	Glu	His	Gln	Ala	Gln	Arg	Ala	Thr	Ser	Ala	Ser
145					150					155					160
Thr	Thr	Ser	Ser	Arg	Ser	Pro	Arg	Pro	Met	Arg	Asn	Arg	Ser	Met	Ala
				165					170					175	
Lys	Glu	Leu	Ala	Gly	Thr	Val	Lys	Glu	Ile	Leu	Gly	Thr	Cys	Val	Ser
			180					185					190		
Val	Gly	Cys	Thr	Val	Asp	Gly	Lys	Asp	Pro	Lys	Asp	Leu	Gln	Gln	Glu
			195				200					205			
Ile	Asp	Asp	Gly	Glu	Val	Glu	Ile	Pro	Ser	Ala					
	210					215									

(2) INFORMATION FOR SEQ ID NO:3273:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 251 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..251  
(D) OTHER INFORMATION: / Ceres Seq. ID 1576275  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3273:

Gln	Pro	Pro	Pro	Ser	Arg	Ile	Thr	Lys	Asn	Ala	Asn	Arg	Cys	Gln	Ser
1				5					10					15	
Lys	Pro	Tyr	Gly	Arg	Arg	Gln	His	Gln	Ala	Pro	Arg	Pro	Asn	Pro	Thr
			20					25					30		
Arg	Thr	Pro	Pro	Pro	Pro	Gln	Pro	Gln	Pro	Arg	Pro	His	Gln	Gln	Ala
			35				40					45			
Glu	Leu	Ala	Ala	Met	Pro	Pro	Lys	Leu	Asp	Pro	Ser	Gln	Val	Val	Glu
			50				55				60				
Val	Phe	Val	Arg	Val	Thr	Gly	Gly	Glu	Val	Gly	Ala	Ala	Ser	Ser	Leu
65					70					75					80
Ala	Pro	Lys	Ile	Gly	Pro	Leu	Gly	Leu	Ser	Pro	Lys	Lys	Ile	Gly	Glu

85 90 95  
Asp Ile Ala Lys Glu Thr Ala Lys Asp Trp Lys Gly Leu Arg Val Thr  
100 105 110  
Val Lys Leu Thr Val Gln Asn Arg Gln Ala Lys Val Ser Val Val Pro  
115 120 125  
Ser Ala Ala Ala Leu Val Ile Lys Ala Leu Lys Glu Pro Glu Arg Asp  
130 135 140  
Arg Lys Lys Val Lys Asn Ile Lys His Ser Gly Gln His Gln Pro Arg  
145 150 155 160  
Arg Arg His Arg Asp Arg Gln Asp Pro Cys Gly Thr Gly Pro Trp Pro  
165 170 175  
Arg Ser Trp Pro Gly Pro Ser Arg Arg Ser Trp Gly Pro Ala Ser Ala  
180 185 190  
Ser Gly Ala Pro Ser Met Gly Arg Thr Pro Arg Thr Cys Ser Arg Arg  
195 200 205  
Ser Met Met Val Arg Ser Arg Ser Pro Gln Leu Lys Gly Tyr Thr Thr  
210 215 220  
Arg Asn His Arg Thr Leu Leu Lys Cys Gly Val Leu Phe Gln Xaa Ser  
225 230 235 240  
Ser Cys Thr Ser Ile Ala Tyr Tyr Cys Leu Leu  
245 250

(2) INFORMATION FOR SEQ ID NO:3274:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 199 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..199

(D) OTHER INFORMATION: / Ceres Seq. ID 1576276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3274:

Met Pro Pro Lys Leu Asp Pro Ser Gln Val Val Glu Val Phe Val Arg  
1 5 10 15  
Val Thr Gly Gly Glu Val Gly Ala Ala Ser Ser Leu Ala Pro Lys Ile  
20 25 30  
Gly Pro Leu Gly Leu Ser Pro Lys Lys Ile Gly Glu Asp Ile Ala Lys  
35 40 45  
Glu Thr Ala Lys Asp Trp Lys Gly Leu Arg Val Thr Val Lys Leu Thr  
50 55 60  
Val Gln Asn Arg Gln Ala Lys Val Ser Val Val Pro Ser Ala Ala Ala  
65 70 75 80  
Leu Val Ile Lys Ala Leu Lys Glu Pro Glu Arg Asp Arg Lys Lys Val  
85 90 95  
Lys Asn Ile Lys His Ser Gly Gln His Gln Pro Arg Arg Arg His Arg  
100 105 110  
Asp Arg Gln Asp Pro Cys Gly Thr Gly Pro Trp Pro Arg Ser Trp Pro  
115 120 125  
Gly Pro Ser Arg Arg Ser Trp Gly Pro Ala Ser Ala Ser Gly Ala Pro  
130 135 140  
Ser Met Gly Arg Thr Pro Arg Thr Cys Ser Arg Arg Ser Met Met Val  
145 150 155 160  
Arg Ser Arg Ser Pro Gln Leu Lys Gly Tyr Thr Thr Arg Asn His Arg  
165 170 175  
Thr Leu Leu Lys Cys Gly Val Leu Phe Gln Xaa Ser Ser Cys Thr Ser  
180 185 190  
Ile Ala Tyr Tyr Cys Leu Leu  
195

(2) INFORMATION FOR SEQ ID NO:3275:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 573 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..573
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1576315
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3275:

acgaagcaca caacaaacct gcagatcccc catggcaggc tccacctccc tcgtwcccoct	60
tcccgctmccc gcccctccat ctgcgccacgc cttccacacg tccacgtccg catcccccccg	120
ccacctgcgc ccttcccctg ctacacgcct ccgcgctgcc cggcgtcggc atccccgacgc	180
cgctggttgc gtcccagatg cccgccctcg ggctggcgat ctatcgggcg ccgccgggtc	240
ctaccgggac ggaagtgagg aggacgaaga cgacgcagat gaagatgagg acgaagacga	300
ggaccgcagc ctggacctac tggcccggtt cctgcactcc gtattcagga aggcctcacg	360
ccGgcGsgcg ccgCgctgcc aggtccgtgc tgcgccttc cgtccccgcc gagctggtga	420
agtttttcggt caatggcgtg ctgtctctga cgttcttatg gatcctgaag ggtcttctcg	480
aggtggtctg cacatttgga agcatggtgt ttggtAattc gattcaagaT tactgtacgc	540
tgccagctct tggagaaaaa aggttttcgg tgc	

(2) INFORMATION FOR SEQ ID NO:3276:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 171 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..171
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1576316
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3276:

Arg Ser Thr Gln Gln Thr Cys Arg Ser Pro Met Ala Gly Ser Thr Ser	
1 5 10 15	
Leu Xaa Pro Leu Pro Xaa Pro Ala Pro Pro Ser Arg His Arg Phe His	
20 25 30	
Thr Ser Thr Ser Ala Ser Pro Arg His Leu Arg Pro Ser Pro Ala Thr	
35 40 45	
Arg Leu Arg Ala Ala Arg Arg Arg His Pro Asp Ala Val Val Val Val	
50 55 60	
Pro Asp Ala Arg Pro Trp Val Gly Asp Leu Ser Gly Ala Ala Ala Ser	
65 70 75 80	
Tyr Arg Asp Gly Ser Glu Glu Asp Glu Asp Asp Ala Asp Glu Asp Glu	
85 90 95	
Asp Glu Asp Glu Asp Arg Ser Leu Asp Leu Leu Ala Arg Phe Leu His	
100 105 110	
Ser Val Phe Arg Lys Ala Ser Arg Arg Xaa Ala Pro Arg Cys Gln Val	
115 120 125	
Arg Ala Ala Ala Phe Arg Pro Arg Arg Ala Gly Glu Val Phe Gly Gln	
130 135 140	
Trp Arg Ala Cys Pro Asp Val Leu Met Asp Pro Glu Gly Ser Ser Arg	
145 150 155 160	
Gly Gly Leu His Ile Trp Lys His Gly Val Trp	
165 170	

(2) INFORMATION FOR SEQ ID NO:3277:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 190 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..190

(D) OTHER INFORMATION: / Ceres Seq. ID 1576317

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3277:

Glu Ala His Asn Lys Pro Ala Asp Pro Pro Trp Gln Ala Pro Pro Pro  
1 5 10 15  
Ser Xaa Pro Phe Pro Xaa Pro Pro Leu His Leu Ala Thr Ala Ser Thr  
20 25 30  
Arg Pro Arg Pro His Pro Pro Ala Thr Cys Ala Pro Pro Leu Leu His  
35 40 45  
Ala Ser Ala Leu Pro Gly Val Gly Ile Pro Thr Pro Ser Leu Ser Ser  
50 55 60  
Gln Met Pro Ala Pro Gly Ser Ala Ile Tyr Arg Ala Pro Pro Arg Pro  
65 70 75 80  
Thr Gly Thr Glu Val Arg Arg Thr Lys Thr Thr Gln Met Lys Met Arg  
85 90 95  
Thr Lys Thr Arg Thr Ala Ala Trp Thr Tyr Trp Pro Gly Ser Cys Thr  
100 105 110  
Pro Tyr Ser Gly Arg Pro His Ala Xaa Arg Arg Ala Ala Arg Ser  
115 120 125  
Val Leu Pro Pro Ser Val Pro Ala Glu Leu Val Lys Phe Ser Val Asn  
130 135 140  
Gly Val Leu Val Leu Thr Phe Leu Trp Ile Leu Lys Gly Leu Leu Glu  
145 150 155 160  
Val Val Cys Thr Phe Gly Ser Met Val Phe Gly Asn Ser Ile Gln Asp  
165 170 175  
Tyr Cys Thr Leu Pro Ala Leu Gly Glu Lys Arg Phe Ser Val  
180 185 190

(2) INFORMATION FOR SEQ ID NO:3278:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 161 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..161

(D) OTHER INFORMATION: / Ceres Seq. ID 1576318

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3278:

Met Ala Gly Ser Thr Ser Leu Xaa Pro Leu Pro Xaa Pro Ala Pro Pro  
1 5 10 15  
Ser Arg His Arg Phe His Thr Ser Thr Ser Ala Ser Pro Arg His Leu  
20 25 30  
Arg Pro Ser Pro Ala Thr Arg Leu Arg Ala Ala Arg Arg His Pro  
35 40 45  
Asp Ala Val Val Val Val Pro Asp Ala Arg Pro Trp Val Gly Asp Leu  
50 55 60  
Ser Gly Ala Ala Ala Ser Tyr Arg Asp Gly Ser Glu Glu Asp Glu Asp  
65 70 75 80  
Asp Ala Asp Glu Asp Glu Asp Glu Asp Glu Asp Arg Ser Leu Asp Leu  
85 90 95  
Leu Ala Arg Phe Leu His Ser Val Phe Arg Lys Ala Ser Arg Arg Xaa  
100 105 110  
Ala Pro Arg Cys Gln Val Arg Ala Ala Phe Arg Pro Arg Arg Ala  
115 120 125  
Gly Glu Val Phe Gly Gln Trp Arg Ala Cys Pro Asp Val Leu Met Asp  
130 135 140  
Pro Glu Gly Ser Ser Arg Gly Gly Leu His Ile Trp Lys His Gly Val  
145 150 155 160

SEQUENCE LISTING

Trp

(2) INFORMATION FOR SEQ ID NO:3279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..447
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3279:

aagacctcct	cgcggtatg	gcgaaGcgtc	tgatcccgtc	gctgaaccgg	gttctggtgg	60
agaagctgct	gaagcccagc	aagagcgccg	gcggcatcct	cctcccggag	accaccaagc	120
agctgaacgc	cgctaaagtc	gttgctgttg	gccctggtga	tcgtgatagg	gatggcaagc	180
tgatccctgt	atctctgagc	gaaggcgaca	ctgttctgct	tccggagtac	ggtgggacag	240
aagtgaagct	tcagaaaaa	gagtaccttc	ttttcagaga	gcacgacata	ctggggaagc	300
tcgaggagta	gctctggact	gttaaaatgg	agttgtttga	aagtaggtat	gcaagagttt	360
tgccacggct	tatctttttt	ttttgtacgg	gggaacaaat	gagaaacaca	acccttgtga	420
gaatgcaata	acactgcctc	attcttg				

(2) INFORMATION FOR SEQ ID NO:3280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..102
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3280:

Asp	Leu	Leu	Ala	Ala	Met	Ala	Lys	Arg	Leu	Ile	Pro	Ser	Leu	Asn	Arg	
1			5					10						15		
Val	Leu	Val	Glu	Lys	Leu	Leu	Lys	Pro	Ser	Lys	Ser	Ala	Gly	Gly	Ile	
			20					25					30			
Leu	Leu	Pro	Glu	Thr	Thr	Lys	Gln	Leu	Asn	Ala	Ala	Lys	Val	Val	Ala	
			35				40						45			
Val	Gly	Pro	Gly	Asp	Arg	Asp	Arg	Asp	Gly	Lys	Leu	Ile	Pro	Val	Ser	
	50				55						60					
Leu	Ser	Glu	Gly	Asp	Thr	Val	Leu	Leu	Pro	Glu	Tyr	Gly	Gly	Thr	Glu	
	65				70				75					80		
Val	Lys	Leu	Ala	Glu	Lys	Glu	Tyr	Leu	Leu	Phe	Arg	Glu	His	Asp	Ile	
			85					90						95		
Leu	Gly	Lys	Leu	Glu	Glu											
			100													

(2) INFORMATION FOR SEQ ID NO:3281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..97
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576331

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3281:

Met Ala Lys Arg Leu Ile Pro Ser Leu Asn Arg Val Leu Val Glu Lys

1 5 10 15  
Leu Leu Lys Pro Ser Lys Ser Ala Gly Gly Ile Leu Leu Pro Glu Thr  
20 25 30  
Thr Lys Gln Leu Asn Ala Ala Lys Val Val Ala Val Gly Pro Gly Asp  
35 40 45  
Arg Asp Arg Asp Gly Lys Leu Ile Pro Val Ser Leu Ser Glu Gly Asp  
50 55 60  
Thr Val Leu Leu Pro Glu Tyr Gly Gly Thr Glu Val Lys Leu Ala Glu  
65 70 75 80  
Lys Glu Tyr Leu Leu Phe Arg Glu His Asp Ile Leu Gly Lys Leu Glu  
85 90 95  
Glu

(2) INFORMATION FOR SEQ ID NO:3282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 798 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..798  
(D) OTHER INFORMATION: / Ceres Seq. ID 1576334

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3282:

gcaaaaccct aaccttgtct tgtgcgcast cogctattaa agtctgcgta cagtccgccc 60  
cggctaggcg accgcatccg catctccctt acgtcttctc gccggtcgcg cacgggcaaaa 120  
gcagcgatgg ctacagcgac ggcagttggt ggacccgaca ggtggagact gcggcgctcgt 180  
ccgcggcggc agtgctggcc gtcgccgttg cctcgsagag tgtrctaggt ctgctcgctc 240  
ttgcggttca aactgtaaat gttggagcag aaatatataa taaagatcag cgggcaatat 300  
acaagtattt atctGggaag aatcaaatct gaaaatgtcc ctgaaaataa ggatgggtca 360  
gacgacgacg atgatgacga cgacgatgaa gacaatgacg atgagggtgg tgacgacgat 420  
gatgatgctg aggaggaatt ctctggagaa gaagatgggg gtgatgacga tgatgaagat 480  
gatgatcctg aagctaattg tgaaggagga agtgacaacg acaatgatga cgacgaagat 540  
ggtgatgatg atggcgatga ggacgatgaa ggtgatgagg acgacgaaga cgaggacgat 600  
gatgaagatg acgaagacca gccaccttcc aagaagaaga aatgatttgc tcatccatgg 660  
atttacctca gcttctccat gctgttagtt gtgttggtta gatcatggac agctttggga 720  
tcaatgtagc ttgttgcttg tcatggtatc gtagtgtagg aaaatttgac atctgatgtt 780  
aaatcactat cctgcttt

(2) INFORMATION FOR SEQ ID NO:3283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..128  
(D) OTHER INFORMATION: / Ceres Seq. ID 1576335

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3283:

Met Leu Glu Gln Lys Tyr Ile Ile Lys Ile Ser Gly Gln Tyr Thr Ser  
1 5 10 15  
Tyr Tyr Leu Gly Arg Ile Lys Ser Glu Asn Val Pro Glu Asn Lys Asp  
20 25 30  
Gly Ser Asp Asp Asp Asp Asp Asp Asp Asp Asp Glu Asp Asn Asp Asp  
35 40 45  
Glu Gly Gly Asp Asp Asp Asp Asp Ala Glu Glu Glu Phe Ser Gly Glu  
50 55 60  
Glu Asp Gly Gly Asp Asp Asp Asp Glu Asp Asp Asp Pro Glu Ala Asn  
65 70 75 80



(2) INFORMATION FOR SEQ ID NO:3284:

(A) LENGTH: 117 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..117

(D) OTHER INFORMATION: / Ceres Seq. ID 1576336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3284:

[illegible]

(2) INFORMATION FOR SEQ ID NO:3285:

(A) LENGTH: 111 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..111

(D) OTHER INFORMATION: / Ceres Seq. ID 1576337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3285:

Met	Gly	Gln	Thr	Thr	Thr	Met	Met	Thr	Thr	Thr	Met	Lys	Thr	Met	Thr
1				5					10					15	
Met	Arg	Val	Val	Thr	Thr	Met	Met	Met	Leu	Arg	Arg	Asn	Ser	Leu	Glu
			20					25					30		
Lys	Lys	Met	Gly	Val	Met	Thr	Met	Met	Lys	Met	Met	Ile	Leu	Lys	Leu
		35					40					45			
Met	Val	Lys	Glu	Glu	Val	Thr	Thr	Thr	Met	Met	Thr	Thr	Lys	Met	Val
	50					55					60				
Met	Met	Met	Ala	Met	Arg	Thr	Met	Lys	Val	Met	Arg	Thr	Thr	Lys	Thr
65					70					75					80
Arg	Thr	Met	Met	Lys	Met	Thr	Lys	Thr	Ser	His	Leu	Pro	Arg	Arg	Arg
				85					90					95	
Asn	Asp	Leu	Leu	Ile	His	Gly	Phe	Thr	Ser	Ala	Ser	Pro	Cys	Cys	

100 105 110

(2) INFORMATION FOR SEQ ID NO:3286:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 646 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..646

(D) OTHER INFORMATION: / Ceres Seq. ID 1576347

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3286:

gacgggagaa aatctccaaa cgcagcaran mccctcgcgc cgccgacctc ttcagcctcg	60
cagcacaccg ccgccagccc gagtgaccgc tgcagcctag ggtttccgtc ggcatggcg	120
ggtaargrag ggaagggtct gctggcgcc aagacgacgg cggccaagag caccgacaag	180
gacaaggaca ggaagaargc ccccggtgctg cgctcctccc gcgccggcct ccagttcccg	240
gtgggtcgca tccaccgcca gctcaagtgc cgtgcctctg cgcacggccg cgtcggcgcc	300
accgcccgcg tctattccgc cgccatcctc gactaccta ccgccgaggt cctcgagctg	360
gGccggcaac gccagcaagg acctcaaggt caagcgcctc accccgcgcc acctgcagct	420
cgccatccgc ggggacgagg agctcgacac cctcatcaag ggaccatcg ccgggggcgg	480
cgatcatccc cacatccaca agtcgctcat caacaagacc gccaaggagt gaatcaaggc	540
cgtgctgctg cttctgcctg actacagtcc catctcgttc tgtacttggt caatctgagt	600
ttaagtgcac gttggcacag ttctagtaaa ctcctcctgt tcacct	

(2) INFORMATION FOR SEQ ID NO:3287:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 186 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..186

(D) OTHER INFORMATION: / Ceres Seq. ID 1576348

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3287:

Asp Gly Arg Lys Ser Pro Asn Ala Ala Xaa Xaa Leu Ala Pro Pro Thr	
1 5 10 15	
Ser Ser Ala Ser Gln His Thr Ala Ala Ser Pro Ser Asp Arg Cys Ser	
20 25 30	
Leu Gly Phe Pro Ser Ala Met Ala Gly Xaa Xaa Gly Lys Gly Leu Leu	
35 40 45	
Ala Ala Lys Thr Thr Ala Ala Lys Ser Thr Asp Lys Asp Lys Asp Arg	
50 55 60	
Lys Xaa Ala Pro Val Ser Arg Ser Ser Arg Ala Gly Leu Gln Phe Pro	
65 70 75 80	
Val Gly Arg Ile His Arg Gln Leu Lys Ser Arg Ala Ser Ala His Gly	
85 90 95	
Arg Val Gly Ala Thr Ala Ala Val Tyr Ser Ala Ala Ile Leu Glu Tyr	
100 105 110	
Leu Thr Ala Glu Val Leu Glu Leu Gly Arg Gln Arg Gln Gln Gly Pro	
115 120 125	
Gln Gly Gln Ala His His Pro Ala Pro Pro Ala Ala Arg His Pro Arg	
130 135 140	
Gly Arg Gly Ala Arg His Pro His Gln Gly His His Arg Arg Gly Arg	
145 150 155 160	
Arg His Pro Ala His Pro Gln Val Ala His Gln Gln Asp Arg Gln Gly	
165 170 175	
Val Asn Gln Gly Arg Ala Ala Ala Ser Ala	
180 185	

(2) INFORMATION FOR SEQ ID NO:3288:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 148 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..148  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1576349  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3288:

Met Ala Gly Xaa Xaa Gly Lys Gly Leu Leu Ala Ala Lys Thr Thr Ala  
1                  5                  10                  15  
Ala Lys Ser Thr Asp Lys Asp Lys Asp Arg Lys Xaa Ala Pro Val Ser  
                  20                  25                  30  
Arg Ser Ser Arg Ala Gly Leu Gln Phe Pro Val Gly Arg Ile His Arg  
                  35                  40                  45  
Gln Leu Lys Ser Arg Ala Ser Ala His Gly Arg Val Gly Ala Thr Ala  
                  50                  55                  60  
Ala Val Tyr Ser Ala Ala Ile Leu Glu Tyr Leu Thr Ala Glu Val Leu  
65                  70                  75                  80  
Glu Leu Gly Arg Gln Arg Gln Gln Gly Pro Gln Gly Gln Ala His His  
                  85                  90                  95  
Pro Ala Pro Pro Ala Ala Arg His Pro Arg Gly Arg Gly Ala Arg His  
                  100                  105                  110  
Pro His Gln Gly His His Arg Arg Gly Arg Arg His Pro Ala His Pro  
                  115                  120                  125  
Gln Val Ala His Gln Gln Asp Arg Gln Gly Val Asn Gln Gly Arg Ala  
130                  135                  140  
Ala Ala Ser Ala  
145

(2) INFORMATION FOR SEQ ID NO:3289:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 454 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..454  
(D) OTHER INFORMATION: / Ceres Seq. ID 1576358

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3289:

tatccaaatt caaatcag acaatgagt atgcagacaa gctagctgct ggcattgcag 60  
cacctgtggg tggagtgat acagagtgtg gtaccaatcc tcctgtcgaa catattctct 120  
cagctgagga tgcagagtgc tgtatctgcc tatgccgta tgaagatggc gtggaactac 180  
gtgagcttcc ttgcaaccac cattttcact gcagctgcat tgacaagtgg cttcacataa 240  
atgctacatg ccattgtgc aagttcgaca tcatcaagag caaccgtgac atagaagagg 300  
tctaggtcac taaggaaaaa acgccgcaaa acttttgtca tgtctctgct gtgttcttca 360  
gtactaccgc taccacattt gcgatcctga gttgtgatta ccggtccttt aggtgatgca 420  
caaatggtac tcgGtgaata ttcttttat tagc

(2) INFORMATION FOR SEQ ID NO:3290:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 100 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..100

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(D) OTHER INFORMATION: / Ceres Seq. ID 1576359

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3290:

Ser Lys Phe Lys Phe Gln Thr Met Ser Asp Ala Asp Lys Leu Ala Ala  
1 5 10 15  
Gly Ile Ala Ala Pro Val Gly Gly Val Met Thr Glu Cys Gly Thr Asn  
20 25 30  
Pro Pro Val Glu His Ile Leu Ser Ala Glu Asp Ala Glu Cys Cys Ile  
35 40 45  
Cys Leu Cys Pro Tyr Glu Asp Gly Val Glu Leu Arg Glu Leu Pro Cys  
50 55 60  
Asn His His Phe His Cys Ser Cys Ile Asp Lys Trp Leu His Ile Asn  
65 70 75 80  
Ala Thr Cys Pro Leu Cys Lys Phe Asp Ile Ile Lys Ser Asn Arg Asp  
85 90 95  
Ile Glu Glu Val  
100

(2) INFORMATION FOR SEQ ID NO:3291:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 93 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..93

(D) OTHER INFORMATION: / Ceres Seq. ID 1576360

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3291:

Met Ser Asp Ala Asp Lys Leu Ala Ala Gly Ile Ala Ala Pro Val Gly  
1 5 10 15  
Gly Val Met Thr Glu Cys Gly Thr Asn Pro Pro Val Glu His Ile Leu  
20 25 30  
Ser Ala Glu Asp Ala Glu Cys Cys Ile Cys Leu Cys Pro Tyr Glu Asp  
35 40 45  
Gly Val Glu Leu Arg Glu Leu Pro Cys Asn His His Phe His Cys Ser  
50 55 60  
Cys Ile Asp Lys Trp Leu His Ile Asn Ala Thr Cys Pro Leu Cys Lys  
65 70 75 80  
Phe Asp Ile Ile Lys Ser Asn Arg Asp Ile Glu Glu Val  
85 90

(2) INFORMATION FOR SEQ ID NO:3292:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..75

(D) OTHER INFORMATION: / Ceres Seq. ID 1576361

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3292:

Met Thr Glu Cys Gly Thr Asn Pro Pro Val Glu His Ile Leu Ser Ala  
1 5 10 15  
Glu Asp Ala Glu Cys Cys Ile Cys Leu Cys Pro Tyr Glu Asp Gly Val  
20 25 30  
Glu Leu Arg Glu Leu Pro Cys Asn His His Phe His Cys Ser Cys Ile  
35 40 45  
Asp Lys Trp Leu His Ile Asn Ala Thr Cys Pro Leu Cys Lys Phe Asp  
50 55 60  
Ile Ile Lys Ser Asn Arg Asp Ile Glu Glu Val

75

(X1) SEQUENCE DISCONTINUITY															
Thr	Thr	Ala	Asn	Thr	Xaa	Cys	Phe	Ala	Phe	Leu	Pro	Ile	Pro	Leu	Arg
1				5					10					15	
Asn	Pro	Asn	Pro	Asn	Xaa	Ala	Pro	His	Arg	Trp	Arg	Pro	Arg	Pro	Arg
			20					25					30		
Arg	Ser	Pro	Arg	Arg	Arg	Ser	Arg	Arg	Arg	Arg	Ser	Pro	Arg	Leu	Arg
		35					40					45			
Arg	Arg	Pro	Pro	Gly	Arg	Ser	Arg	Gly	Gly	Gly	Cys	Ser	Leu	Pro	Pro
	50					55					60				

Ser Asp Leu Ala Trp Gln Gln Glu Gly Ser Ser Glu  
65 70 75

(2) INFORMATION FOR SEQ ID NO:3296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..46
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576365

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3296:

Gln Gln Arg Thr Xaa Ser Ala Ser His Phe Phe Pro Ser Pro Phe Ala  
1 5 10 15  
Thr Gln Thr Pro Xaa Ser Leu Arg Ile Asp Gly Ala Gln Gly Arg Glu  
20 25 30  
Glu Ala Arg Gly Glu Glu Ala Gly Gly Gly Gly Ala Arg Gly  
35 40 45

(2) INFORMATION FOR SEQ ID NO:3297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 634 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..634
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3297:

acccaagtcc aagcaccttc ccaaaaaaat cccccatttt cttcgaggcg aggagagcgt	60
gaaagacagg gcaccggcag cgacgatgtc ggggcgcggc aagggcggca aaggtctggs	120
caaggcgga Gcaaagcggc accgtaaggT gctccgtgac aacatccagg gcatcaccaa	180
gcccgcgatc cgtaggctgg ctccggagggg cggcgtgaag cgcatttcgg ggcttatcta	240
cgaggagggt aagactgtgg acctctatgt ccccaggaag tgctcggcca caaacaggat	300
catcactgcc aaggaccatg cctctgtcca gatcaacatt ggccacttgg atgcgaatgg	360
cctgtatgat ggtcacttca caacgtttgc tctctctggg tttgtccgtg ctcagggtga	420
cgcagacagc tccttggaca ggctgtggca aaagaagaag gctgatatca agcagtagat	480
tttacatcta gtttaccaag aattggacac cgccttagct atgttttgaa ttcattgtcac	540
tatatgcAat gttgtgattt cagctgggtac cttaaactctg aagatttagt atctttgttg	600
ggttccttct gagtttgatg tgtggtgttc gttt	

(2) INFORMATION FOR SEQ ID NO:3298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..158
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576373

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3298:

Pro Lys Ser Lys His Leu Pro Lys Lys Ile Pro His Phe Leu Arg Gly  
1 5 10 15  
Glu Glu Ser Val Lys Asp Arg Ala Pro Ala Ala Thr Met Ser Gly Arg  
20 25 30  
Gly Lys Gly Gly Lys Gly Leu Xaa Lys Gly Gly Ala Lys Arg His Arg  
35 40 45

Lys Val Leu Arg Asp Asn Ile Gln Gly Ile Thr Lys Pro Ala Ile Arg  
50 55 60  
Arg Leu Ala Arg Arg Gly Gly Val Lys Arg Ile Ser Gly Leu Ile Tyr  
65 70 75 80  
Glu Glu Gly Lys Thr Val Asp Leu Tyr Val Pro Arg Lys Cys Ser Ala  
85 90 95  
Thr Asn Arg Ile Ile Thr Ala Lys Asp His Ala Ser Val Gln Ile Asn  
100 105 110  
Ile Gly His Leu Asp Ala Asn Gly Leu Tyr Asp Gly His Phe Thr Thr  
115 120 125  
Phe Ala Leu Ser Gly Phe Val Arg Ala Gln Gly Asp Ala Asp Ser Ser  
130 135 140  
Leu Asp Arg Leu Trp Gln Lys Lys Lys Ala Asp Ile Lys Gln  
145 150 155

(2) INFORMATION FOR SEQ ID NO:3299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..130
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576374

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3299:

Met Ser Gly Arg Gly Lys Gly Gly Lys Gly Leu Xaa Lys Gly Gly Ala  
1 5 10 15  
Lys Arg His Arg Lys Val Leu Arg Asp Asn Ile Gln Gly Ile Thr Lys  
20 25 30  
Pro Ala Ile Arg Arg Leu Ala Arg Arg Gly Gly Val Lys Arg Ile Ser  
35 40 45  
Gly Leu Ile Tyr Glu Glu Gly Lys Thr Val Asp Leu Tyr Val Pro Arg  
50 55 60  
Lys Cys Ser Ala Thr Asn Arg Ile Ile Thr Ala Lys Asp His Ala Ser  
65 70 75 80  
Val Gln Ile Asn Ile Gly His Leu Asp Ala Asn Gly Leu Tyr Asp Gly  
85 90 95  
His Phe Thr Thr Phe Ala Leu Ser Gly Phe Val Arg Ala Gln Gly Asp  
100 105 110  
Ala Asp Ser Ser Leu Asp Arg Leu Trp Gln Lys Lys Lys Ala Asp Ile  
115 120 125  
Lys Gln  
130

(2) INFORMATION FOR SEQ ID NO:3300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 847 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..847
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576379

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3300:

acaaaatgaa gatgaagatg aagaagttga tgaaagtga gaagctgcag atgattcacg	60
caagcctgca acatcaattg gctcagcata cagactgctt actccatcag taaaggtcca	120
gttggttgata tacttcatgc tgaaatacgc aatggagatt ttgctttcag agtctagtgt	180
tatcactaat cactatttca gttggaacac aagcgcagtg gncaattttt ctagcaatcc	240
ttgggttgac ggtgcttcct gttaatgctg ttgttggaac atacatcagc aatatgtttg	300

aggacaggca actgctcatg gtctctcaaa ttacgttgct agtaggcatt atcttcagct 360  
tcaaggttac gagtacatac tctgttgctc agtatgttgt ctcagcactt gtcacatttg 420  
tttctgcaga agttcttgaa ggtgtgaacc ttccctcct atcaagcgtg atgtcatctc 480  
gcctctcccg tggcacatac aacggtggcc tcctctcgac ggaggccVgg gaccctggcg 540  
aggggtggctg ctgactgcac catcactgcg gcggggtacc tgggcgtggg gaagcttctc 600  
aacgtcaccc tgctaccatc cctggtgata tgtgttgctg ccattgcctg caccttcctg 660  
acataatact cgcttttctg atggagcttc acaatgtatt tgtgtcatca tgattcgttc 720  
catattagcg caaatcaagg cagctgggag accgccattg ccattgcccg aaggggctat 780  
tgtattacta ttattatatg ttogtcgatt tgattgctat aaattgattg ataaaatgat 840  
tgtagcg

(2) INFORMATION FOR SEQ ID NO:3301:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 87 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..87

(D) OTHER INFORMATION: / Ceres Seq. ID 1576380

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3301:

Gln Asn Glu Asp Glu Asp Glu Glu Val Asp Glu Ser Glu Glu Ala Ala  
1 5 10 15  
Asp Asp Ser Arg Lys Pro Ala Thr Ser Ile Gly Ser Ala Tyr Arg Leu  
20 25 30  
Leu Thr Pro Ser Val Lys Val Gln Leu Leu Ile Tyr Phe Met Leu Lys  
35 40 45  
Tyr Ala Met Glu Ile Leu Leu Ser Glu Ser Ser Val Ile Thr Asn His  
50 55 60  
Tyr Phe Ser Trp Asn Thr Ser Ala Val Xaa Asn Phe Ser Ser Asn Pro  
65 70 75 80  
Trp Val Asp Gly Ala Ser Cys  
85

(2) INFORMATION FOR SEQ ID NO:3302:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 86 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..86

(D) OTHER INFORMATION: / Ceres Seq. ID 1576381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3302:

Met Phe Glu Asp Arg Gln Leu Leu Met Val Ser Gln Ile Thr Leu Leu  
1 5 10 15  
Val Gly Ile Ile Phe Ser Phe Lys Val Thr Ser Thr Tyr Ser Val Val  
20 25 30  
Gln Tyr Val Val Ser Ala Leu Val Thr Phe Val Ser Ala Glu Val Leu  
35 40 45  
Glu Gly Val Asn Leu Ser Leu Leu Ser Ser Val Met Ser Ser Arg Leu  
50 55 60  
Ser Arg Gly Thr Tyr Asn Gly Gly Leu Leu Ser Thr Glu Ala Xaa Asp  
65 70 75 80  
Pro Gly Glu Gly Gly Arg  
85

(2) INFORMATION FOR SEQ ID NO:3303:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 amino acids



(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..78  
(D) OTHER INFORMATION: / Ceres Seq. ID 1576382  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3303:  
Met Val Ser Gln Ile Thr Leu Leu Val Gly Ile Ile Phe Ser Phe Lys  
1 5 10 15  
Val Thr Ser Thr Tyr Ser Val Val Gln Tyr Val Val Ser Ala Leu Val  
20 25 30  
Thr Phe Val Ser Ala Glu Val Leu Glu Gly Val Asn Leu Ser Leu Leu  
35 40 45  
Ser Ser Val Met Ser Ser Arg Leu Ser Arg Gly Thr Tyr Asn Gly Gly  
50 55 60  
Leu Leu Ser Thr Glu Ala Xaa Asp Pro Gly Glu Gly Gly Arg  
65 70 75

(2) INFORMATION FOR SEQ ID NO:3304:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 688 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..688  
(D) OTHER INFORMATION: / Ceres Seq. ID 1576401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3304:

ccacccaccc ccacacccac gagcccgcg gcggtgtctc tgctgtctgc tctgcaccca 60  
ggaccttcgg ccacaggagc tcagccctat ccctcgacgg tgctcgcggc cggcgcgcg 120  
cggtcgcacc ctccccatc tccagctcca cgccgtctcc accgcctgga atccagggcc 180  
tccgacgcca cccacctcc accgcctgga atcgaggacc gtcggcgtcc ttcagatcag 240  
cggcgagcgc aacaaggagc aggaggagaa gacggacacc tggcaccgcg tggagcggag 300  
cagcgggaga ttctgcgca ggttccgact gcccgagaac gccaagacgg agcagatcag 360  
ggccgccatg gagaacggcg tgcttacagt cactgtgcc aaggaggacg ccaagaagcc 420  
CCtgaagtga agtccattca gatctccggc tagacctcgg tctgcggtcg tctgtacctgc 480  
gtggtttgag gaacggcagt tcgcctcggc cgttctgtga aataaaattg gggtacaaga 540  
attatggcgt ttgtcaatat gatcgtaatg tcgtaggatg gtggaatgtg gtcacaaact 600  
ttgcgtatgt tgggtctact ggtggtgtct actctgaatc tatgtatgga tgtcatgagt 660  
tccagttcct gtggtgttcg tatgatgc

(2) INFORMATION FOR SEQ ID NO:3305:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 150 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..150  
(D) OTHER INFORMATION: / Ceres Seq. ID 1576402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3305:

Pro Pro Thr Pro Thr Pro Thr Ser Pro Ala Ala Cys Ser Leu Leu Ser  
1 5 10 15  
Ala Leu His Pro Gly Pro Ser Ala Thr Gly Ala Gln Pro Tyr Pro Ser  
20 25 30  
Thr Val Leu Ala Ala Gly Ala Arg Arg Leu Asp Pro Ser Pro Ser Pro  
35 40 45

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Ala Pro Arg Arg Leu His Arg Leu Glu Ser Arg Ala Ser Asp Ala Thr  
50 55 60  
Pro Pro Pro Pro Pro Gly Ile Glu Asp Arg Arg Arg Pro Ser Asp Gln  
65 70 75 80  
Arg Arg Ala Gln Gln Gly Ala Gly Gly Glu Asp Gly His Leu Ala Pro  
85 90 95  
Arg Gly Ala Glu Gln Arg Glu Ile Pro Ala Gln Val Pro Thr Ala Arg  
100 105 110  
Glu Arg Gln Asp Gly Ala Asp Gln Gly Arg His Gly Glu Arg Arg Ala  
115 120 125  
Tyr Ser His Cys Ala Gln Gly Arg Gln Glu Ala Pro Glu Val Lys  
130 135 140  
Ser Ile Gln Ile Ser Gly  
145 150

(2) INFORMATION FOR SEQ ID NO:3306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..142
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3306:

His Pro Pro Pro His Pro Arg Ala Arg Arg Ala Leu Cys Cys Leu  
1 5 10 15  
Leu Cys Thr Gln Asp Leu Arg Pro Gln Glu Leu Ser Pro Ile Pro Arg  
20 25 30  
Arg Cys Ser Arg Pro Ala Arg Gly Gly Ser Thr Leu Pro His Leu Gln  
35 40 45  
Leu His Ala Val Ser Thr Ala Trp Asn Pro Gly Pro Pro Thr Pro Pro  
50 55 60  
His Leu His Arg Leu Glu Ser Arg Thr Val Gly Val Leu Gln Ile Ser  
65 70 75 80  
Gly Glu Arg Asn Lys Glu Gln Glu Glu Lys Thr Asp Thr Trp His Arg  
85 90 95  
Val Glu Arg Ser Ser Gly Arg Phe Leu Arg Arg Phe Arg Leu Pro Glu  
100 105 110  
Asn Ala Lys Thr Glu Gln Ile Arg Ala Ala Met Glu Asn Gly Val Leu  
115 120 125  
Thr Val Thr Val Pro Lys Glu Asp Ala Lys Lys Pro Leu Lys  
130 135 140

(2) INFORMATION FOR SEQ ID NO:3307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..140
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3307:

Thr His Pro His Thr His Glu Pro Gly Gly Val Leu Ser Ala Val Cys  
1 5 10 15  
Ser Ala Pro Arg Thr Phe Gly His Arg Ser Ser Ala Leu Ser Leu Asp  
20 25 30  
Gly Ala Arg Gly Arg Arg Ala Ala Ala Arg Pro Phe Pro Ile Ser Ser

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35	40	45
Ser Thr Pro Ser Pro Pro Pro Gly Ile Gln Gly Leu Arg Arg His Pro		
50	55	60
Thr Ser Thr Ala Trp Asn Arg Gly Pro Ser Ala Ser Phe Arg Ser Ala		
65	70	75
Ala Ser Ala Thr Arg Ser Arg Arg Arg Arg Arg Thr Pro Gly Thr Ala		
85	90	95
Trp Ser Gly Ala Ala Gly Asp Ser Cys Ala Gly Ser Asp Cys Pro Arg		
100	105	110
Thr Pro Arg Arg Ser Arg Ser Gly Pro Pro Trp Arg Thr Ala Cys Leu		
115	120	125
Gln Ser Leu Cys Pro Arg Arg Thr Pro Arg Ser Pro		
130	135	140

(2) INFORMATION FOR SEQ ID NO:3308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..425
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3308:

atccagttac agtccggagt ctggttagta ctccgcatgt tcgttctttt tacgccgacg	60
gaaatcaacc tgcgcogctg ctttctccgt tctcgccgtc gcctccgcct ccgctgccgc	120
cgcgccaggtc aggggtcatgt cgatcttcga gtacaacggg agcgccgtgg tggcgatggt	180
ggggaagaac tgCttcgcca tcgccagcga ccgccgcctc ggcgtgcagc tgcagacgat	240
cgccaccgac ttccgacggg tgttcaaggt ccacgacaag ctctacatcg ggctctcggg	300
gctcgccacc gacgccaga cgctgtatca gcgctggtg ttcaggcaca agttgtacca	360
gctgagggag gagagggaca tgaagccga agcctttgcc agccttgttt cagccctcct	420
ctatg	

(2) INFORMATION FOR SEQ ID NO:3309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..141
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3309:

Ile Gln Leu Gln Ser Gly Val Trp Leu Val Leu Arg Met Phe Val Leu	
1	5
Phe Thr Pro Thr Glu Ile Asn Leu Arg Arg Cys Leu Leu Arg Ser Arg	10
20	25
Arg Arg Leu Arg Leu Arg Cys Arg Arg Ala Gly Gln Gly His Val Asp	30
35	40
Leu Arg Val Gln Arg Glu Arg Arg Gly Gly Asp Gly Gly Glu Glu Leu	45
50	55
Leu Arg Asp Arg Gln Arg Pro Pro Pro Arg Arg Ala Ala Ala Asp Asp	60
65	70
Arg His Arg Leu Pro Thr Gly Val Gln Gly Pro Arg Gln Ala Leu His	75
85	90
Arg Ala Leu Gly Ala Arg His Arg Arg Pro Asp Ala Val Ser Ala Ala	95
100	105
Gly Val Gln Ala Gln Val Val Pro Ala Glu Gly Gly Glu Gly His Glu	110
115	120

Ala Arg Ser Leu Cys Gln Pro Cys Phe Ser Pro Pro Leu  
130 135 140

(2) INFORMATION FOR SEQ ID NO:3310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..120

(D) OTHER INFORMATION: / Ceres Seq. ID 1576407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3310:

Pro Val Thr Val Arg Ser Leu Val Ser Thr Pro His Val Arg Ser Phe  
1 5 10 15  
Tyr Ala Asp Gly Asn Gln Pro Ala Pro Leu Pro Ser Pro Phe Ser Pro  
20 25 30  
Ser Pro Pro Pro Leu Pro Pro Arg Arg Ser Gly Ser Cys Arg Ser  
35 40 45  
Ser Ser Thr Thr Gly Ala Pro Trp Trp Arg Trp Trp Gly Arg Thr Ala  
50 55 60  
Ser Arg Ser Pro Ala Thr Ala Ala Ser Ala Cys Ser Cys Arg Arg Ser  
65 70 75 80  
Pro Pro Thr Ser Asp Gly Cys Ser Arg Ser Thr Thr Ser Ser Thr Ser  
85 90 95  
Gly Ser Arg Gly Ser Pro Pro Thr Pro Arg Arg Cys Ile Ser Gly Trp  
100 105 110  
Cys Ser Gly Thr Ser Cys Thr Ser  
115 120

(2) INFORMATION FOR SEQ ID NO:3311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..129

(D) OTHER INFORMATION: / Ceres Seq. ID 1576408

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3311:

Met Phe Val Leu Phe Thr Pro Thr Glu Ile Asn Leu Arg Arg Cys Leu  
1 5 10 15  
Leu Arg Ser Arg Arg Arg Leu Arg Leu Arg Cys Arg Arg Ala Gly Gln  
20 25 30  
Gly His Val Asp Leu Arg Val Gln Arg Glu Arg Arg Gly Gly Asp Gly  
35 40 45  
Gly Glu Glu Leu Leu Arg Asp Arg Gln Arg Pro Pro Pro Arg Arg Ala  
50 55 60  
Ala Ala Asp Asp Arg His Arg Leu Pro Thr Gly Val Gln Gly Pro Arg  
65 70 75 80  
Gln Ala Leu His Arg Ala Leu Gly Ala Arg His Arg Arg Pro Asp Ala  
85 90 95  
Val Ser Ala Ala Gly Val Gln Ala Gln Val Val Pro Ala Glu Gly Gly  
100 105 110  
Glu Gly His Glu Ala Arg Ser Leu Cys Gln Pro Cys Phe Ser Pro Pro  
115 120 125  
Leu

(2) INFORMATION FOR SEQ ID NO:3312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 986 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..986
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576429

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3312:

aacgctgcct tcccgcggtt atcctttccc acgactcctc tccccgcggt gagaacatgc 60  
cccgcgtcct tgtccaggca ccattgccgc cggccgctgc ctcccttgca ccatcggcct 120  
ctacagatga agctcaaagg aagtgaactc aaattatcac tcaagaatct caagagcatt 180  
tggtgaagag tgtttctctg attttgtgaa tgtccagtat gcagtgaact tctagaagtt 240  
tttatttatg tatgcatgtt ttaaatactt tgatcaatgg atgcttataa agattctatg 300  
gaatttctgg aggagttatc tgtctttgat cttcatctgt ggaggccgtg gtggccggtt 360  
cggcggcggg ttccgcgcagc agggcccgcgc cgcagaggtc gtcgaggtgt cgacgttcgt 420  
gcacgcgtgc gaggggagac cggtgacgaa actcaccaac gagaaGgtgc cctacttcaa 480  
cgcgcccata tacctgcaga acaagactca ggtcggcaag gtcgacgaga tcttcggccc 540  
catcaacgaa tcctatttct ctgtgaagat gatggaagg atcattgcaa catcgtacaa 600  
ggaaggcgac aagttctata tcgaccccat gaaattgctg cctctttcgc gcttctctgcc 660  
gcaaccaag ggacaatctc aaggagcacc tagaggtggt ggccgtgtgg aaggggtggt 720  
ggccgaggcc gtggtggttc gttccggggt ggaagaggac caccaagggg tgggtggcca 780  
ggtccaaggg gtggaagccg tgggtggttt agagggcgag gaaggttcta ggtgtagttt 840  
gagtttgatg atgttttttt ttgttgaggc atcatagcta cccaattgga aacttccatg 900  
ttcttgtaac ctgatatgtt taaggtagca gaacactttg tttgtggaac ttggattctc 960  
aattgaaaca aagggtttgt acctgt

(2) INFORMATION FOR SEQ ID NO:3313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..209
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576430

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3313:

Met Tyr Ala Cys Phe Lys Tyr Phe Asp Gln Trp Met Leu Ile Lys Ile  
1 5 10 15  
Leu Trp Asn Phe Trp Arg Ser Tyr Leu Ser Leu Ile Phe Ile Cys Gly  
20 25 30  
Gly Arg Gly Gly Arg Phe Gly Gly Phe Arg Asp Glu Gly Pro Pro  
35 40 45  
Ala Glu Val Val Glu Val Ser Thr Phe Val His Ala Cys Glu Gly Asp  
50 55 60  
Ala Val Thr Lys Leu Thr Asn Glu Lys Val Pro Tyr Phe Asn Ala Pro  
65 70 75 80  
Ile Tyr Leu Gln Asn Lys Thr Gln Val Gly Lys Val Asp Glu Ile Phe  
85 90 95  
Gly Pro Ile Asn Glu Ser Tyr Phe Ser Val Lys Met Met Glu Gly Ile  
100 105 110  
Ile Ala Thr Ser Tyr Lys Glu Gly Asp Lys Phe Tyr Ile Asp Pro Met  
115 120 125  
Lys Leu Leu Pro Leu Ser Arg Phe Leu Pro Gln Pro Lys Gly Gln Ser  
130 135 140  
Gln Gly Ala Pro Arg Gly Gly Gly Arg Val Glu Gly Val Val Ala Glu  
145 150 155 160  
Ala Val Val Val Arg Ser Gly Val Glu Glu Asp His Gln Gly Val Val

	165		170		175										
Ala	Glu	Val	Gln	Gly	Val	Glu	Ala	Val	Val	Val	Leu	Glu	Gly	Glu	Glu
	180						185						190		
Gly	Ser	Arg	Cys	Ser	Leu	Ser	Leu	Met	Met	Phe	Phe	Phe	Val	Glu	Ala
	195						200						205		
Ser															

(2) INFORMATION FOR SEQ ID NO:3314:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 138 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..138

(D) OTHER INFORMATION: / Ceres Seq. ID 1576431

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3314:

Met	Asp	Ala	Tyr	Lys	Asp	Ser	Met	Glu	Phe	Leu	Glu	Glu	Leu	Ser	Val
1			5					10						15	
Phe	Asp	Leu	His	Leu	Trp	Arg	Pro	Trp	Trp	Pro	Val	Arg	Arg	Arg	Val
		20					25						30		
Pro	Arg	Arg	Gly	Pro	Ala	Arg	Arg	Gly	Arg	Arg	Gly	Val	Asp	Val	Arg
		35				40						45			
Ala	Arg	Val	Arg	Gly	Arg	Arg	Gly	Asp	Glu	Thr	His	Gln	Arg	Glu	Gly
		50				55					60				
Ala	Leu	Leu	Gln	Arg	Ala	His	Ile	Pro	Ala	Glu	Gln	Asp	Ser	Gly	Arg
65			70						75					80	
Gln	Gly	Arg	Arg	Asp	Leu	Arg	Pro	His	Gln	Arg	Ile	Leu	Phe	Leu	Cys
			85					90						95	
Glu	Asp	Asp	Gly	Arg	Asp	His	Cys	Asn	Ile	Val	Gln	Gly	Arg	Arg	Gln
		100					105						110		
Val	Leu	Tyr	Arg	Pro	His	Glu	Ile	Ala	Ala	Ser	Phe	Ala	Leu	Pro	Ala
		115				120						125			
Ala	Thr	Lys	Gly	Thr	Ile	Ser	Arg	Ser	Thr						
		130				135									

(2) INFORMATION FOR SEQ ID NO:3315:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 198 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..198

(D) OTHER INFORMATION: / Ceres Seq. ID 1576432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3315:

Met	Leu	Ile	Lys	Ile	Leu	Trp	Asn	Phe	Trp	Arg	Ser	Tyr	Leu	Ser	Leu
1			5					10						15	
Ile	Phe	Ile	Cys	Gly	Gly	Arg	Gly	Gly	Arg	Phe	Gly	Gly	Gly	Phe	Arg
		20					25						30		
Asp	Glu	Gly	Pro	Pro	Ala	Glu	Val	Glu	Val	Ser	Thr	Phe	Val	His	
		35				40					45				
Ala	Cys	Glu	Gly	Asp	Ala	Val	Thr	Lys	Leu	Thr	Asn	Glu	Lys	Val	Pro
		50				55				60					
Tyr	Phe	Asn	Ala	Pro	Ile	Tyr	Leu	Gln	Asn	Lys	Thr	Gln	Val	Gly	Lys
65			70						75					80	
Val	Asp	Glu	Ile	Phe	Gly	Pro	Ile	Asn	Glu	Ser	Tyr	Phe	Ser	Val	Lys
			85					90						95	

Met Met Glu Gly Ile Ile Ala Thr Ser Tyr Lys Glu Gly Asp Lys Phe  
100 105 110  
Tyr Ile Asp Pro Met Lys Leu Leu Pro Leu Ser Arg Phe Leu Pro Gln  
115 120 125  
Pro Lys Gly Gln Ser Gln Gly Ala Pro Arg Gly Gly Gly Arg Val Glu  
130 135 140  
Gly Val Val Ala Glu Ala Val Val Val Arg Ser Gly Val Glu Glu Asp  
145 150 155 160  
His Gln Gly Val Val Ala Glu Val Gln Gly Val Glu Ala Val Val Val  
165 170 175  
Leu Glu Gly Glu Gly Ser Arg Cys Ser Leu Ser Leu Met Met Phe  
180 185 190  
Phe Phe Val Glu Ala Ser  
195

(2) INFORMATION FOR SEQ ID NO:3316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 582 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..582
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576433

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3316:

atccaggcgt	acagccctcc	gcctcgtgaa	ggcaaagcac	gcgcaaagcc	accacagcgt	60
cgctcctctt	gtctccagtc	caagcaagcg	aagagcaccc	ctcgagatct	ctccctcccc	120
gcgccgccat	ggacgcagtt	gactcggtag	tcgacccgct	ccgggagttc	gccaaggaca	180
gcatccgcct	cgtaagcgc	tgccacaagc	cggaccgcaa	ggagttcacc	aaggtcgccg	240
cgcggactgc	gacgggttc	gtcgtcatgg	gattcgtcgg	cttctttgtc	aagctcatct	300
tcatccctat	caacaacatc	atcgtcggct	ccggctgata	cgttcacctc	aggctagtgg	360
ctgcaggagt	ggacaatggc	gtcactacct	tggaggcagc	accgttttca	gctctgattt	420
ccgcaaagca	attcctttag	gacttggtgt	gttaaagggc	aactccctta	tcttttcctc	480
tcttgaggtc	gtgtggtaga	tctggaactc	ttttgtacct	ggtgccgaat	agtcttttgg	540
ggatcagcgg	gtgacaaaat	tTaaatgggt	actgtcttgg	gg		

(2) INFORMATION FOR SEQ ID NO:3317:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..49
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576434

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3317:

Ile Gln Ala Tyr Ser Pro Pro Pro Arg Glu Gly Lys Ala Arg Ala Lys  
1 5 10 15  
Pro Pro Gln Arg Arg Pro Leu Arg Leu Gln Ser Lys Gln Ala Lys Ser  
20 25 30  
Thr Pro Arg Asp Leu Ser Leu Pro Ala Pro Pro Trp Thr Gln Leu Thr  
35 40 45  
Arg

(2) INFORMATION FOR SEQ ID NO:3318:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..46  
(D) OTHER INFORMATION: / Ceres Seq. ID 1576435

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3318:

```
Ser Arg Arg Thr Ala Leu Arg Leu Val Lys Ala Lys His Ala Gln Ser
1           5           10           15
His His Ser Val Val Leu Phe Val Ser Ser Pro Ser Lys Arg Arg Ala
20           25           30
Pro Leu Glu Ile Ser Pro Ser Pro Arg Arg His Gly Arg Ser
35           40           45
```

(2) INFORMATION FOR SEQ ID NO:3319:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 69 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..69  
(D) OTHER INFORMATION: / Ceres Seq. ID 1576436

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3319:

```
Met Asp Ala Val Asp Ser Val Val Asp Pro Leu Arg Glu Phe Ala Lys
1           5           10           15
Asp Ser Ile Arg Leu Val Lys Arg Cys His Lys Pro Asp Arg Lys Glu
20           25           30
Phe Thr Lys Val Ala Ala Arg Thr Ala Ile Gly Phe Val Val Met Gly
35           40           45
Phe Val Gly Phe Phe Val Lys Leu Ile Phe Ile Pro Ile Asn Asn Ile
50           55           60
Ile Val Gly Ser Gly
65
```

(2) INFORMATION FOR SEQ ID NO:3320:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 810 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..810  
(D) OTHER INFORMATION: / Ceres Seq. ID 1576437

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3320:

```
aacgacccaa gtcccaacgg aacttagctg ccgagcgccc aaagcccccac cgccgctccc      60
atcaagcggc gctaaagggt tcctcgcccc caacgcgatg ccgaagaaca agggaaaggg      120
aggcaagaac cggaagcggg gcaagaacga rgcggacgac gagaagcggg agctggntgt      180
tcaaggagga cgggcaggag tacgcgcagg tgacgcggat gctgggcaac ggccgctgcg      240
aggcgctctg catcgacggc accaagcgcc tctgccacat ccggggcaag atgcacaaga      300
aggtgtggat cgccgccggg gacatcgtgc tcgtcggcct gcgcgactac caGggacgac      360
aaggcggacg tcatcctcaa gtacatgaac gacgaggccc gcctgctcaa gGCctacggc      420
gagatccccg acaacgtcag gctcaacgag ggcgtcgttg atgaggagga agccggcgcg      480
caggatgact atatacagtt cgaggacgag gacatcgaca agatctgatg atgcctctt      540
ccacacggtc cctttccatg gtaaaactaaa cgtatgcaaa acaattgtat ccttctgttt      600
tgtggtggct accatgactg aagaatggta gtcgtgggtg tggtataatg atttgggcgg      660
agagtactgt gtataatgat ttgggggcac ttgttgtgcc caataacccc atatggtgat      720
atagcaagta tgggactgaa cgaaccgttc ctctcccttt ctgttaatat gatatatattg      780
gttgggcatg atccaatttt ttttttttct
```



(2) INFORMATION FOR SEQ ID NO:3321:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..128

(D) OTHER INFORMATION: / Ceres Seq. ID 1576438

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3321:

Thr Thr Gln Val Thr Glu Leu Ser Cys Arg Ala Pro Lys Ala Pro  
1 5 10 15  
Pro Pro Leu Pro Ser Ser Gly Ala Lys Gly Phe Leu Ala Arg Asn Ala  
20 25 30  
Met Pro Lys Asn Lys Gly Lys Gly Gly Lys Asn Arg Lys Arg Gly Lys  
35 40 45  
Asn Xaa Ala Asp Asp Glu Lys Arg Glu Leu Xaa Val Gln Gly Gly Arg  
50 55 60  
Ala Gly Val Arg Ala Gly Asp Ala Asp Ala Gly Gln Arg Pro Leu Arg  
65 70 75 80  
Gly Ala Leu His Arg Arg His Gln Ala Pro Leu Pro His Pro Gly Gln  
85 90 95  
Asp Ala Gln Glu Gly Val Asp Arg Arg Arg Gly His Arg Ala Arg Arg  
100 105 110  
Pro Ala Arg Leu Pro Gly Thr Thr Arg Arg Thr Ser Ser Ser Ser Thr  
115 120 125

(2) INFORMATION FOR SEQ ID NO:3322:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 152 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..152

(D) OTHER INFORMATION: / Ceres Seq. ID 1576439

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3322:

Arg Pro Lys Ser Gln Arg Asn Leu Ala Ala Glu Arg Pro Lys Pro His  
1 5 10 15  
Arg Arg Ser His Gln Ala Ala Leu Lys Val Ser Ser Pro Ala Thr Arg  
20 25 30  
Cys Arg Arg Thr Arg Glu Arg Glu Ala Arg Thr Gly Ser Gly Ala Arg  
35 40 45  
Thr Xaa Arg Thr Thr Arg Ser Gly Ser Trp Xaa Phe Lys Glu Asp Gly  
50 55 60  
Gln Glu Tyr Ala Gln Val Thr Arg Met Leu Gly Asn Gly Arg Cys Glu  
65 70 75 80  
Ala Leu Cys Ile Asp Gly Thr Lys Arg Leu Cys His Ile Arg Gly Lys  
85 90 95  
Met His Lys Lys Val Trp Ile Ala Ala Gly Asp Ile Val Leu Val Gly  
100 105 110  
Leu Arg Asp Tyr Gln Gly Arg Gln Gly Gly Arg His Pro Gln Val His  
115 120 125  
Glu Arg Arg Gly Pro Pro Ala Gln Gly Leu Arg Arg Asp Pro Arg Gln  
130 135 140  
Arg Gln Ala Gln Arg Gly Arg Arg

145 150

(2) INFORMATION FOR SEQ ID NO:3323:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..96

(D) OTHER INFORMATION: / Ceres Seq. ID 1576440

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3323:

Met	Pro	Lys	Asn	Lys	Gly	Lys	Gly	Gly	Lys	Asn	Arg	Lys	Arg	Gly	Lys
1			5						10					15	
Asn	Xaa	Ala	Asp	Asp	Glu	Lys	Arg	Glu	Leu	Xaa	Val	Gln	Gly	Gly	Arg
			20					25					30		
Ala	Gly	Val	Arg	Ala	Gly	Asp	Ala	Asp	Ala	Gly	Gln	Arg	Pro	Leu	Arg
		35				40					45				
Gly	Ala	Leu	His	Arg	Arg	His	Gln	Ala	Pro	Leu	Pro	His	Pro	Gly	Gln
	50					55				60					
Asp	Ala	Gln	Glu	Gly	Val	Asp	Arg	Arg	Arg	Gly	His	Arg	Ala	Arg	Arg
65					70				75					80	
Pro	Ala	Arg	Leu	Pro	Gly	Thr	Thr	Arg	Arg	Thr	Ser	Ser	Ser	Ser	Thr
			85					90						95	

(2) INFORMATION FOR SEQ ID NO:3324:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1030 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1030

(D) OTHER INFORMATION: / Ceres Seq. ID 1576441

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3324:

gtcggtaggt	gtccctccct	ttactccctc	cgccctccca	cagtcccact	gcccttctcc	60
tcgggtccatc	gcaagtcctt	gcgggtccctg	ctacggcgct	acggcgggcat	ccacccttct	120
gccgcatcgt	ctttctcaag	acgctgcccc	aggtccatcg	cgcctagggg	tcgccgagtc	180
cggcgggcgt	aagataatga	gtggggcaccg	aaacagtc	ggaaagcgct	actctgatta	240
tactgaaact	ggaggcggta	agagaagaaa	tcctgggtgat	gatacctatg	cccctgggtcc	300
tgatgacact	gtgtatcgct	acctctgcgc	ctctagaaaa	atTgggagta	tcattggcag	360
gggtggagaa	atTgcaaagc	agttgaggac	tgagacccaa	gctaAgatca	ggattgggtga	420
gagtgtccct	ggatgtgaag	agcgagttat	taccatat	agctcaagtc	gaagaactaa	480
taccatcgat	gatgctgaag	ataaggtttg	ccctgctcag	gatgccctct	ttagagttca	540
tgagaggcct	gccactgatg	agagtttttg	taacgaagac	agcgaagaaa	tttcacctca	600
agttactgtt	cgctgcttg	tgccatcaga	ccagattgga	tgcatctctg	gaaaagggtg	660
gcacatcatc	caaggaatcc	gcagtgcgac	tggtgcgcaa	atacgcgtgc	ttagtaagga	720
tcatatccct	gcatgtgcc	ttagtggcga	tgaacttctc	cagatatctg	gggacatggt	780
agttgtcaaa	aaggctcttt	gtcaagtgtc	atctcgccctc	cataacaacc	catccaagtc	840
acagcatctt	cttgcaccca	gcttgaccca	accgtatcca	gggggtaccc	accttgggtg	900
ttcctctgct	gcacctgttg	tagggatcac	tccagtaatt	cctccttatg	gaggctacaa	960
aggtgacgtg	gcaggagatt	ggccctcttt	ataccaaccc	cgacgggatg	agagctctgc	1020
aaaggagttt						

(2) INFORMATION FOR SEQ ID NO:3325:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 343 amino acids

(B) TYPE: amino acid

- (C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..343  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1576442  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3325:

Ser Val Gly Val Pro Pro Phe Thr Pro Ser Ala Leu Pro Gln Ser His  
1 5 10 15  
Cys Pro Ser Pro Arg Ser Ile Ala Ser Ser Cys Gly Pro Ala Tyr Gly  
20 25 30  
Arg Thr Ala Ala Ser Thr Leu Leu Pro His Arg Leu Ser Gln Asp Ala  
35 40 45  
Ala Pro Gly Pro Ser Arg Leu Gly Phe Ala Glu Ser Gly Gly Ala Lys  
50 55 60  
Ile Met Ser Gly His Arg Asn Ser His Gly Lys Arg Tyr Ser Asp Tyr  
65 70 75 80  
Thr Glu Thr Gly Gly Gly Lys Arg Arg Asn Pro Gly Asp Asp Thr Tyr  
85 90 95  
Ala Pro Gly Pro Asp Asp Thr Val Tyr Arg Tyr Leu Cys Ala Ser Arg  
100 105 110  
Lys Ile Gly Ser Ile Ile Gly Arg Gly Gly Glu Ile Ala Lys Gln Leu  
115 120 125  
Arg Thr Glu Thr Gln Ala Lys Ile Arg Ile Gly Glu Ser Val Pro Gly  
130 135 140  
Cys Glu Glu Arg Val Ile Thr Ile Phe Ser Ser Arg Arg Thr Asn  
145 150 155 160  
Thr Ile Asp Asp Ala Glu Asp Lys Val Cys Pro Ala Gln Asp Ala Leu  
165 170 175  
Phe Arg Val His Glu Arg Leu Ala Thr Asp Glu Ser Phe Gly Asn Glu  
180 185 190  
Asp Ser Glu Glu Ile Ser Pro Gln Val Thr Val Arg Leu Leu Val Pro  
195 200 205  
Ser Asp Gln Ile Gly Cys Ile Leu Gly Lys Gly Gly His Ile Ile Gln  
210 215 220  
Gly Ile Arg Ser Glu Thr Gly Ala Gln Ile Arg Val Leu Ser Lys Asp  
225 230 235 240  
His Ile Pro Ala Cys Ala Ile Ser Gly Asp Glu Leu Leu Gln Ile Ser  
245 250 255  
Gly Asp Met Val Val Val Lys Lys Ala Leu Cys Gln Val Ser Ser Arg  
260 265 270  
Leu His Asn Asn Pro Ser Lys Ser Gln His Leu Leu Ala Ser Ser Leu  
275 280 285  
Thr Gln Pro Tyr Pro Gly Gly Thr His Leu Gly Gly Ser Ser Ala Ala  
290 295 300  
Pro Val Val Gly Ile Thr Pro Val Ile Pro Pro Tyr Gly Gly Tyr Lys  
305 310 315 320  
Gly Asp Val Ala Gly Asp Trp Pro Ser Leu Tyr Gln Pro Arg Arg Asp  
325 330 335  
Glu Ser Ser Ala Lys Glu Phe  
340

- (2) INFORMATION FOR SEQ ID NO:3326:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 278 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide

U.S. PAT. & TRADEMARK OFFICE

(B) LOCATION: 1..278

(D) OTHER INFORMATION: / Ceres Seq. ID 1576443

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3326:

Met Ser Gly His Arg Asn Ser His Gly Lys Arg Tyr Ser Asp Tyr Thr  
1 5 10 15  
Glu Thr Gly Gly Gly Lys Arg Arg Asn Pro Gly Asp Asp Thr Tyr Ala  
20 25 30  
Pro Gly Pro Asp Asp Thr Val Tyr Arg Tyr Leu Cys Ala Ser Arg Lys  
35 40 45  
Ile Gly Ser Ile Ile Gly Arg Gly Gly Glu Ile Ala Lys Gln Leu Arg  
50 55 60  
Thr Glu Thr Gln Ala Lys Ile Arg Ile Gly Glu Ser Val Pro Gly Cys  
65 70 75 80  
Glu Glu Arg Val Ile Thr Ile Phe Ser Ser Ser Arg Arg Thr Asn Thr  
85 90 95  
Ile Asp Asp Ala Glu Asp Lys Val Cys Pro Ala Gln Asp Ala Leu Phe  
100 105 110  
Arg Val His Glu Arg Leu Ala Thr Asp Glu Ser Phe Gly Asn Glu Asp  
115 120 125  
Ser Glu Glu Ile Ser Pro Gln Val Thr Val Arg Leu Leu Val Pro Ser  
130 135 140  
Asp Gln Ile Gly Cys Ile Leu Gly Lys Gly Gly His Ile Ile Gln Gly  
145 150 155 160  
Ile Arg Ser Glu Thr Gly Ala Gln Ile Arg Val Leu Ser Lys Asp His  
165 170 175  
Ile Pro Ala Cys Ala Ile Ser Gly Asp Glu Leu Leu Gln Ile Ser Gly  
180 185 190  
Asp Met Val Val Val Lys Lys Ala Leu Cys Gln Val Ser Ser Arg Leu  
195 200 205  
His Asn Asn Pro Ser Lys Ser Gln His Leu Leu Ala Ser Ser Leu Thr  
210 215 220  
Gln Pro Tyr Pro Gly Gly Thr His Leu Gly Gly Ser Ser Ala Ala Pro  
225 230 235 240  
Val Val Gly Ile Thr Pro Val Ile Pro Pro Tyr Gly Gly Tyr Lys Gly  
245 250 255  
Asp Val Ala Gly Asp Trp Pro Ser Leu Tyr Gln Pro Arg Arg Asp Glu  
260 265 270  
Ser Ser Ala Lys Glu Phe  
275

(2) INFORMATION FOR SEQ ID NO:3327:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 713 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..713

(D) OTHER INFORMATION: / Ceres Seq. ID 1576444

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3327:

taggataatt	cttgggtgctg	ctgcaacaga	aatagagctg	gcaaagagat	tgaaggagtt	60
ctctttgaag	gaaacaggtt	tggaccagta	tgctgttgcg	aaatttgctg	aaastttgaa	120
atgggtccaa	gaaccctggc	agaaaatgcc	ggacttagcg	caatggatgt	aatatcctct	180
ctttatgctg	agcatgctag	tggcaatgtg	aaagttggca	ttgacctgga	ggaagggtgcc	240
tgaaggaca	tcacgacctt	gaaaatatgg	gacctttatg	tcacaaagtt	ctttgcccta	300
aaatattctg	ccgatgccgc	atgcaccgtg	ctgcgggttg	accagatcat	tatggcgaaG	360
csggcaggag	gtccaagaag	agatgcccg	cttgggtggcg	ggatggacga	ggactagttt	420
gactgtgatt	gttctctttg	tgtatcacgt	acgcaagggt	tcagagcagg	gaacatcatg	480
tcttatttag	ggtttggttc	tgtagaaggt	tttgggtgct	gtagttcacg	tttggaaaggg	540
ttgcacggct	gtgctggtat	cgtatgggga	atttgcttgt	tctttcctgg	tgtattattg	600

cagtgccgat gtattattca ttcgagggtt ctttccttca gttcatcaca ccgactgagc 660  
tcatatgagt sytacttcag tttttttatt atagaagcaa aaatgttaca gcc

(2) INFORMATION FOR SEQ ID NO:3328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..98
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576445

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3328:

Met	Val	Pro	Arg	Thr	Leu	Ala	Glu	Asn	Ala	Gly	Leu	Ser	Ala	Met	Asp
1				5					10					15	
Val	Ile	Ser	Ser	Leu	Tyr	Ala	Glu	His	Ala	Ser	Gly	Asn	Val	Lys	Val
			20					25					30		
Gly	Ile	Asp	Leu	Glu	Glu	Gly	Ala	Cys	Lys	Asp	Ile	Thr	Thr	Leu	Lys
		35					40					45			
Ile	Trp	Asp	Leu	Tyr	Val	Thr	Lys	Phe	Phe	Ala	Leu	Lys	Tyr	Ser	Ala
	50					55					60				
Asp	Ala	Ala	Cys	Thr	Val	Leu	Arg	Val	Asp	Gln	Ile	Ile	Met	Ala	Lys
65					70				75					80	
Xaa	Ala	Gly	Gly	Pro	Arg	Arg	Asp	Ala	Gln	Pro	Gly	Gly	Gly	Met	Asp
				85				90						95	

Glu Asp

(2) INFORMATION FOR SEQ ID NO:3329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..84
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576446

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3329:

Met	Asp	Val	Ile	Ser	Ser	Leu	Tyr	Ala	Glu	His	Ala	Ser	Gly	Asn	Val
1				5					10					15	
Lys	Val	Gly	Ile	Asp	Leu	Glu	Glu	Gly	Ala	Cys	Lys	Asp	Ile	Thr	Thr
			20					25					30		
Leu	Lys	Ile	Trp	Asp	Leu	Tyr	Val	Thr	Lys	Phe	Phe	Ala	Leu	Lys	Tyr
		35				40						45			
Ser	Ala	Asp	Ala	Ala	Cys	Thr	Val	Leu	Arg	Val	Asp	Gln	Ile	Ile	Met
	50					55					60				
Ala	Lys	Xaa	Ala	Gly	Gly	Pro	Arg	Arg	Asp	Ala	Gln	Pro	Gly	Gly	Gly
65					70				75					80	

Met Asp Glu Asp

(2) INFORMATION FOR SEQ ID NO:3330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..78

(D) OTHER INFORMATION: / Ceres Seq. ID 1576447

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3330:

```
Met Ser Tyr Leu Gly Phe Gly Ser Val Glu Gly Phe Gly Ala Cys Ser
1           5           10           15
Ser Arg Leu Glu Gly Leu His Gly Cys Ala Gly Ile Val Trp Gly Ile
          20          25          30
Cys Leu Phe Phe Pro Gly Val Leu Leu Gln Cys Arg Cys Ile Ile His
          35          40          45
Ser Arg Val Leu Ser Phe Ser Ser Ser His Arg Leu Ser Ser Tyr Glu
          50          55          60
Xaa Tyr Phe Ser Phe Phe Ile Ile Glu Ala Lys Met Leu Gln
65          70          75
```

(2) INFORMATION FOR SEQ ID NO:3331:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 927 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..927

(D) OTHER INFORMATION: / Ceres Seq. ID 1576470

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3331:

```
atttgcacatc gagttcctga ttgttgattt ccagtttctt ctgtgagttt tgtgggacrc 60
craggaagaa ctagaaggat gtcgtgctgc rgargcaact rcrggtvcvg cgccggctgc 120
aagtrcggca rcggctgcgg aggggtgcaag atgtaccgga acatggctga rcaggtgacc 180
accactaccc agactctcat catgggtgtw gcaccctcct rmccgcccgc ccgctcccgc 240
tcccagctcg tgttccgctt cttgcagccg tcgcccgcga gctccagaga acttccgtca 300
acatggggaa racacgtggt atggrarccg ggcgcaagct caagaccac cgcagaacca 360
gcggtgggct gacaaggcat acaagaagag ccatttgggS caatgagtgg aagaaaccct 420
tcgctgggtc atcccatgcc aagggcattg ycctggagaa gatttggtatt gaggccaagc 480
agcccaactc cgctatccgt aagtgtgtct gtgttcagct tgttaagaat ggcaagaaga 540
ttgctgcctt cgtgccaaat gacggttggt tgaactacat tgaggaaaat gatgaggtct 600
tgattgctgg atttggtcgt aaggggccacg ctgtgggaga tattcctggt gtccggttca 660
agtgctcaa ggtttccggt gtgtctctgc ttgccctttt caaggagaag aaagagaagc 720
caagtccta gattgctctt gctaccaaa tcagcaagcg tggagttgaa acgggagggc 780
gttagatgat taagaagaat ggttgcttgc tatgtttgca gtgcattcgt gcaattgtta 840
acctaagatt ttgttggtga aaacgatttc ttttcagact tgcttctggt gagtgcctac 900
attccatata aatgtacttc ctcttct
```

(2) INFORMATION FOR SEQ ID NO:3332:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..97

(D) OTHER INFORMATION: / Ceres Seq. ID 1576471

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3332:

```
Met Ser Cys Cys Xaa Xaa Asn Xaa Xaa Xaa Ala Gly Cys Lys Xaa
1           5           10           15
Gly Xaa Gly Cys Gly Gly Cys Lys Met Tyr Pro Asp Met Ala Xaa Gln
          20          25          30
Val Thr Thr Thr Thr Gln Thr Leu Ile Met Gly Xaa Ala Pro Ser Xaa
          35          40          45
Arg Arg Arg Arg Ser Arg Ser Gln Leu Val Phe Arg Phe Leu Gln Pro
          50          55          60
```

Ser Pro Arg Ser Ser Arg Glu Leu Pro Ser Thr Trp Gly Xaa His Val  
65 70 75 80  
Val Trp Xaa Pro Gly Ala Ser Ser Arg Pro Thr Ala Glu Pro Ala Val  
85 90 95  
Gly

(2) INFORMATION FOR SEQ ID NO:3333:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 142 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..142

(D) OTHER INFORMATION: / Ceres Seq. ID 1576472

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3333:

Met Gly Xaa Thr Arg Gly Met Xaa Xaa Gly Arg Lys Leu Lys Thr His  
1 5 10 15  
Arg Arg Thr Ser Gly Gly Leu Thr Arg His Thr Arg Arg Ala Ile Trp  
20 25 30  
Xaa Asn Glu Trp Lys Lys Pro Phe Ala Gly Ser Ser His Ala Lys Gly  
35 40 45  
Ile Xaa Leu Glu Lys Ile Gly Ile Glu Ala Lys Gln Pro Asn Ser Ala  
50 55 60  
Ile Arg Lys Cys Ala Arg Val Gln Leu Val Lys Asn Gly Lys Lys Ile  
65 70 75 80  
Ala Ala Phe Val Pro Asn Asp Gly Cys Leu Asn Tyr Ile Glu Glu Asn  
85 90 95  
Asp Glu Val Leu Ile Ala Gly Phe Gly Arg Lys Gly His Ala Val Gly  
100 105 110  
Asp Ile Pro Gly Val Arg Phe Lys Val Val Lys Val Ser Gly Val Ser  
115 120 125  
Leu Leu Ala Leu Phe Lys Glu Lys Lys Glu Lys Pro Arg Ser  
130 135 140

(2) INFORMATION FOR SEQ ID NO:3334:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 136 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..136

(D) OTHER INFORMATION: / Ceres Seq. ID 1576473

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3334:

Met Xaa Xaa Gly Arg Lys Leu Lys Thr His Arg Arg Thr Ser Gly Gly  
1 5 10 15  
Leu Thr Arg His Thr Arg Arg Ala Ile Trp Xaa Asn Glu Trp Lys Lys  
20 25 30  
Pro Phe Ala Gly Ser Ser His Ala Lys Gly Ile Xaa Leu Glu Lys Ile  
35 40 45  
Gly Ile Glu Ala Lys Gln Pro Asn Ser Ala Ile Arg Lys Cys Ala Arg  
50 55 60  
Val Gln Leu Val Lys Asn Gly Lys Lys Ile Ala Ala Phe Val Pro Asn  
65 70 75 80  
Asp Gly Cys Leu Asn Tyr Ile Glu Glu Asn Asp Glu Val Leu Ile Ala  
85 90 95  
Gly Phe Gly Arg Lys Gly His Ala Val Gly Asp Ile Pro Gly Val Arg

100 105 110  
Phe Lys Val Val Lys Val Ser Gly Val Ser Leu Leu Ala Leu Phe Lys  
115 120 125  
Glu Lys Lys Glu Lys Pro Arg Ser  
130 135

(2) INFORMATION FOR SEQ ID NO:3335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 440 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..440
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576485

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3335:

aaaccctagc cgccgccaga ccattcgctt ctcgcgagcc atcgcttctg taattctcag	60
gcattccggaa gaaatggcca agtcgaagaa ccacacggcg cacaaccagt cgttcaaggc	120
gcacaagaac ggcattaaga aacccaagcg ccaccgccag acctccacca aggggatgga	180
ccccaaagttc ctgaggaacc tgaggtattc taggaaggcg aacaaaaaga gtggtgaggc	240
tgaagctgag gactaggaag gaaagcatgg ctttgtttcc tctgttttta gctcagttcc	300
accttttagga cctgggggtt tgctaaagat ggGaacttaa gtggtgttac tgtatgatgg	360
caaggacctt ttgctgccga agGttatggt ttgaagttca tgctacctt taaagtacgg	420
attaccttgt gcctatgttc	

(2) INFORMATION FOR SEQ ID NO:3336:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..84
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576486

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3336:

Asn Pro Ser Arg Gln Thr Ile Arg Phe Ser Arg Ala Ile Ala Ser	
1 5 10 15	
Val Ile Leu Arg His Pro Glu Glu Met Ala Lys Ser Lys Asn His Thr	
20 25 30	
Ala His Asn Gln Ser Phe Lys Ala His Lys Asn Gly Ile Lys Lys Pro	
35 40 45	
Lys Arg His Arg Gln Thr Ser Thr Lys Gly Met Asp Pro Lys Phe Leu	
50 55 60	
Arg Asn Leu Arg Tyr Ser Arg Lys Gly Asn Lys Lys Ser Gly Glu Ala	
65 70 75 80	
Glu Ala Glu Glu	

(2) INFORMATION FOR SEQ ID NO:3337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..60
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576487

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3337:



Met Ala Lys Ser Lys Asn His Thr Ala His Asn Gln Ser Phe Lys Ala  
1 5 10 15  
His Lys Asn Gly Ile Lys Lys Pro Lys Arg His Arg Gln Thr Ser Thr  
20 25 30  
Lys Gly Met Asp Pro Lys Phe Leu Arg Asn Leu Arg Tyr Ser Arg Lys  
35 40 45  
Gly Asn Lys Lys Ser Gly Glu Ala Glu Ala Glu Glu  
50 55 60

(2) INFORMATION FOR SEQ ID NO:3338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 577 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..577
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3338:

gagccgaact caacccaact tctctccctc tccctcgctt gcctgccgtt ccgcgtttga	60
ccaactcccc cgcaccgtaa ccctagcagc agatcgccca tggagagctg ggcgacctgg	120
gtggggacaa gcgtcacctc cgccttcttc gcctccctcg agcgtctgtc ctgcatcaac	180
ctctccaccg acgacgacga cgacgacgag gaccacgacg aggccaagga ccggcccctc	240
atcctcgccg ccgccccacg ccacgactcc gccgccaagc ccgatccaga ctccgcgcgc	300
gaggaccagg acgaccagaa gcaagagcag ccgccMgctg ccgccgtatg aatcaaacc	360
gattccttgc ttgtactagc tgctactgct gttatgtcgc caaataaagt cgtgtgtgcg	420
tgtgcagtca gtactactgc tctgctgcta ctatcctagt cctagtatat tagtatatta	480
tacagtccctc tctgtgaaat ttgaatcgac tcgaaaatca aacccccacca atatgagctt	540
gttaatatatt gtctcccgga atcaaccagc gcttggt	

(2) INFORMATION FOR SEQ ID NO:3339:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..125
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576492

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3339:

Ser Arg Thr Gln Pro Asn Phe Ser Pro Ser Pro Ser Pro Ala Cys Arg	
1 5 10 15	
Ser Ala Phe Asp Gln Leu Pro Arg Thr Val Thr Leu Ala Ala Asp Arg	
20 25 30	
Pro Trp Arg Ala Gly Arg Pro Gly Trp Gly Gln Ala Ser Pro Pro Pro	
35 40 45	
Ser Ser Pro Pro Ser Ser Ala Ala Pro Ala Ser Thr Ser Pro Pro Thr	
50 55 60	
Thr Thr Thr Thr Thr Arg Thr Thr Thr Arg Pro Arg Thr Gly Pro Ser	
65 70 75 80	
Ser Ser Pro Pro Pro His Ala Thr Thr Pro Pro Pro Ser Pro Ile Gln	
85 90 95	
Thr Pro Pro Pro Arg Thr Arg Thr Thr Arg Ser Lys Ser Ser Arg Xaa	
100 105 110	
Leu Pro Pro Tyr Glu Ser Asn Pro Ile Pro Cys Leu Tyr	
115 120 125	

(2) INFORMATION FOR SEQ ID NO:3340:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids

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- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..83
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1576493

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3340:

Met Glu Ser Trp Ala Thr Trp Val Gly Thr Ser Val Thr Ser Ala Phe  
1 5 10 15  
Phe Ala Ser Leu Glu Arg Cys Ser Cys Ile Asn Leu Ser Thr Asp Asp  
20 25 30  
Asp Asp Asp Asp Glu Asp His Asp Glu Ala Lys Asp Arg Pro Leu Ile  
35 40 45  
Leu Ala Ala Ala Pro Arg His Asp Ser Ala Ala Lys Pro Asp Pro Asp  
50 55 60  
Ser Ala Ala Glu Asp Gln Asp Asp Gln Lys Gln Glu Gln Pro Xaa Ala  
65 70 75 80  
Ala Ala Val

(2) INFORMATION FOR SEQ ID NO:3341:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 618 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..618
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1576494

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3341:

agccgactga atcttccacc tcgtcttcgcg cctccggctc cgcgccgggc ccgcataatc 60  
tgtgctcggg atcgctctt cccgcggcaa atgggggccc actccgagga cgccgtcaag 120  
cagctcagcc tcctcatgga gcaagtdgag gccccgctga agagatcgtt tcagaatatg 180  
caccagggct atcctaaaga aacactgggt cgtttcctta aggctagaga gtggaatgta 240  
gcaaaggctc ataaaatgat tgtagaatgt ttgaattgga ggattcaaaa tgaaattgat 300  
agtgtgctag agaggcctat agtcccagta gatttataca ggtcaatacg tgattcacaa 360  
cttattggcc tgtcaggata cacaaaggag ggtctcccaa tttttggcat tgggtgttggg 420  
catagcacat atgacaaagc ttcgggtccac tactatgtgc aatctcatat ccagattaac 480  
gagtaccgtg atcgataat tttgcctagg ctgacacaac agtttgggcg gcctgttacc 540  
agctgtataa aagtgtctgga tatgactggt ttgaagctat cagcactaag ccaaataaag 600  
atgttgactT ccatatcg

(2) INFORMATION FOR SEQ ID NO:3342:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 206 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..206
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1576495

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3342:

Ser Arg Leu Asn Leu Pro Pro Arg Phe Ala Pro Pro Ala Pro Arg Arg  
1 5 10 15  
Ala Arg Ile Ile Cys Ala Arg Asp Arg Leu Phe Pro Arg Gln Met Gly  
20 25 30  
Ala Asp Ser Glu Asp Ala Val Lys Gln Leu Ser Leu Leu Met Glu Gln

35 40 45  
Xaa Glu Ala Pro Leu Lys Arg Ser Phe Gln Asn Met His Gln Gly Tyr  
50 55 60  
Pro Lys Glu Thr Leu Val Arg Phe Leu Lys Ala Arg Glu Trp Asn Val  
65 70 75 80  
Ala Lys Ala His Lys Met Ile Val Glu Cys Leu Asn Trp Arg Ile Gln  
85 90 95  
Asn Glu Ile Asp Ser Val Leu Glu Arg Pro Ile Val Pro Val Asp Leu  
100 105 110  
Tyr Arg Ser Ile Arg Asp Ser Gln Leu Ile Gly Leu Ser Gly Tyr Thr  
115 120 125  
Lys Glu Gly Leu Pro Ile Phe Gly Ile Gly Val Gly His Ser Thr Tyr  
130 135 140  
Asp Lys Ala Ser Val His Tyr Tyr Val Gln Ser His Ile Gln Ile Asn  
145 150 155 160  
Glu Tyr Arg Asp Arg Ile Ile Leu Pro Arg Leu Thr Gln Gln Phe Gly  
165 170 175  
Arg Pro Val Thr Ser Cys Ile Lys Val Leu Asp Met Thr Gly Leu Lys  
180 185 190  
Leu Ser Ala Leu Ser Gln Ile Lys Met Leu Thr Ser Ile Ser  
195 200 205

(2) INFORMATION FOR SEQ ID NO:3343:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 176 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..176

(D) OTHER INFORMATION: / Ceres Seq. ID 1576496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3343:

Met Gly Ala Asp Ser Glu Asp Ala Val Lys Gln Leu Ser Leu Leu Met  
1 5 10 15  
Glu Gln Xaa Glu Ala Pro Leu Lys Arg Ser Phe Gln Asn Met His Gln  
20 25 30  
Gly Tyr Pro Lys Glu Thr Leu Val Arg Phe Leu Lys Ala Arg Glu Trp  
35 40 45  
Asn Val Ala Lys Ala His Lys Met Ile Val Glu Cys Leu Asn Trp Arg  
50 55 60  
Ile Gln Asn Glu Ile Asp Ser Val Leu Glu Arg Pro Ile Val Pro Val  
65 70 75 80  
Asp Leu Tyr Arg Ser Ile Arg Asp Ser Gln Leu Ile Gly Leu Ser Gly  
85 90 95  
Tyr Thr Lys Glu Gly Leu Pro Ile Phe Gly Ile Gly Val Gly His Ser  
100 105 110  
Thr Tyr Asp Lys Ala Ser Val His Tyr Tyr Val Gln Ser His Ile Gln  
115 120 125  
Ile Asn Glu Tyr Arg Asp Arg Ile Ile Leu Pro Arg Leu Thr Gln Gln  
130 135 140  
Phe Gly Arg Pro Val Thr Ser Cys Ile Lys Val Leu Asp Met Thr Gly  
145 150 155 160  
Leu Lys Leu Ser Ala Leu Ser Gln Ile Lys Met Leu Thr Ser Ile Ser  
165 170 175

(2) INFORMATION FOR SEQ ID NO:3344:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 161 amino acids

(B) TYPE: amino acid

- (C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..161  
(D) OTHER INFORMATION: / Ceres Seq. ID 1576497  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3344:

Met Glu Gln Xaa Glu Ala Pro Leu Lys Arg Ser Phe Gln Asn Met His  
1 5 10 15  
Gln Gly Tyr Pro Lys Glu Thr Leu Val Arg Phe Leu Lys Ala Arg Glu  
20 25 30  
Trp Asn Val Ala Lys Ala His Lys Met Ile Val Glu Cys Leu Asn Trp  
35 40 45  
Arg Ile Gln Asn Glu Ile Asp Ser Val Leu Glu Arg Pro Ile Val Pro  
50 55 60  
Val Asp Leu Tyr Arg Ser Ile Arg Asp Ser Gln Leu Ile Gly Leu Ser  
65 70 75 80  
Gly Tyr Thr Lys Glu Gly Leu Pro Ile Phe Gly Ile Gly Val Gly His  
85 90 95  
Ser Thr Tyr Asp Lys Ala Ser Val His Tyr Tyr Val Gln Ser His Ile  
100 105 110  
Gln Ile Asn Glu Tyr Arg Asp Arg Ile Ile Leu Pro Arg Leu Thr Gln  
115 120 125  
Gln Phe Gly Arg Pro Val Thr Ser Cys Ile Lys Val Leu Asp Met Thr  
130 135 140  
Gly Leu Lys Leu Ser Ala Leu Ser Gln Ile Lys Met Leu Thr Ser Ile  
145 150 155 160  
Ser

- (2) INFORMATION FOR SEQ ID NO:3345:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 768 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..768  
(D) OTHER INFORMATION: / Ceres Seq. ID 1576508  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3345:

ttccttcggt attgccacag ccacacccgg cgcctcttcc tcttccctcg gacagggaga 60  
gaccctttcc atccaagcta gccaaaccct agccacccgc ggttccaatc tgccaacgtc 120  
tcgtccgctg gttggtggct cggcgccatg gcctcgtccg cctacgccgc ttgggacgcc 180  
gcggaggagg cggacatcga cgcctccgca tcgcaggagg agctcatcgg ccgcgcccgc 240  
ttcatctccc gtgacaatga ggaggagggg gagggggagg gggaggagga ggaggaggtc 300  
gagtggttca gcacgccgcc tctcacgcat caggaccgcg agagtcaggg ggaagaagtc 360  
atcgatcatgt gctccatccc cttcacccag cctgacccca cccctcccm cgCtcccgt 420  
ccctccctc cctcggacag taagagtcgc cgtccggagc ggggtcaaatt gaagccgcgg 480  
aagaaggtct gcaagaggaa gaggggtctgc aagaggaagg tgagaagagc caacaagatc 540  
aggtctccga ctccgagccg cagccccgaa ctggaccytc tcgccagggc cgtgctcatg 600  
atcccaaccg ctctttctac aatcacccgt ggtgaggata tctctgaggt tgctcgcagc 660  
cgcgcatct tctagatcta ctagttgcct gtgtattttg tgcattgtag cgtagtcctt 720  
tgtgtttctg ccgatcaatc catatgctat ggcctggctg gattttgt

- (2) INFORMATION FOR SEQ ID NO:3346:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 156 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(2) INFORMATION FOR SEQ ID NO:3348:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 102 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..102  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1576511  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3348:  
Met Cys Ser Ile Pro Phe Thr Gln Pro Asp Pro Thr Pro Pro Xaa Ala  
1                    5                    10                    15  
Pro Ala Pro Ser Pro Pro Ser Asp Ser Lys Ser Arg Arg Pro Glu Arg  
                    20                    25                    30  
Val Lys Leu Lys Pro Arg Lys Lys Val Cys Lys Arg Lys Arg Val Cys  
                    35                    40                    45  
Lys Arg Lys Val Arg Arg Ala Asn Lys Ile Arg Ser Pro Thr Pro Ser  
50                    55                    60  
Arg Ser Pro Glu Leu Asp Xaa Leu Ala Arg Ala Val Leu Met Ile Pro  
65                    70                    75                    80  
Thr Ala Pro Ser Thr Ile Thr Gly Gly Glu Asp Ile Leu Glu Val Ala  
                    85                    90                    95  
Arg Ser Arg Gly Ile Phe  
                    100

(2) INFORMATION FOR SEQ ID NO:3349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 663 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..663
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576523

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3349:

```
aggtgtgtct agtctctagt ctagctaggc actactctag ctccaagtg gccaaagtata      60
ctcgccagag tacgtagagt gtaGbtgagc gtcgtcgaag gatggcgtGg acytcccgcc      120
gcatgggtcgc gtcgcgcgtc gtcttctctgc tgatgctgct cgccgcctca gagatgggga      180
cgacgaggkt ggcggaggcg aggcactgca cgtcgcagag ccaccggttc gtcggcgcct      240
gcatgagcaa gagcaactgc gagaacgtct gcaggacgga gggcttccc tggggcgagt      300
gcaggtggca cgcatagag cgcaagtgcc actgcaagcg gatctgctag taattaacta      360
gccggctggc cagcgcgatgc atgcacgacg accgacctac ctgctgctgg tccgtttgcg      420
tttgtttctt gtcctttggg ccttgctgtg gcgcgcagtc ttgcgtacgt gcgtgtgcgt      480
gtgtcttttc agttactctc aattagtcac agcagacgtg cgtgggtgcg agcgtgtgtc      540
tcgttgcatc gatgaaccgg cttcacgtgc tgtggtttta cagtttctga tgtgttttag      600
ctaactctga ataataaata ataaggcccc gtcttcacgc agttgcgtac tgggtgctta      660
cgt
```

(2) INFORMATION FOR SEQ ID NO:3350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..82
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576524

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3350:

Met Ala Trp Xaa Ser Arg Arg Met Val Ala Ser Ala Leu Val Phe Leu  
1 5 10 15  
Leu Met Leu Leu Ala Ala Ser Glu Met Gly Thr Thr Arg Xaa Ala Glu  
20 25 30  
Ala Arg His Cys Thr Ser Gln Ser His Arg Phe Val Gly Ala Cys Met  
35 40 45  
Ser Lys Ser Asn Cys Glu Asn Val Cys Arg Thr Glu Gly Phe Pro Trp  
50 55 60  
Gly Glu Cys Arg Trp His Gly Ile Glu Arg Lys Cys His Cys Lys Arg  
65 70 75 80  
Ile Cys

(2) INFORMATION FOR SEQ ID NO:3351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..75
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576525

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3351:

Met Val Ala Ser Ala Leu Val Phe Leu Leu Met Leu Leu Ala Ala Ser  
1 5 10 15  
Glu Met Gly Thr Thr Arg Xaa Ala Glu Ala Arg His Cys Thr Ser Gln  
20 25 30  
Ser His Arg Phe Val Gly Ala Cys Met Ser Lys Ser Asn Cys Glu Asn  
35 40 45  
Val Cys Arg Thr Glu Gly Phe Pro Trp Gly Glu Cys Arg Trp His Gly  
50 55 60  
Ile Glu Arg Lys Cys His Cys Lys Arg Ile Cys  
65 70 75

(2) INFORMATION FOR SEQ ID NO:3352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..75
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576526

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3352:

Met His Ala Arg Arg Pro Thr Tyr Leu Leu Val Arg Leu Arg Leu  
1 5 10 15  
Phe Leu Val Leu Trp Ala Leu Leu Trp Arg Ala Val Leu Arg Thr Cys  
20 25 30  
Val Cys Val Cys Leu Phe Ser Tyr Ser Gln Leu Val Ile Ala Asp Val  
35 40 45  
Arg Gly Cys Glu Arg Val Ser Arg Cys Ile Asp Glu Pro Ala Ser Arg  
50 55 60  
Ala Val Val Leu Gln Phe Leu Met Cys Phe Ser  
65 70 75

(2) INFORMATION FOR SEQ ID NO:3353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 906 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3353:

(2) INFORMATION FOR SEQ ID NO:3354:

(A) LENGTH: 203 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..203

(D) OTHER INFORMATION: / Ceres Seq. ID 1576536

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3354:

Met	Lys	Phe	Asn	Ile	Ala	Asn	Pro	Ser	Thr	Gly	Cys	Gln	Lys	Lys	Leu
1				5					10					15	
Glu	Ile	Asp	Asp	Asp	Gln	Lys	Leu	Arg	Ala	Phe	Tyr	Asp	Arg	Arg	Ser
			20					25					30		
Pro	Arg	Arg	Ser	Val	Val	Met	Leu	Trp	Val	Arg	Ser	Leu	Arg	Val	Met
			35				40					45			
Ser	Ser	Arg	Ser	Trp	Val	Asp	Val	Ser	Gln	Asp	Leu	Ser	Val	Ile	Asn
	50					55					60				
Leu	Val	Ile	Val	Lys	Lys	Gly	Glu	Asn	Asp	Leu	Pro	Gly	Leu	Thr	Asp
65				70						75				80	
Thr	Glu	Lys	Pro	Arg	Met	Arg	Gly	Pro	Lys	Arg	Ala	Ser	Lys	Ile	Arg
				85					90					95	
Lys	Leu	Phe	Asn	Leu	Ala	Lys	Asp	Asp	Asp	Val	Arg	Lys	Tyr	Val	Asn
			100					105					110		
Thr	Tyr	Arg	Arg	Thr	Phe	Thr	Thr	Lys	Asn	Gly	Lys	Lys	Val	Ser	Lys
		115					120					125			
Ala	Pro	Lys	Ile	Gln	Arg	Leu	Val	Thr	Pro	Leu	Thr	Leu	Gln	Arg	Lys
		130				135					140				
Arg	Ala	Arg	Ile	Ala	Asp	Lys	Lys	Lys	Arg	Ile	Ala	Lys	Lys	Lys	Ser
145				150						155				160	
Glu	Ala	Ala	Glu	Tyr	Gln	Lys	Leu	Leu	Ala	Gln	Arg	Leu	Lys	Glu	Gln
			165						170					175	
Arg	Asp	Arg	Arg	Ser	Glu	Ser	Leu	Ala	Lys	Arg	Arg	Ser	Lys	Leu	Ser
			180				185						190		
Ala	Ala	Ala	Lys	Ala	Ser	Ala	Ala	Thr	Ser	Ala					
		195					200								



(2) INFORMATION FOR SEQ ID NO:3355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..165

(D) OTHER INFORMATION: / Ceres Seq. ID 1576537

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3355:

Met Leu Trp Val Arg Ser Leu Arg Val Met Ser Ser Arg Ser Trp Val  
1 5 10 15  
Asp Val Ser Gln Asp Leu Ser Val Ile Asn Leu Val Ile Val Lys Lys  
20 25 30  
Gly Glu Asn Asp Leu Pro Gly Leu Thr Asp Thr Glu Lys Pro Arg Met  
35 40 45  
Arg Gly Pro Lys Arg Ala Ser Lys Ile Arg Lys Leu Phe Asn Leu Ala  
50 55 60  
Lys Asp Asp Asp Val Arg Lys Tyr Val Asn Thr Tyr Arg Arg Thr Phe  
65 70 75 80  
Thr Thr Lys Asn Gly Lys Lys Val Ser Lys Ala Pro Lys Ile Gln Arg  
85 90 95  
Leu Val Thr Pro Leu Thr Leu Gln Arg Lys Arg Ala Arg Ile Ala Asp  
100 105 110  
Lys Lys Lys Arg Ile Ala Lys Lys Ser Glu Ala Ala Glu Tyr Gln  
115 120 125  
Lys Leu Leu Ala Gln Arg Leu Lys Glu Gln Arg Asp Arg Arg Ser Glu  
130 135 140  
Ser Leu Ala Lys Arg Arg Ser Lys Leu Ser Ala Ala Ala Lys Ala Ser  
145 150 155 160  
Ala Ala Thr Ser Ala  
165

(2) INFORMATION FOR SEQ ID NO:3356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..156

(D) OTHER INFORMATION: / Ceres Seq. ID 1576538

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3356:

Met Ser Ser Arg Ser Trp Val Asp Val Ser Gln Asp Leu Ser Val Ile  
1 5 10 15  
Asn Leu Val Ile Val Lys Lys Gly Glu Asn Asp Leu Pro Gly Leu Thr  
20 25 30  
Asp Thr Glu Lys Pro Arg Met Arg Gly Pro Lys Arg Ala Ser Lys Ile  
35 40 45  
Arg Lys Leu Phe Asn Leu Ala Lys Asp Asp Asp Val Arg Lys Tyr Val  
50 55 60  
Asn Thr Tyr Arg Arg Thr Phe Thr Thr Lys Asn Gly Lys Lys Val Ser  
65 70 75 80  
Lys Ala Pro Lys Ile Gln Arg Leu Val Thr Pro Leu Thr Leu Gln Arg  
85 90 95  
Lys Arg Ala Arg Ile Ala Asp Lys Lys Lys Arg Ile Ala Lys Lys Lys  
100 105 110  
Ser Glu Ala Ala Glu Tyr Gln Lys Leu Leu Ala Gln Arg Leu Lys Glu

115 120 125  
Gln Arg Asp Arg Arg Ser Glu Ser Leu Ala Lys Arg Arg Ser Lys Leu  
130 135 140  
Ser Ala Ala Ala Lys Ala Ser Ala Ala Thr Ser Ala  
145 150 155

(2) INFORMATION FOR SEQ ID NO:3357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 782 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..782
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576543

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3357:

agtgggtcgt	ccactgtgac	gtgaagccgg	agaacatact	tctgaccg	gatttcgatg	60
ccaagatagc	agactttggg	ctggccaagc	tcgcgaacaa	gggagcacta	gtctgaactt	120
cacccatag	agaggcacca	tgggctacat	ggcgccggaa	tgggcgctca	actcgccgat	180
carcgcgaa	gttgatgtgt	acarctacgg	ggtcrtgstt	ctrgagatcg	tractgggat	240
carggcttcg	artggcatag	tgctagatga	gagRgcagat	agactttcgg	cagtttgtac	300
aggaggctaa	gcatatcctg	tctactggga	gtgtcagtga	tatcggtgat	gatagattgc	360
aaggccattt	tcacgcggac	caagcgggtt	cgatgggtcaa	aatagccttt	tcatgcctcg	420
aggaaagacg	caagaggcca	acgatggatg	agattgtcaa	ggtgctcatg	tcgtgtgggtg	480
atgacgatga	ctaccatcct	gcttattcat	attgacttgc	aacagatgtg	aaggtttccc	540
aaaagaaaac	agatgcaaag	atttgagagg	cagaggcaag	tgtacctttg	atcaatgata	600
gaagctgaac	tgaactgact	gatgaaatat	attcgaaagc	gtgccaaaatt	gtgatatttg	660
tgtagagtat	gttgggggtat	ctccatatct	ggtagattaa	aattgagtaa	tgttgttttg	720
ctctatttct	aaggggaggtg	tcttgcccta	taagtggaat	actataatat	tctctccggtt	780

cc

(2) INFORMATION FOR SEQ ID NO:3358:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..60
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576544

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3358:

Met	Arg	Gly	Thr	Met	Gly	Tyr	Met	Ala	Pro	Glu	Trp	Ala	Leu	Asn	Ser
1				5					10					15	
Pro	Ile	Xaa	Ala	Lys	Val	Asp	Val	Tyr	Xaa	Tyr	Gly	Val	Xaa	Xaa	Xaa
				20				25					30		
Glu	Ile	Xaa	Thr	Gly	Ile	Xaa	Ala	Ser	Xaa	Gly	Ile	Val	Leu	Asp	Glu
				35				40					45		
Xaa	Ala	Asp	Arg	Leu	Ser	Ala	Val	Cys	Thr	Gly	Gly				
				50				55					60		

(2) INFORMATION FOR SEQ ID NO:3359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..56

(D) OTHER INFORMATION: / Ceres Seq. ID 1576545

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3359:

Met Gly Tyr Met Ala Pro Glu Trp Ala Leu Asn Ser Pro Ile Xaa Ala  
1 5 10 15  
Lys Val Asp Val Tyr Xaa Tyr Gly Val Xaa Xaa Xaa Glu Ile Xaa Thr  
20 25 30  
Gly Ile Xaa Ala Ser Xaa Gly Ile Val Leu Asp Glu Xaa Ala Asp Arg  
35 40 45  
Leu Ser Ala Val Cys Thr Gly Gly  
50 55

(2) INFORMATION FOR SEQ ID NO:3360:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 82 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..82

(D) OTHER INFORMATION: / Ceres Seq. ID 1576546

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3360:

Met Arg Xaa Gln Ile Asp Phe Arg Gln Phe Val Gln Glu Ala Lys His  
1 5 10 15  
Ile Leu Ser Thr Gly Ser Val Ser Asp Ile Val Asp Asp Arg Leu Gln  
20 25 30  
Gly His Phe His Ala Asp Gln Ala Val Ala Met Val Lys Ile Ala Phe  
35 40 45  
Ser Cys Leu Glu Glu Arg Arg Lys Arg Pro Thr Met Asp Glu Ile Val  
50 55 60  
Lys Val Leu Met Ser Cys Gly Asp Asp Asp Tyr His Pro Ala Tyr  
65 70 75 80  
Ser Tyr

(2) INFORMATION FOR SEQ ID NO:3361:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 746 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..746

(D) OTHER INFORMATION: / Ceres Seq. ID 1576564

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3361:

gccgtgtgca tagcagcaaa tagtggtcgg cctgttggtta ctctatatcg tcccttccag 60  
tgtaccogtc ctccagccca ttatacatca tacttgctcc agataagacc aagagcatca 120  
tggccaaacgc cttgcctctc atcgtcgcgc tggtcgccgc cgccgggtgc gcggcgctgg 180  
cttcggccac gtctacacc gtcggcgact cgcagggtg gacgaccacc ggcgtcgact 240  
acagcagctg ggccagccgc aacactttcg tcgtcggaga cacactagtg ttcaactacg 300  
tgagcaaggc gcacacggtg acggaggtga gcaaggccgg ctacgacgcc tgctccggcg 360  
ccaacgcgct cagcgacgac gacaccggct ccaccaccat cacgtccag accccgggca 420  
cgcactatct catctgcaac gtccccggcc actgcgccaG cggcatgaag ctacgggtcg 480  
cogtctccgc ctgcgccctcg ggcacggccc cttccaccgg agccctgcag gttccggcga 540  
tggcatccgt cgtegcgcg cgcgggcgc tgccatcaag ctgcgcgtct tctgacggag 600  
cacggccggg tcgtctcagg ggagagacag tgcattcaga ctacgttctt ggcggttgat 660  
agtttcccgc tggcgattgt tcgccgcgca gttcatgtac gtatgtatgt gtgtatgcta 720  
ctctgcggtg gcgaatgctt tttctg

(2) INFORMATION FOR SEQ ID NO:3362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..95
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1576565
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3362:

Ala Val Cys Ile Ala Ala Asn Ser Gly Arg Pro Val Gly Thr Leu Tyr  
1 5 10 15  
Arg Pro Phe Gln Cys Thr Arg Pro Pro Ala His Tyr Thr Ser Tyr Leu  
20 25 30  
Leu Gln Ile Arg Pro Arg Ala Ser Trp Pro Thr Pro Cys Leu Ser Ser  
35 40 45  
Ser Arg Trp Ser Pro Pro Pro Gly Ala Arg Arg Trp Leu Arg Pro Arg  
50 55 60  
Arg Thr Pro Ser Ala Thr Arg Arg Ala Gly Arg Pro Pro Ala Ser Thr  
65 70 75 80  
Thr Ala Ala Gly Pro Ala Ala Thr Leu Ser Ser Ser Glu Thr His  
85 90 95

(2) INFORMATION FOR SEQ ID NO:3363:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 179 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..179
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1576566
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3363:

Met Ala Asn Ala Leu Pro Leu Ile Val Ala Leu Val Ala Ala Gly  
1 5 10 15  
Cys Ala Ala Leu Ala Ser Ala Thr Ser Tyr Thr Val Gly Asp Ser Gln  
20 25 30  
Gly Trp Thr Thr Thr Gly Val Asp Tyr Ser Ser Trp Ala Ser Arg Asn  
35 40 45  
Thr Phe Val Val Gly Asp Thr Leu Val Phe Asn Tyr Val Ser Lys Ala  
50 55 60  
His Thr Val Thr Glu Val Ser Lys Ala Gly Tyr Asp Ala Cys Ser Gly  
65 70 75 80  
Ala Asn Ala Leu Ser Asp Asp Asp Thr Gly Ser Thr Thr Ile Thr Leu  
85 90 95  
Gln Thr Pro Gly Thr His Tyr Phe Ile Cys Asn Val Pro Gly His Cys  
100 105 110  
Ala Ser Gly Met Lys Leu Ala Val Ala Val Ser Ala Ser Pro Ser Gly  
115 120 125  
Thr Ala Pro Ser Thr Gly Ala Leu Gln Val Pro Ala Met Ala Ser Val  
130 135 140  
Val Ala Arg Pro Arg Ala Leu Pro Ser Ser Ser Arg Ser Ser Asp Gly  
145 150 155 160  
Ala Arg Pro Gly Arg Leu Arg Gly Glu Thr Val His Ala Asp Tyr Val  
165 170 175  
Leu Gly Gly

(2) INFORMATION FOR SEQ ID NO:3364:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 782 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..782
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1576575

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3364:

```
actcgccac caaccttccc gtccccgatg ggcgatcatgg cggccaccgc cactgccgtg      60
gcttccccct ccagctccac ctgcgccaggt cccctccaac ccagcccccg cttcctccct      120
cccgctccca cgcccgctcg ctgccatctc ctccccaagc cgcggcggtg gtgcgcgcgc      180
ctccacatcg agcgtcgggg ggccgctcggc agcgacgtgt cctcgtccca tgacgtggct      240
gcmgaggagg ccgctgctgc gtccaaggtc gggaagcscg tgcgcgtcMa cggtgcccgt      300
ccgctgccac cacgttgcca aggcgcccgg cctggacctg cgcggcctgg agggcgctcg      360
caagcagtac atcggcggtt ggaaggggaa ggcgatcacg gccaatctcc cttcaagggt      420
ggagttcgag ctcaagctgg acggccatga caagccggtc cggttcatca cccacctccg      480
cgagcaagag ttcgagatcc tcggggagga atagagctct ggactagaga ataacgcgct      540
ctcatcggcg gctgtggcat ctgtatacta ttgtgtctgc gctaaagaag aacgtggctc      600
agggtgcggg gagaatagga gattgcaact ttgctagtaa gttcctgttt gtttgcttat      660
ttgcggtgcg cttctccctt ctccaccctt taacattgaa attttcatat gtgaggattg      720
aggaattggt cgattgttga tacttatgat ccaaagtaat taaactgagg aatctgttca      780
gc
```

(2) INFORMATION FOR SEQ ID NO:3365:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 149 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..149
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1576576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3365:

```
Thr Arg Pro Pro Thr Phe Pro Ser Pro Met Ala Ile Met Ala Ala Thr
1          5          10          15
Ala Thr Ala Val Ala Ser Pro Ser Ser Thr Ser Pro Gly Pro Leu
20          25          30
Gln Pro Ser Pro Arg Phe Leu Pro Pro Val Ser Thr Pro Ala Arg Cys
35          40          45
His Leu Leu Pro Lys Pro Arg Arg Trp Cys Ala Arg Leu His Ile Glu
50          55          60
Arg Arg Val Ala Val Gly Ser Asp Val Ser Ser His Asp Val Ala
65          70          75          80
Xaa Glu Glu Ala Ala Ala Ser Lys Val Gly Lys Xaa Val Arg Val
85          90          95
Xaa Gly Ala Arg Pro Arg Pro Pro Arg Cys Gln Gly Ala Arg Pro Gly
100         105         110
Pro Ala Arg His Gly Gly Arg Arg Gln Ala Val His Arg Arg Leu Glu
115         120         125
Gly Glu Ala His His Gly Gln Ser Pro Leu Gln Gly Gly Val Arg Ala
130         135         140
Gln Ala Gly Arg Pro
145
```

(2) INFORMATION FOR SEQ ID NO:3366:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 170 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..170  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1576577

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3366:

Leu Ala His Gln Pro Ser Arg Pro Arg Trp Arg Ser Trp Arg Pro Pro  
1                    5                    10                    15  
Pro Leu Pro Trp Leu Pro Pro Pro Ala Pro Pro Arg Gln Val Pro Ser  
                    20                    25                    30  
Asn Pro Ala Pro Ala Ser Ser Leu Pro Ser Pro Arg Pro Leu Ala Ala  
                    35                    40                    45  
Ile Ser Ser Pro Ser Arg Gly Gly Gly Ala Arg Ala Ser Thr Ser Ser  
50                    55                    60  
Val Gly Trp Pro Ser Ala Ala Thr Cys Pro Arg Pro Met Thr Trp Leu  
65                    70                    75                    80  
Xaa Arg Arg Pro Leu Leu Arg Pro Arg Ser Gly Ser Xaa Cys Ala Xaa  
                    85                    90                    95  
Thr Val Pro Val Arg Val His His Val Ala Lys Ala Pro Gly Leu Asp  
                    100                    105                    110  
Leu Arg Gly Met Glu Gly Val Val Lys Gln Tyr Ile Gly Val Trp Lys  
                    115                    120                    125  
Gly Lys Arg Ile Thr Ala Asn Leu Pro Phe Lys Val Glu Phe Glu Leu  
130                    135                    140  
Lys Leu Asp Gly His Asp Lys Pro Val Arg Phe Ile Thr His Leu Arg  
145                    150                    155                    160  
Glu Gln Glu Phe Glu Ile Leu Gly Glu Glu  
                    165                    170

(2) INFORMATION FOR SEQ ID NO:3367:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 140 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..140  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1576578

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3367:

Met Ala Ile Met Ala Ala Thr Ala Thr Ala Val Ala Ser Pro Ser Ser  
1                    5                    10                    15  
Ser Thr Ser Pro Gly Pro Leu Gln Pro Ser Pro Arg Phe Leu Pro Pro  
                    20                    25                    30  
Val Ser Thr Pro Ala Arg Cys His Leu Leu Pro Lys Pro Arg Arg Trp  
                    35                    40                    45  
Cys Ala Arg Leu His Ile Glu Arg Arg Val Ala Val Gly Ser Asp Val  
50                    55                    60  
Ser Ser Ser His Asp Val Ala Xaa Glu Glu Ala Ala Ala Ala Ser Lys  
65                    70                    75                    80  
Val Gly Lys Xaa Val Arg Val Xaa Gly Ala Arg Pro Arg Pro Pro Arg  
                    85                    90                    95  
Cys Gln Gly Ala Arg Pro Gly Pro Ala Arg His Gly Gly Arg Arg Gln  
                    100                    105                    110  
Ala Val His Arg Arg Leu Glu Gly Glu Ala His His Gly Gln Ser Pro  
115                    120                    125  
Leu Gln Gly Gly Val Arg Ala Gln Ala Gly Arg Pro  
130                    135                    140

(2) INFORMATION FOR SEQ ID NO:3368:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 810 base pairs

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3368:

(2) INFORMATION FOR SEQ ID NO:3369:

(A) LENGTH: 206 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..206

(D) OTHER INFORMATION: / Ceres Seq. ID 1576583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3369:

Thr 1	Gly	Lys	His	Leu 5	Ala	Thr	Cys	Ala	Leu 10	Thr	Arg	Leu	Arg	Ala 15	Arg
Gly	Gln	Gln	Gly 20	Thr	Ile	Thr	Val	Pro 25	Leu	Trp	Ser	Ile	Gly 30	Ala	His
Ser	Thr	Ala 35	Gln	Gly	Glu	Ala	Glu 40	Lys	Arg	Phe	Ser	Arg 45	Ser	Arg	Ser
Asp	Lys 50	Ser	Glu	Leu	Ala	Gly 55	Ala	His	Arg	His	Gly 60	Gly	His	Gly	Val
Leu 65	Arg	Gly	Ala	Pro	Arg 70	Arg	Arg	Ala	Pro	Pro 75	Arg	Arg	Ser	Ala	Leu 80
Arg	Pro	Pro	Pro	Ser 85	Ala	Xaa	Val	Cys	Gln 90	Leu	Arg	Phe	Gln 95	Asp	Ala
Pro	Arg	Leu 100	Ser	Leu	Leu	Arg	Ala	Lys 105	Ala	Ala	Ser	Glu	Asp 110	Thr	Ser
Ala	Ser	Gly 115	Asp	Glu	Leu	Ile	Glu 120	Asp	Leu	Lys	Ala	Lys 125	Trp	Asp	Ala
Val	Glu 130	Asp	Lys	Pro	Thr	Val 135	Leu	Leu	Tyr	Gly	Gly 140	Gly	Ala	Val	Val
Ala 145	Leu	Trp	Leu	Thr	Ser 150	Val	Val	Val	Gly	Ala 155	Ile	Asn	Ala	Val	Pro 160
Leu	Leu	Pro	Lys 165	Ile	Leu	Glu	Leu	Val	Gly 170	Leu	Gly	Tyr	Thr 175	Gly	Trp
Phe	Val	Tyr 180	Arg	Tyr	Leu	Leu	Phe	Lys 185	Glu	Ser	Arg	Lys	Glu 190	Leu	Ala
Ala	Asp	Ile 195	Glu	Thr	Leu	Lys	Lys 200	Lys	Ile	Ala	Gly	Thr 205	Glu		

(2) INFORMATION FOR SEQ ID NO:3370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..461
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576592

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3370:

aactcagatt	cagtacaagc	tcaagccagg	cacacagcaa	gacatcgacc	atggctgcct	60
accaacaagc	tcccgcctctc	ctgtgcgccct	gcctgatgct	cgtgctcatg	gcggggcgcg	120
catccggcgg	ccgcgtagac	gtggaagaca	tgctgatgat	ggaccggttc	cgcgcgtggc	180
aagccacgta	caaccgctcg	tacctgaccg	ccgcggagyg	Tctgcgccgg	ttcgaggtgt	240
accgccagaa	catggagctc	atcgaggcca	cgaaccgccc	cgccgagctc	tcgtaccagc	300
tcggcgagac	cccgttcacc	gacctcacca	gcgaggagtt	cctcgccaca	cacaccatgt	360
ccacgcgcct	gcctgcgtcc	gaggccgctc	ggcggcaccg	ggagctcatc	acgacgcacg	420
caggccccgt	cagcgacgGc	ggtcgcCagt	ggaaccggcg	g		

(2) INFORMATION FOR SEQ ID NO:3371:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..153
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576593

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3371:

Thr	Gln	Ile	Gln	Tyr	Lys	Leu	Lys	Pro	Gly	Thr	Gln	Gln	Asp	Ile	Asp	
1				5				10						15		
His	Gly	Cys	Leu	Pro	Thr	Ser	Ser	Arg	Ser	Pro	Val	Arg	Leu	Pro	Asp	
			20					25					30			
Ala	Arg	Ala	His	Gly	Gly	Arg	Gly	Ile	Arg	Arg	Pro	Arg	Arg	Arg	Gly	
			35				40					45				
Arg	His	Ala	Asp	Asp	Gly	Pro	Val	Pro	Arg	Val	Ala	Ser	His	Val	Gln	
			50			55				60						
Pro	Leu	Val	Pro	Asp	Arg	Arg	Gly	Xaa	Ser	Ala	Pro	Val	Arg	Gly	Val	
65				70				75						80		
Pro	Pro	Glu	His	Gly	Ala	His	Arg	Gly	His	Glu	Pro	Pro	Arg	Arg	Ala	
			85				90							95		
Leu	Val	Pro	Ala	Arg	Arg	Asp	Pro	Val	His	Arg	Pro	His	Gln	Arg	Gly	
			100				105						110			
Val	Pro	Arg	His	Thr	His	His	Val	His	Ala	Pro	Ala	Cys	Val	Arg	Gly	
			115				120					125				
Arg	Ser	Ala	Ala	Pro	Gly	Ala	His	His	Asp	Ala	Arg	Arg	Pro	Arg	Gln	
			130				135					140				
Arg	Arg	Arg	Ser	Pro	Val	Glu	Pro	Ala								
145						150										

(2) INFORMATION FOR SEQ ID NO:3372:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide



(B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1576594

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3372:

Leu	Arg	Phe	Ser	Thr	Ser	Ser	Ser	Gln	Ala	His	Ser	Lys	Thr	Ser	Thr
1			5						10					15	
Met	Ala	Ala	Tyr	Gln	Gln	Ala	Pro	Ala	Leu	Leu	Cys	Ala	Cys	Leu	Met
			20					25					30		
Leu	Val	Leu	Met	Ala	Gly	Ala	Ala	Ser	Gly	Gly	Arg	Val	Asp	Val	Glu
			35				40					45			
Asp	Met	Leu	Met	Met	Asp	Arg	Phe	Arg	Ala	Trp	Gln	Ala	Thr	Tyr	Asn
50					55						60				
Arg	Ser	Tyr	Leu	Thr	Ala	Glu	Xaa	Leu	Arg	Arg	Phe	Glu	Val	Tyr	
65				70				75						80	
Arg	Gln	Asn	Met	Glu	Leu	Ile	Glu	Ala	Thr	Asn	Arg	Arg	Ala	Glu	Leu
			85					90						95	
Ser	Tyr	Gln	Leu	Gly	Glu	Thr	Pro	Phe	Thr	Asp	Leu	Thr	Ser	Glu	Glu
			100					105					110		
Phe	Leu	Ala	Thr	His	Thr	Met	Ser	Thr	Arg	Leu	His	Ala	Ser	Glu	Ala
		115					120					125			
Ala	Arg	Arg	His	Arg	Glu	Leu	Ile	Thr	Thr	His	Ala	Gly	Pro	Val	Ser
130					135						140				
Asp	Gly	Gly	Arg	Gln	Trp	Asn	Arg	Arg							
145				150											

(2) INFORMATION FOR SEQ ID NO:3373:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 137 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..137

(D) OTHER INFORMATION: / Ceres Seq. ID 1576595

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3373:

Met	Ala	Ala	Tyr	Gln	Gln	Ala	Pro	Ala	Leu	Leu	Cys	Ala	Cys	Leu	Met
1			5						10					15	
Leu	Val	Leu	Met	Ala	Gly	Ala	Ala	Ser	Gly	Gly	Arg	Val	Asp	Val	Glu
			20					25					30		
Asp	Met	Leu	Met	Met	Asp	Arg	Phe	Arg	Ala	Trp	Gln	Ala	Thr	Tyr	Asn
			35				40					45			
Arg	Ser	Tyr	Leu	Thr	Ala	Ala	Glu	Xaa	Leu	Arg	Arg	Phe	Glu	Val	Tyr
50					55						60				
Arg	Gln	Asn	Met	Glu	Leu	Ile	Glu	Ala	Thr	Asn	Arg	Arg	Ala	Glu	Leu
65				70					75					80	
Ser	Tyr	Gln	Leu	Gly	Glu	Thr	Pro	Phe	Thr	Asp	Leu	Thr	Ser	Glu	Glu
			85					90						95	
Phe	Leu	Ala	Thr	His	Thr	Met	Ser	Thr	Arg	Leu	His	Ala	Ser	Glu	Ala
			100					105					110		
Ala	Arg	Arg	His	Arg	Glu	Leu	Ile	Thr	Thr	His	Ala	Gly	Pro	Val	Ser
			115				120					125			
Asp	Gly	Gly	Arg	Gln	Trp	Asn	Arg	Arg							
130				135											

(2) INFORMATION FOR SEQ ID NO:3374:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 677 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..677

(D) OTHER INFORMATION: / Ceres Seq. ID 1576618

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3374:

aattgcgatt	gogagtcttc	caaaccatgg	cgctcgccct	ggcctctcca	atggcgtctc	60
tctccttcca	ctccgggagg	atctcggcgg	cgtctatcgg	aggcgtcggc	cgcactcgca	120
gggcgccccc	ggtggGcgta	tccgcctcgc	cgttcCtccg	gagctccttc	gtctcgtcct	180
cctccacgtc	gtccgcctcc	gcctccgcct	ccvccgcttc	gctcgcggcg	gctgtctcgg	240
cgtctctggc	atttacgtcc	tcctccgcgt	ttgcggggttc	atctttggga	atcgagttca	300
gctacagtat	aatgacaaca	cggagatccc	gtggtatgca	gattagggct	ggaaaaggctg	360
ccctctgcat	gaccaagagg	tcaaggtcta	ggaagtcact	tgcccgtaca	catggtttcc	420
gcagGcggat	gcggaactact	tctggaagga	aggtactgaa	gCgcaggcgc	gccaaaggca	480
ggaaggttct	ttgcacaagg	acaaactcaa	acagtgggaa	gaaaagaatg	ttctaattac	540
actgcaattt	gatgtgctcg	caactgtaag	tgtaatgtct	acttgcaatc	ttctaagccg	600
ccatctatgt	gtaacaatca	tgtagcatcc	tattcctgtt	taattgggta	aaaatatctg	660
gatcaccttc	tgcttcc					

(2) INFORMATION FOR SEQ ID NO:3375:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..177

(D) OTHER INFORMATION: / Ceres Seq. ID 1576619

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3375:

Leu	Arg	Leu	Arg	Val	Leu	Gln	Thr	Met	Ala	Leu	Ala	Leu	Ala	Ser	Pro
1				5					10					15	
Met	Ala	Ser	Leu	Ser	Phe	His	Ser	Gly	Arg	Ile	Ser	Ala	Ala	Ser	Ile
				20				25					30		
Gly	Gly	Val	Gly	Arg	Thr	Arg	Arg	Ala	Ala	Pro	Val	Gly	Val	Ser	Ala
				35				40					45		
Ser	Pro	Phe	Leu	Arg	Ser	Ser	Phe	Val	Ser	Ser	Ser	Ser	Thr	Ser	Ser
				50			55				60				
Ala	Ser	Ala	Ser	Ala	Ser	Xaa	Ala	Ser	Leu	Ala	Ala	Ala	Val	Ser	Ala
65					70					75				80	
Ser	Leu	Ala	Phe	Thr	Ser	Ser	Ser	Ala	Phe	Ala	Gly	Ser	Ser	Leu	Gly
				85						90				95	
Ile	Glu	Phe	Ser	Tyr	Ser	Ile	Met	Thr	Thr	Arg	Arg	Ser	Arg	Gly	Met
				100					105				110		
Gln	Ile	Arg	Ala	Gly	Lys	Ala	Ala	Leu	Cys	Met	Thr	Lys	Arg	Ser	Arg
				115			120					125			
Ser	Arg	Lys	Ser	Leu	Ala	Arg	Thr	His	Gly	Phe	Arg	Arg	Arg	Met	Arg
				130			135				140				
Thr	Thr	Ser	Gly	Arg	Lys	Val	Leu	Lys	Arg	Arg	Ala	Lys	Gly	Arg	
145					150					155				160	
Lys	Val	Leu	Cys	Thr	Arg	Thr	Asn	Ser	Asn	Ser	Gly	Lys	Lys	Arg	Met
				165					170					175	
Phe															

(2) INFORMATION FOR SEQ ID NO:3376:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 169 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..169

(D) OTHER INFORMATION: / Ceres Seq. ID 1576620

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3376:

Met Ala Leu Ala Leu Ala Ser Pro Met Ala Ser Leu Ser Phe His Ser  
1 5 10 15  
Gly Arg Ile Ser Ala Ala Ser Ile Gly Gly Val Gly Arg Thr Arg Arg  
20 25 30  
Ala Ala Pro Val Gly Val Ser Ala Ser Pro Phe Leu Arg Ser Ser Phe  
35 40 45  
Val Ser Ser Ser Ser Thr Ser Ser Ala Ser Ala Ser Xaa Ala  
50 55 60  
Ser Leu Ala Ala Ala Val Ser Ala Ser Leu Ala Phe Thr Ser Ser Ser  
65 70 75 80  
Ala Phe Ala Gly Ser Ser Leu Gly Ile Glu Phe Ser Tyr Ser Ile Met  
85 90 95  
Thr Thr Arg Arg Ser Arg Gly Met Gln Ile Arg Ala Gly Lys Ala Ala  
100 105 110  
Leu Cys Met Thr Lys Arg Ser Arg Ser Arg Lys Ser Leu Ala Arg Thr  
115 120 125  
His Gly Phe Arg Arg Arg Met Arg Thr Thr Ser Gly Arg Lys Val Leu  
130 135 140  
Lys Arg Arg Arg Ala Lys Gly Arg Lys Val Leu Cys Thr Arg Thr Asn  
145 150 155 160  
Ser Asn Ser Gly Lys Lys Arg Met Phe  
165

(2) INFORMATION FOR SEQ ID NO:3377:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 161 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..161

(D) OTHER INFORMATION: / Ceres Seq. ID 1576621

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3377:

Met Ala Ser Leu Ser Phe His Ser Gly Arg Ile Ser Ala Ala Ser Ile  
1 5 10 15  
Gly Gly Val Gly Arg Thr Arg Arg Ala Ala Pro Val Gly Val Ser Ala  
20 25 30  
Ser Pro Phe Leu Arg Ser Ser Phe Val Ser Ser Ser Ser Thr Ser Ser  
35 40 45  
Ala Ser Ala Ser Ala Ser Xaa Ala Ser Leu Ala Ala Val Ser Ala  
50 55 60  
Ser Leu Ala Phe Thr Ser Ser Ala Phe Ala Gly Ser Ser Leu Gly  
65 70 75 80  
Ile Glu Phe Ser Tyr Ser Ile Met Thr Thr Arg Arg Ser Arg Gly Met  
85 90 95  
Gln Ile Arg Ala Gly Lys Ala Ala Leu Cys Met Thr Lys Arg Ser Arg  
100 105 110  
Ser Arg Lys Ser Leu Ala Arg Thr His Gly Phe Arg Arg Met Arg  
115 120 125  
Thr Thr Ser Gly Arg Lys Val Leu Lys Arg Arg Arg Ala Lys Gly Arg  
130 135 140  
Lys Val Leu Cys Thr Arg Thr Asn Ser Asn Ser Gly Lys Lys Arg Met  
145 150 155 160  
Phe

(2) INFORMATION FOR SEQ ID NO:3378:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..479

(D) OTHER INFORMATION: / Ceres Seq. ID 1576636

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3378:

gttgcccgtt	gtgctctctc	tctctattcg	ttccccgcct	camccccgagc	cagccgtctc	60
gctaggggtt	cgccgcgcgc	gcgcgcgcgc	ccgcgcgtat	gcctcgccgc	agctcaggcg	120
cggaatgg	caggcggcag	ggttgacat	gctaccctca	agggccccag	cgtggtgaag	180
gagatcttca	ttggactgac	cctGgggtct	gatcgctgga	ggtatgtgga	agatgcacca	240
ctggaacgag	cagaggaaaa	ctagatcctt	ctacgacatg	cttgacaagg	gccagatcgt	300
cgctcgtagag	gagtagttcc	cacgtgtcac	ctcagaagtt	ttttttttcc	agtgttttt	360
gaaaactcac	tctggagagc	acgacaaagt	gaatgctgtg	gagatttggc	ttgaaaataa	420
gcataacat	ttgagaacac	cagcttctgt	tgaattgtct	tttcttgtca	tgactat	

(2) INFORMATION FOR SEQ ID NO:3379:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 87 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..87

(D) OTHER INFORMATION: / Ceres Seq. ID 1576637

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3379:

Val	Ala	Arg	Cys	Ala	Leu	Ser	Leu	Tyr	Ser	Phe	Pro	Ala	Ser	Xaa	Arg
1			5					10						15	
Ala	Ser	Arg	Leu	Ala	Arg	Val	Ser	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro
			20					25						30	
Leu	Cys	Leu	Ala	Ala	Ala	Gln	Ala	Arg	Gln	Met	Ala	Gly	Gly	Arg	Val
			35					40						45	
Ala	His	Ala	Thr	Leu	Lys	Gly	Pro	Ser	Val	Val	Lys	Glu	Ile	Phe	Ile
			50					55				60			
Gly	Leu	Thr	Leu	Gly	Ser	Asp	Arg	Trp	Arg	Tyr	Val	Glu	Asp	Ala	Pro
65						70				75				80	
Leu	Glu	Arg	Ala	Glu	Glu	Asn									
						85									

(2) INFORMATION FOR SEQ ID NO:3380:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..58

(D) OTHER INFORMATION: / Ceres Seq. ID 1576638

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3380:

Leu	Pro	Val	Val	Ser	Leu	Ser	Ile	Arg	Ser	Pro	Pro	Xaa	Pro	Glu
1				5				10					15	
Pro	Ala	Val	Ser	Leu	Gly	Phe	Arg	Arg	Arg	Arg	Arg	Arg	Arg	Arg
				20				25					30	
Tyr	Ala	Ser	Pro	Gln	Leu	Arg	Arg	Gly	Lys	Trp	Gln	Ala	Gly	Leu
				35				40					45	
His	Met	Leu	Pro	Ser	Arg	Ala	Pro	Ala	Trp					

50 55  
(2) INFORMATION FOR SEQ ID NO:3381:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 45 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..45  
(D) OTHER INFORMATION: / Ceres Seq. ID 1576639  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3381:  
Met Ala Gly Gly Arg Val Ala His Ala Thr Leu Lys Gly Pro Ser Val  
1 5 10 15  
Val Lys Glu Ile Phe Ile Gly Leu Thr Leu Gly Ser Asp Arg Trp Arg  
20 25 30  
Tyr Val Glu Asp Ala Pro Leu Glu Arg Ala Glu Glu Asn  
35 40 45

(2) INFORMATION FOR SEQ ID NO:3382:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 719 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..719  
(D) OTHER INFORMATION: / Ceres Seq. ID 1576648  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3382:  
gttgatatatg cggatctcca ttaccaaatc gccttctctgt cgccctcccg ctggtgctcgg 60  
cgaacgcgat ctgttcccca acctccgcag ccgctccacc gtctctccact ccggctgccg 120  
aatcgaccog ccccgatcca gatcaggagc tgagggatgg acgcgaacag gcgccagagt 180  
gggatccagc agttgctggc tgcggaScag gaggtcagc aaattgtgaa tgccCgctag 240  
agctgccaaag tcagcgaggc tcaggcaagc aaaagaggag gctgagcggg aaatagccga 300  
ataccgtgcc cagatggagg ctgagtttca gaggaaggtt gcagagagca gcggcgactc 360  
cggtgcaaac gtcaagcgtc tcgaggaaga aacggcggcg aagatcgagc aactcaccca 420  
gcaggccgca agcatctccc cggatgtcat tcagatgctt ctgcggcatg tcaccaccgt 480  
caagaactga ggagtgtctg tcccgaacta tgctcgaga cttgtaccgt cgatctattt 540  
atttttgtca agagtgagag tggtaggaa taatatgcc gcttgatatcc ataattcctg 600  
ttcgtaaacta cggaataagc cgccgcagct ttagcggcaa acgtgactag tactgtcaga 660  
acctaccatt gttatttggt acaattggta aataatattg ttttaaactg gatttttcg

(2) INFORMATION FOR SEQ ID NO:3383:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 75 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..75  
(D) OTHER INFORMATION: / Ceres Seq. ID 1576649  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3383:  
Leu Tyr Met Arg Ile Ser Ile His Gln Ser Pro Ser Cys Arg Pro Pro  
1 5 10 15  
Ala Arg Leu Gly Glu Arg Asp Leu Phe Pro Asn Leu Arg Ser Arg Ser  
20 25 30  
Thr Val Leu His Ser Gly Cys Arg Ile Asp Pro Pro Arg Ser Arg Ser  
35 40 45

Gly Ala Glu Gly Trp Thr Arg Thr Gly Ala Arg Val Gly Ser Ser Ser  
50 55 60  
Cys Trp Leu Arg Xaa Arg Arg Leu Ser Lys Leu  
65 70 75

(2) INFORMATION FOR SEQ ID NO:3384:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..97
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576650

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3384:

Cys Ile Cys Gly Ser Pro Phe Thr Asn Arg Leu Pro Val Ala Leu Pro  
1 5 10 15  
Leu Gly Ser Ala Asn Ala Ile Cys Ser Pro Thr Ser Ala Ala Pro  
20 25 30  
Pro Ser Ser Thr Pro Ala Ala Glu Ser Thr Arg Pro Asp Pro Asp Gln  
35 40 45  
Glu Leu Arg Asp Gly Arg Glu Gln Ala Pro Glu Trp Asp Pro Ala Val  
50 55 60  
Ala Gly Cys Gly Xaa Gly Gly Ser Ala Asn Cys Glu Cys Pro Leu Glu  
65 70 75 80  
Leu Pro Ser Gln Arg Gly Ser Gly Lys Gln Lys Arg Arg Leu Ser Gly  
85 90 95  
Lys

(2) INFORMATION FOR SEQ ID NO:3385:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..86
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576651

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3385:

Met Pro Ala Arg Ala Ala Lys Ser Ala Arg Leu Arg Gln Ala Lys Glu  
1 5 10 15  
Glu Ala Glu Arg Glu Ile Ala Glu Tyr Arg Ala Gln Met Glu Ala Glu  
20 25 30  
Phe Gln Arg Lys Val Ala Glu Ser Ser Gly Asp Ser Gly Ala Asn Val  
35 40 45  
Lys Arg Leu Glu Glu Glu Thr Ala Ala Lys Ile Glu Gln Leu Thr Gln  
50 55 60  
Gln Ala Ala Ser Ile Ser Pro Asp Val Ile Gln Met Leu Leu Arg His  
65 70 75 80  
Val Thr Thr Val Lys Asn  
85

(2) INFORMATION FOR SEQ ID NO:3386:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 756 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..756
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576665

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3386:

atagggttct aagcctcggc cgttttcttcg tctccacagc tcccgcgcgc gcggaccagc	60
gcgtcactct accgggttcc ggcgtctccc cgtacccgta gcgcggcatc catggcggas	120
agacggaaag ggctttcttg aagcagccca aggtgtttct ctgttccaag aaggccacca	180
aggtaaacaac acctggcaag ggaggaaaca gattctggaa gaacattggc cttggtttca	240
agacacccag ggaagccatt gaaggaacct acattgataa gaagtgtcca ttcaccggca	300
ctgtgtctat caggggtcgc atcatcgccg gaacatgcca cagtgtctaa atgaatagga	360
ccatcattgt tcgttagaat tatcttctac tcgtcaagaa gtaccagagg tatgagaaga	420
gacactccaa catccctgcg cacatttcac catgcttccg tgtcaaggaa ggagatcatg	480
tgatcattgg ccagtgcagg ccagtgtcga agactgNtaa ggttcaatgt ggtcaaagtt	540
attcctgcag gttcgaagag tggagcagtg aagaaagctt tctactgccg ttaagatcat	600
gacgagttca tcatccatgg cccggaaaag ctctgtgtta taacgttttg atgctgccta	660
ttagcctttt tccccgtaac tactatatgt gtacttgga ttggacttga attacatcca	720
gaacttgaaa tcctgaaaaa aaatcataac cctttg	

(2) INFORMATION FOR SEQ ID NO:3387:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..83
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576666

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3387:

Met Asn Arg Thr Ile Ile Val Arg Arg Asn Tyr Leu His Phe Val Lys	
1 5 10 15	
Lys Tyr Gln Arg Tyr Glu Lys Arg His Ser Asn Ile Pro Ala His Ile	
20 25 30	
Ser Pro Cys Phe Arg Val Lys Glu Gly Asp His Val Ile Ile Gly Gln	
35 40 45	
Cys Arg Pro Val Ser Lys Thr Xaa Lys Val Gln Cys Gly Gln Ser Tyr	
50 55 60	
Ser Cys Arg Phe Glu Glu Trp Ser Ser Glu Glu Ser Phe His Cys Arg	
65 70 75 80	
Leu Arg Ser	

(2) INFORMATION FOR SEQ ID NO:3388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1034 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1034
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576671

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3388:

gtgtctctta tttctttgtg tgtttggttg ctggaaaggg agtggacttt tacaacttct	60
catgtcccta ttgttgggag gggttcggagt ccggtatcggg atttgccaca accagattgt	120
tcaacactcg gaaggctcac caaatcgtcc tacgcttctg ctctctcctc cacgaggtga	180
ggaaacccta gcgactgacc atggcgttgc tcccgcgcac cgcacggttg gccttctct	240
ctaccccgcg gtcgtactcc gccgcgcgcg ctgcgggcgc ctccccgacc tccccagcgc	300
catacggggg cgcgccccca ccggcgatgt cgaagaggnc cgagttcgtg gtctccaagg	360
ttgatgacct gatgaactgg gcgcgtaagg gctcgatttg gcccatgacc tttgggctcg	420

```
cctgctgcr c ggtcgagatg atgcacgccg gcgCgtcccg ctacgacttc gaccggGttc 480
ggcgctcatct tccgtccctc gccgcgcmag tccgattgca tgatcgtcgc cggcacgytc 540
accaacaaaa tggctccagc cctccgcaag gtttatgacc aaatgcctga gcctagatgg 600
gttatttcaa tgggcagctg tgccaacggt ggtggatact accattactc ctactctggt 660
gtacgtggat gtgacggtat agtccccgtg gacatctacg tccctgggtg cccaccaact 720
gctgaggcac tgctgtacgg tgttcttcag ctccaaaaga agatcaacag gcgtaaggat 780
ttccttctact ggtggaccaaa gtgaagcatg cttctgctgt tgctcgcttg ctacgtttct 840
ttgcactcga cctacctgtc ttatctgaaa taaggacgga ctttgctcgg attcacaaaat 900
ttgttggtgcc tggaaggatg tatgcccagg ttgtgacgaa catataactt gtgtactttg 960
agtcagttcg cctgtaatgg acaccagacc tgctgtgaat ctgtttttaa gcttccattg 1020
taatacagca atac
```

(2) INFORMATION FOR SEQ ID NO:3389:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..120
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576672

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3389:

```
Cys Leu Leu Phe Leu Cys Val Phe Gly Cys Trp Lys Gly Ser Gly Leu
1      5      10      15
Leu Gln Leu Leu Met Ser Leu Leu Leu Gly Gly Phe Gly Val Arg Ile
20      25      30
Gly Ile Cys His Asn Gln Ile Val Gln His Ser Glu Gly Ser Pro Asn
35      40      45
Arg Pro Thr Leu Leu Leu Pro Pro Arg Gly Glu Glu Thr Leu Ala
50      55      60
Thr Asp His Gly Val Ala Pro Ala His Arg Thr Val Gly Leu Pro Leu
65      70      75      80
Tyr Pro Ala Val Val Leu Arg Arg Arg Arg Cys Gly Arg Leu Pro Asp
85      90      95
Leu Pro Ser Ala Ile Arg Gly Arg Ala Pro Thr Gly Asp Val Glu Glu
100     105     110
Xaa Arg Val Arg Gly Leu Gln Gly
115     120
```

(2) INFORMATION FOR SEQ ID NO:3390:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..100
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576673

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3390:

```
Met Ser Leu Leu Leu Gly Gly Phe Gly Val Arg Ile Gly Ile Cys His
1      5      10      15
Asn Gln Ile Val Gln His Ser Glu Gly Ser Pro Asn Arg Pro Thr Leu
20      25      30
Leu Leu Pro Pro Pro Arg Gly Glu Glu Thr Leu Ala Thr Asp His Gly
35      40      45
Val Ala Pro Ala His Arg Thr Val Gly Leu Pro Leu Tyr Pro Ala Val
50      55      60
Val Leu Arg Arg Arg Arg Cys Gly Arg Leu Pro Asp Leu Pro Ser Ala
65      70      75      80
```

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Ile Arg Gly Arg Ala Pro Thr Gly Asp Val Glu Glu Xaa Arg Val Arg  
85 90 95  
Gly Leu Gln Gly  
100

(2) INFORMATION FOR SEQ ID NO:3391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..125
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576674

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3391:

Met Ala Leu Leu Pro Arg Thr Ala Arg Leu Ala Phe Leu Ser Thr Pro  
1 5 10 15  
Arg Ser Tyr Ser Ala Ala Ala Ala Gly Ala Ser Pro Thr Ser Pro  
20 25 30  
Ala Pro Tyr Gly Gly Ala Pro Pro Ala Met Ser Lys Arg Xaa Glu  
35 40 45  
Phe Val Val Ser Lys Val Asp Asp Leu Met Asn Trp Ala Arg Lys Gly  
50 55 60  
Ser Ile Trp Pro Met Thr Phe Gly Leu Ala Cys Cys Xaa Val Glu Met  
65 70 75 80  
Met His Ala Gly Ala Ser Arg Tyr Asp Phe Asp Arg Val Arg Arg His  
85 90 95  
Leu Pro Ser Leu Ala Ala Xaa Val Arg Leu His Asp Arg Arg Arg His  
100 105 110  
Xaa His Gln Gln Asn Gly Ser Ser Pro Pro Gln Gly Leu  
115 120 125

(2) INFORMATION FOR SEQ ID NO:3392:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 868 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..868
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576682

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3392:

adgcctctcc aaaattcgaa caccctcgcc tggaaccttc tacgagccag ctccgagcgg 60  
ttgccgtccc ataattctgag agacggtgcc gtgggtttgc rgcgcctggg tcgccagtaa 120  
agtgcgggcc gagatggagt cctcgctgctc rggcggcggg ctggcgcggc ggcgagtag 180  
cggcggtctgg ggcagcttca gcggcgacac ggaccggttc gacatccccg cgaagggcgc 240  
acccctcgag cggttagga agtggcgga agcagccctt gtgctgaatg catcaaggcg 300  
ctttaggtac acactcgatt ttggaagagc attggccttg gtttcaagac tcccagcgaa 360  
Gcaattgaag ggacctacat tgacaagaaa tgtccattca ctggaaccgt ttctatcaga 420  
ggcagaatta ttgctggaac atgccacagt gctaagatga acagaaccat cattgttcgc 480  
aggaactatc tccactttgt taagaaatac cagaggtatg aaaagaggca ctccaacatt 540  
ccagctcaca tctccccatg cttcogtgtg aagggaaggc accatgtcat cattggccag 600  
tgcaggcccc tatcaaaaac tgtgagggtc aatgtcgtca aagtcattcc agctggatct 660  
gctgctgccg gcaagaaggc tttcacccga gcctgagttt aagactatgt tccatgagta 720  
gtttatatag tgatgtcttt ttttgttaaa aaaactgcct tctaggcttg tgcctttcga 780  
ctatggtttg gagattgttc ccattctaata gaagtccaat catctgaaca tgttactgtt 840  
tattgtacct tgtcgtgcaa agttttcc

(2) INFORMATION FOR SEQ ID NO:3393:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..108
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1576683
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3393:

Met Glu Ser Ser Ser Xaa Gly Gly Gly Leu Ala Arg Arg Arg Ser Ser  
1 5 10 15  
Gly Gly Trp Gly Ser Phe Ser Gly Asp Thr Asp Pro Phe Asp Ile Pro  
20 25 30  
Ala Lys Gly Ala Pro Leu Glu Arg Leu Arg Lys Trp Arg Gln Ala Ala  
35 40 45  
Leu Val Leu Asn Ala Ser Arg Arg Phe Arg Tyr Thr Leu Asp Phe Gly  
50 55 60  
Arg Ala Leu Ala Leu Val Ser Arg Leu Pro Ala Lys Gln Leu Lys Gly  
65 70 75 80  
Pro Thr Leu Thr Arg Asn Val His Ser Leu Glu Pro Phe Leu Ser Glu  
85 90 95  
Ala Glu Leu Leu Leu Glu His Ala Thr Val Leu Arg  
100 105

(2) INFORMATION FOR SEQ ID NO:3394:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 79 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..79
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1576684
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3394:

Met Asn Arg Thr Ile Ile Val Arg Arg Asn Tyr Leu His Phe Val Lys  
1 5 10 15  
Lys Tyr Gln Arg Tyr Glu Lys Arg His Ser Asn Ile Pro Ala His Ile  
20 25 30  
Ser Pro Cys Phe Arg Val Lys Glu Gly Asp His Val Ile Ile Gly Gln  
35 40 45  
Cys Arg Pro Leu Ser Lys Thr Val Arg Phe Asn Val Val Lys Val Ile  
50 55 60  
Pro Ala Gly Ser Ala Ala Gly Lys Lys Ala Phe Thr Ala Ala  
65 70 75

(2) INFORMATION FOR SEQ ID NO:3395:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 63 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..63
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1576685
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3395:

Met Leu Pro Cys Glu Gly Arg Arg Pro Cys His His Trp Pro Val Gln  
1 5 10 15  
Ala Pro Ile Lys Asn Cys Glu Val Gln Cys Arg Gln Ser His Ser Ser

20 25 30  
Trp Ile Cys Cys Arg Gln Glu Gly Phe His Arg Ser Leu Ser Leu  
35 40 45  
Arg Leu Cys Ser Met Ser Ser Leu Tyr Ser Asp Val Phe Phe Cys  
50 55 60

(2) INFORMATION FOR SEQ ID NO:3396:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 921 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..921
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576713

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3396:

atcctctagc tctctctctc tctcttctct cacacacaca cacagtcaca gacaccccta 60  
tcaattagac tgtgctagta ggtagcggcc gcgtaatgga gcaggagctc agccttgagc 120  
tcacctctct ccacctctcg gcctcgccgc cggagccacc gggctacttc gtctgcatgt 180  
actgcgaccg caagttcttc agctcgagg ctctcggtgg ccaccagaac gcgcacaagt 240  
acgagcgcas ctggccaagc gccgcaggga gatagccgcc gccctgcgcy gcgcacggggc 300  
ggcgcgccacc gmaccgggcg cyccggagga cgacgmcgyc gccgcgatgg gctctcgca 360  
tgtccccgcc aggccacaag gcacgggtac cggagtcgtc gtcgttgaag atgagagtgc 420  
aaccaggatg atggGacaag cagaaggctc ctgctgctga tgacgasstc ccgcgaccgc 480  
gtcgtcgagc aacatgaaga ggtcgtcgga gtacggctac ggcgtcgagg agctggatct 540  
ctccctcagg ctttgattgg ttctctcttc tcctccacyn nnanatataa ttgcggccgt 600  
tngetnagat aattcgatct ttgtggtcag tgcaatcatc tgtttcgcgt gcgtggatc 660  
tcagtgtctg atccgtcact ttcttctca tgtagttgtt gtgcagttat attcttccat 720  
ccgatgatgg aacctatcgg caagaactat tgcggccca tcctgctatc caaagggcgt 780  
ggatatttgg gtgctctttt cggttttctg ccttgagtct tctttgtgcy atctaaattc 840  
gcagcttggt ttttccaaaa cggcggaac agttttgccg caatttcgtt tggacctttt 900  
tcaagtgact ctaaattggg c

(2) INFORMATION FOR SEQ ID NO:3397:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..59
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576714

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3397:

Met Glu Gln Glu Ser Leu Glu Leu Thr Leu Leu His Pro Ser Ala  
1 5 10 15  
Ser Pro Pro Glu Pro Pro Gly Tyr Phe Val Cys Met Tyr Cys Asp Arg  
20 25 30  
Lys Phe Phe Ser Ser Gln Ala Leu Gly Gly His Gln Asn Ala His Lys  
35 40 45  
Tyr Glu Arg Xaa Trp Pro Ser Ala Ala Gly Arg  
50 55

(2) INFORMATION FOR SEQ ID NO:3398:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..37  
(D) OTHER INFORMATION: / Ceres Seq. ID 1576715  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3398:  
Met Gly Ser Arg Asp Val Pro Ala Arg Pro Gln Gly Thr Gly Thr Gly  
1 5 10 15  
Val Val Val Val Glu Asp Glu Ser Ala Thr Arg Met Met Gly Gln Ala  
20 25 30  
Glu Gly Ser Cys Cys  
35

(2) INFORMATION FOR SEQ ID NO:3399:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..50

(D) OTHER INFORMATION: / Ceres Seq. ID 1576716

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3399:

Met Thr Xaa Ser Arg Asp Arg Val Val Glu Gln His Glu Glu Val Val  
1 5 10 15  
Gly Val Arg Leu Arg Arg Arg Gly Ala Gly Ser Leu Pro Gln Ala Leu  
20 25 30  
Ile Gly Ser Ser Ser Ser Ser Xaa Xaa Xaa Tyr Asn Ser Pro Arg Xaa  
35 40 45  
Xaa Arg  
50

(2) INFORMATION FOR SEQ ID NO:3400:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 831 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..831

(D) OTHER INFORMATION: / Ceres Seq. ID 1576730

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3400:

tcaagcacct ataatagtagt acctcataat ggcaggcaaa aacctaatac cattggggct	60
cattatcctc atgaccatgg gattagccaa tgctgttagg gtggttagat actctagtgc	120
cgatggtact ggcacaggac agggagaagg tgggtgatat gtgaatggcg ggggatcagg	180
gtctgggtct ggcaccgat caggtgatag tggctcttat ggtgcacatg caagtrctag	240
tmgagggtgt ggaggggtg gaactagcca gtacgggtgg tctggatatg gttctgggtc	300
agggtcaggg tcaggatcta gtacatatag tcaaggaggg tattctgggtt atggagaatc	360
ttctagtgtt ggtRggcatc ggtgggggtg gaggtggagg acaagctgca ggcgcatgga	420
attccaatgc tcaaggatcc ggtagtggaa ctggttcttg ctctagctat gctaacagg	480
attggtacgg atcaagtga gcaagggtgca gtgctaattg caatgggtgt ggacaggaa	540
atagtcaaaa cgggtggaagt ggtggtggct caggtgctgg atctgggttt ggcaatgcct	600
acccctaatt tctatatcta agtcaacct tagttggagc ccaacagtat ttgtcatttc	660
aagttgtggt attagttagt ttgtttgtac ctctattaca cttttgctag aactaaataa	720
ataaagggcc caactattct agtaattgca gcagtttagt gtgaggttca gcttgtaaga	780
atttggtgta aacatgtcag tctatgaatg aaataataac ttcccttttag c	

(2) INFORMATION FOR SEQ ID NO:3401:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 138 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..138  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1576731  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3401:

Met Ala Gly Lys Asn Leu Ile Pro Leu Gly Leu Ile Ile Leu Met Thr  
1                  5                  10                  15  
Met Gly Leu Ala Asn Ala Val Arg Val Val Arg Tyr Ser Ser Ala Asp  
                  20                  25                  30  
Gly Thr Gly Thr Gly Gln Gly Glu Gly Gly Gly Tyr Val Asn Gly Gly  
                  35                  40                  45  
Gly Ser Gly Ser Gly Ser Gly Thr Gly Ser Gly Asp Ser Gly Pro Tyr  
                  50                  55                  60  
Gly Ala His Ala Ser Xaa Ser Xaa Gly Gly Gly Gly Gly Gly Thr Ser  
65                  70                  75                  80  
Gln Tyr Gly Gly Ser Gly Tyr Gly Ser Gly Ser Gly Ser Gly Ser Gly  
                  85                  90                  95  
Ser Ser Thr Tyr Ser Gln Gly Gly Tyr Ser Gly Tyr Gly Glu Ser Ser  
                  100                 105                 110  
Ser Ala Gly Xaa His Arg Trp Gly Trp Arg Trp Arg Thr Ser Cys Arg  
                 115                 120                 125  
Arg Met Glu Phe Gln Cys Ser Arg Ile Arg  
130                 135

(2) INFORMATION FOR SEQ ID NO:3402:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 147 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..147  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1576732

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3402:

Met Ala Gly Asp Gln Gly Leu Gly Leu Ala Pro Asp Gln Val Ile Val  
1                  5                  10                  15  
Val Leu Met Val His Met Gln Xaa Leu Xaa Glu Val Val Glu Gly Val  
                  20                  25                  30  
Glu Leu Ala Ser Thr Val Gly Leu Asp Met Val Leu Gly Gln Gly Gln  
                  35                  40                  45  
Gly Gln Asp Leu Val His Ile Val Lys Glu Gly Ile Leu Val Met Glu  
                  50                  55                  60  
Asn Leu Leu Val Leu Xaa Gly Ile Gly Gly Gly Gly Gly Gly Gln  
65                  70                  75                  80  
Ala Ala Gly Ala Trp Asn Ser Asn Ala Gln Gly Ser Gly Ser Gly Thr  
                  85                  90                  95  
Gly Ser Gly Ser Ser Tyr Ala Asn Arg Tyr Trp Tyr Gly Ser Ser Glu  
                 100                 105                 110  
Ala Gly Ala Ser Ala Asn Gly Asn Gly Gly Gly Thr Gly Asn Ser Gln  
                 115                 120                 125  
Asn Gly Gly Ser Gly Gly Gly Ser Gly Ala Gly Ser Gly Phe Gly Asn  
130                 135                 140  
Ala Tyr Pro  
145

(2) INFORMATION FOR SEQ ID NO:3403:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 129 amino acids  
    (B) TYPE: amino acid

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- (C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..129  
(D) OTHER INFORMATION: / Ceres Seq. ID 1576733  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3403:

Met Val His Met Gln Xaa Leu Xaa Glu Val Val Glu Gly Val Glu Leu  
1 5 10 15  
Ala Ser Thr Val Gly Leu Asp Met Val Leu Gly Gln Gly Gln Gly Gln  
20 25 30  
Asp Leu Val His Ile Val Lys Glu Gly Ile Leu Val Met Glu Asn Leu  
35 40 45  
Leu Val Leu Xaa Gly Ile Gly Gly Gly Gly Gly Gly Gly Gln Ala Ala  
50 55 60  
Gly Ala Trp Asn Ser Asn Ala Gln Gly Ser Gly Ser Gly Thr Gly Ser  
65 70 75 80  
Gly Ser Ser Tyr Ala Asn Arg Tyr Trp Tyr Gly Ser Ser Glu Ala Gly  
85 90 95  
Ala Ser Ala Asn Gly Asn Gly Gly Gly Thr Gly Asn Ser Gln Asn Gly  
100 105 110  
Gly Ser Gly Gly Gly Ser Gly Ala Gly Ser Gly Phe Gly Asn Ala Tyr  
115 120 125  
Pro

- (2) INFORMATION FOR SEQ ID NO:3404:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 744 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..744  
(D) OTHER INFORMATION: / Ceres Seq. ID 1576754

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3404:

ctcacgtca cggccgcgc ctccaccgt cgccgttcc tcccgtaga ctaggtagg 60  
ctaggctagg gtgtcgacca gctcgcggt atggtggcct tcaggttcca tcagtaccag 120  
gwggtggggc gcgcgctgcc gacgcccgc gacgagcacc ccaagatcta ccgcatgaag 180  
ctctgggcca ccaacgaagt ccgcgccaa agcaagttct ggtacttctt gaggaagttg 240  
aagaaggtta agaagagcaa cggtcagggtc ctggccatca acgagatctt cgagcgtaac 300  
ccgacgacga tcaagaacta tggcatctgg Ctgcgctacc agagcagaac cggctaccac 360  
aacatgtaca aggagtaccg cgacacaacc ctgaacggcg ctgtagagca gatgtacaat 420  
gagatggctt ctgcgccacc cgtgagggtc cctgcattcc agatcatcaa gaccgccaca 480  
gtacacttca agctgtgcaa gagggacaac accaagcagt ttcacaacag tgagatcaag 540  
ttcccaactcg tgtaccgcaa ggtcaggccg ccgaccagga agctgaagac cacgttcaag 600  
gcttcgaggc ccaacctgtt catgtgattt agctgtggtc agtgtatgtg atcgtaagaa 660  
tctgtgtttt aagttttgac gctaagactt gggtggtttg aagattcaac tcgttttgaa 720  
acgtgcatgg tgaaccattt gccg

- (2) INFORMATION FOR SEQ ID NO:3405:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 178 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..178

000001-166666

(D) OTHER INFORMATION: / Ceres Seq. ID 1576755

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3405:

Met Val Ala Phe 5 Phe His Gln Tyr Gln Xaa Val Gly Arg Ala Leu 15  
1 10  
Pro Thr Pro Gly Asp Glu His Pro Lys Ile Tyr Arg Met Lys Leu Trp 30  
20 25  
Ala Thr Asn Glu Val Arg Ala Lys Ser Lys Phe Trp Tyr Phe Leu Arg 45  
35 40  
Lys Leu Lys Lys Val Lys Lys Ser Asn Gly Gln Val Leu Ala Ile Asn 60  
50 55  
Glu Ile Phe Glu Arg Asn Pro Thr Thr Ile Lys Asn Tyr Gly Ile Trp 80  
65 70 75  
Leu Arg Tyr Gln Ser Arg Thr Gly Tyr His Asn Met Tyr Lys Glu Tyr 95  
85 90  
Arg Asp Thr Thr Leu Asn Gly Ala Val Glu Gln Met Tyr Asn Glu Met 110  
100 105  
Ala Ser Arg His Arg Val Arg Ser Pro Cys Ile Gln Ile Ile Lys Thr 125  
115 120  
Ala Thr Val His Phe Lys Leu Cys Lys Arg Asp Asn Thr Lys Gln Phe 140  
130 135  
His Asn Ser Glu Ile Lys Phe Pro Leu Val Tyr Arg Lys Val Arg Pro 160  
145 150 155  
Pro Thr Arg Lys Leu Lys Thr Thr Phe Lys Ala Ser Arg Pro Asn Leu 175  
165 170  
Phe Met

(2) INFORMATION FOR SEQ ID NO:3406:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..150

(D) OTHER INFORMATION: / Ceres Seq. ID 1576756

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3406:

Met Lys Leu Trp Ala Thr Asn Glu Val Arg Ala Lys Ser Lys Phe Trp 15  
1 10  
Tyr Phe Leu Arg Lys Leu Lys Lys Val Lys Lys Ser Asn Gly Gln Val 30  
20 25  
Leu Ala Ile Asn Glu Ile Phe Glu Arg Asn Pro Thr Thr Ile Lys Asn 45  
35 40  
Tyr Gly Ile Trp Leu Arg Tyr Gln Ser Arg Thr Gly Tyr His Asn Met 60  
50 55  
Tyr Lys Glu Tyr Arg Asp Thr Thr Leu Asn Gly Ala Val Glu Gln Met 80  
65 70 75  
Tyr Asn Glu Met Ala Ser Arg His Arg Val Arg Ser Pro Cys Ile Gln 95  
85 90  
Ile Ile Lys Thr Ala Thr Val His Phe Lys Leu Cys Lys Arg Asp Asn 110  
100 105  
Thr Lys Gln Phe His Asn Ser Glu Ile Lys Phe Pro Leu Val Tyr Arg 125  
115 120  
Lys Val Arg Pro Pro Thr Arg Lys Leu Lys Thr Thr Phe Lys Ala Ser 140  
130 135  
Arg Pro Asn Leu Phe Met 150  
145 150

(2) INFORMATION FOR SEQ ID NO:3407:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 654 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..654
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1576757

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3407:

ggacctttct atcgcgcgca ttttctttcc gaccagccga vcgccgcgc cctccggcag	60
gtcttctttcc cgccacgac caccacgccc aggtctttccc ggccccgaac gcgagcacc	120
agccctcctc caggtctttcc ccggcgacga gcgcgtagaa gaggggatcc ttagcacaat	180
ggaagaagga gcaccagggc cgtcgcaagc catcccggat tctggagaca cgtaccgcaa	240
cagctccacc gcgcccgtag gcagcagctc accgtctgtc gcgaagCtcc ggaagctgct	300
gttccggcgg atgctcatcg gcgtcaacga cggccgctac ttccacggcc tgttccaactg	360
catcgacaag cagggaacaa tcctcttcca ggacgccgta gactaccgca gcgcccgcca	420
ctgctcgctt ccgacggagc agcgggtgctt ggggctcatc ctgatcccg gcgcctgccg	480
gtcgtcgtgc caggtcgatt gctccgttga agagaagatg tcgctcctgt gttttgagtg	540
aatcgtgctt caaagggaat acactacgca tgtactaagt tactggggct catctctgct	600
atctgaaact gagaggcatg attggtgttt cctatttttg aaggattgtt tatt	

(2) INFORMATION FOR SEQ ID NO:3408:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 179 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..179
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1576758

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3408:

Asp	Leu	Ser	Ile	Ala	Arg	Ile	Phe	Phe	Pro	Thr	Ser	Arg	Xaa	Pro	Pro
1				5					10					15	
Pro	Ser	Gly	Arg	Ser	Ser	Ser	Arg	Pro	Arg	Pro	Pro	Thr	Pro	Gly	Leu
				20				25					30		
Pro	Gly	Pro	Glu	Arg	Glu	His	Pro	Ala	Leu	Leu	Gln	Val	Phe	Pro	Gly
		35				40					45				
Asp	Glu	Arg	Val	Glu	Glu	Gly	Ile	Leu	Ser	Thr	Met	Glu	Glu	Gly	Ala
	50					55					60				
Pro	Gly	Pro	Ser	Gln	Ala	Ile	Pro	Asp	Ser	Gly	Asp	Thr	Tyr	Arg	Asn
	65				70					75				80	
Ser	Ser	Thr	Ala	Pro	Val	Gly	Ser	Ser	Ser	Pro	Ser	Val	Ala	Lys	Leu
				85					90					95	
Arg	Lys	Leu	Leu	Phe	Arg	Arg	Met	Leu	Ile	Gly	Val	Asn	Asp	Gly	Arg
		100						105					110		
Tyr	Phe	His	Gly	Leu	Phe	His	Cys	Ile	Asp	Lys	Gln	Gly	Asn	Ile	Ile
		115				120						125			
Leu	Gln	Asp	Ala	Val	Glu	Tyr	Arg	Ser	Ala	Arg	His	Cys	Ser	Pro	Pro
	130					135					140				
Thr	Glu	Gln	Arg	Cys	Leu	Gly	Leu	Ile	Leu	Ile	Pro	Ala	Ala	Cys	Arg
	145				150					155				160	
Ser	Ser	Cys	Gln	Val	Asp	Cys	Ser	Val	Glu	Lys	Met	Ser	Leu	Leu	
				165					170				175		
Cys	Phe	Glu													

(2) INFORMATION FOR SEQ ID NO:3409:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 120 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:



- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..120  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1576759  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3409:

Met Glu Glu Gly Ala Pro Gly Pro Ser Gln Ala Ile Pro Asp Ser Gly  
1                  5                  10                  15  
Asp Thr Tyr Arg Asn Ser Ser Thr Ala Pro Val Gly Ser Ser Ser Pro  
                  20                  25                  30  
Ser Val Ala Lys Leu Arg Lys Leu Phe Arg Arg Met Leu Ile Gly  
                  35                  40                  45  
Val Asn Asp Gly Arg Tyr Phe His Gly Leu Phe His Cys Ile Asp Lys  
                  50                  55                  60  
Gln Gly Asn Ile Ile Leu Gln Asp Ala Val Glu Tyr Arg Ser Ala Arg  
65                  70                  75                  80  
His Cys Ser Pro Pro Thr Glu Gln Arg Cys Leu Gly Leu Ile Leu Ile  
                  85                  90                  95  
Pro Ala Ala Cys Arg Ser Ser Cys Gln Val Asp Cys Ser Val Glu Glu  
                  100                  105                  110  
Lys Met Ser Leu Leu Cys Phe Glu  
                  115                  120

(2) INFORMATION FOR SEQ ID NO:3410:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 555 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..555  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1576763  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3410:

gactccacgc cgccagtcac gaccacgccg cgcctccgcc tggaaccctt tagccgagcg          60  
gasaagggaa gaaatgggga aggggtacggg cagcttcggc aagcgccgga acaagacgca          120  
cacgtcttgc atccgctgcg gcggccggcg tggagcgggc gcgtcaagaa cccgcatcta          180  
aatcgggcgc ccagccccga gagctccgac gccgagtgc atgagaagcg agcgagcagc          240  
agcagcagca gccaccgcaa aggtcaacg acgacgacgt ccgttgttgc gacggcgccc          300  
agcgcagCat gccgctgtcg tcttcgttcg tatccacgta cgtacgacgg cccagctgac          360  
ccgtttgcct acccgtccgt tctgtgcgac tggatggtcg gtcggcgggc gtcgcggcga          420  
gggctttcgg tacgtcgtgg ataagcacga ggggagggcg ggcaggcggg aacggaggcg          480  
gaggcgggcg ccccaagtgg cggctcttcc aaatgtcaaa aaggacagct gtaacagtga          540  
taagaaaaac aagtc

(2) INFORMATION FOR SEQ ID NO:3411:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 72 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..72  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1576764  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3411:

Asp Ser Thr Pro Pro Val Thr Thr Thr Pro Arg Leu Arg Leu Glu Pro  
1                  5                  10                  15  
Phe Ser Arg Ala Xaa Lys Gly Arg Asn Gly Glu Gly Tyr Gly Gln Leu  
                  20                  25                  30

(A) NAME/KEY: -

(D) OTHER INFORMATION: / Ceres Seq. ID 1576795

gccagttcac	ctccgcctcc	gtctctcccc	tccccctccc	gtctgtccat	ggccaccgca	60
gcacgcgccc	tctgtgcgc	acgcccggca	cggcgcgtgc	tgcgtctcg	ggcctccc	120
tctctcttt	ccatccgtcc	cgcgcggcaa	cgtgctggcg	tgggtgcgt	ccgtgcattg	180
gtcgcggcgc	cggattccac	ctattccccg	ctgcgttcgg	gccagggcgg	tgaccgtgca	240
ccgactgaaa	tggcgcctct	gttccctggc	tgcgactacg	agcactggct	catcgctcatg	300
gacaagcccc	ggggcgaggg	cgcaccaaag	cagcaaatga	tagattgtta	cattccagacc	360
cttgcccagg	tgttagggag	tgaagaggag	gcgaagaaga	ggatatataa	tgtgtcctgc	420
gagcgtctatt	ttggattcgg	atgcgaattt	gacgaggaga	cctCccaaca	aactcgaagg	480
ccttccaggg	gttctttttg	tgttctctga	ctcttacggt	gatgctgaga	acaaggatta	540
tgggtgctgag	ttatttgtga	acggtgaaat	cgttcagcga	tctccagaaa	ggcagagaag	600
ggtggagcca	gtgcctcaga	gagctcagga	tgcaccacgg	tacagtgacc	ggaccgcgta	660
tgtgaagcgg	agggagaacc	aatcttacca	gagatgatgt	ttccgtctct	gaagatgtaa	720
aatgtcacgg	tttccacaag	tgtccaaatg	cggtagtgaa	gatgcagcag	caactcccca	780
ctactcatat	gagaattgga	tccgttctgt	ttgccgcgca	ttttaagctg	tatatgctta	840
ttatgcattt	ggccttgtac	ctcagtcgat	atgaacgatg	tatcctttga	actaacgcatt	900
tataattttt	gaaaccgttt	taqcc				

(i) SEQUENCE CHARACTERISTICS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..169

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3415:

(2) INFORMATION FOR SEQ ID NO:3416:

(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..112
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576797

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3416:

Pro	Val	His	Leu	Arg	Leu	Arg	Ser	Ser	Pro	Pro	Pro	Pro	Val	Leu	Pro
1			5						10				15		
Trp	Pro	Pro	Gln	His	Ala	Pro	Ser	Ser	Pro	His	Ala	Arg	His	Gly	Arg
			20					25					30		
Cys	Cys	Arg	Leu	Gly	Ala	Ser	Arg	Pro	Pro	Leu	Pro	Ser	Val	Pro	Arg
		35					40					45			
Gly	Asn	Val	Leu	Ala	Ser	Gly	Ala	Ser	Ala	Ala	Trp	Leu	Gly	Gly	Arg
	50					55					60				
Ile	Pro	Pro	Ile	Pro	Arg	Cys	Val	Arg	Ala	Arg	Ala	Val	Thr	Val	His
65					70				75						80
Arg	Leu	Lys	Trp	Arg	Leu	Cys	Ser	Leu	Ala	Ala	Thr	Thr	Ser	Thr	Gly
			85						90					95	
Ser	Ser	Ser	Trp	Thr	Ser	Pro	Gly	Ala	Arg	Ala	Pro	Pro	Ser	Ser	Lys
			100					105					110		

(2) INFORMATION FOR SEQ ID NO:3417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..153
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576798

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3417:

Met	Ala	Thr	Ala	Ala	Arg	Ala	Leu	Val	Ala	Ala	Arg	Pro	Ala	Arg	Pro
1			5						10				15		
Leu	Leu	Pro	Ser	Arg	Arg	Leu	Pro	Ser	Ser	Ser	Ser	Ile	Arg	Pro	Ala
			20					25					30		
Arg	Gln	Arg	Ala	Gly	Val	Gly	Cys	Val	Arg	Cys	Met	Ala	Arg	Arg	Pro
		35					40					45			
Asp	Ser	Thr	Tyr	Ser	Pro	Leu	Arg	Ser	Gly	Gln	Gly	Gly	Asp	Arg	Ala
	50					55					60				
Pro	Thr	Glu	Met	Ala	Pro	Leu	Phe	Pro	Gly	Cys	Asp	Tyr	Glu	His	Trp
65				70					75						80
Leu	Ile	Val	Met	Asp	Lys	Pro	Gly	Gly	Glu	Gly	Ala	Thr	Lys	Gln	Gln
			85						90					95	
Met	Ile	Asp	Cys	Tyr	Ile	Gln	Thr	Leu	Ala	Gln	Val	Val	Gly	Ser	Glu
		100						105					110		
Glu	Glu	Ala	Lys	Lys	Arg	Ile	Tyr	Asn	Val	Ser	Cys	Glu	Arg	Tyr	Phe
		115					120					125			
Gly	Phe	Gly	Cys	Glu	Ile	Asp	Glu	Glu	Thr	Ser	Gln	Gln	Thr	Arg	Arg
	130					135					140				
Pro	Ser	Arg	Gly	Ser	Phe	Cys	Ala	Ser							
145						150									

(2) INFORMATION FOR SEQ ID NO:3418:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..545

(D) OTHER INFORMATION: / Ceres Seq. ID 1576799

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3418:

aatcttccag	cccaaagtgc	catccattg	ctcgtctgt	ccctccgttc	acaacctcct	60
ccacgaccga	acgagcagag	cagacccttc	cccctcacca	gctccgggtt	ccagcggcgg	120
cggcggcgaa	gatgatcata	ccggtgcgct	gcttcaCctg	cggcaaggtg	attgggaaca	180
agtgggacct	ctacctcgac	ctcctccagg	ccgactactc	ggaaggggat	gctctggatg	240
ctttggaatt	gttccgctac	tgctgcaggc	gaatgctcat	gacccatgtt	gacctcattg	300
agaagtgtgt	caactacaac	acactggaga	agactgagac	aagttaagtg	agcaagcata	360
tcatgctctg	aaagcactac	tgtttcgcag	tatcatatat	attgtaggcg	gtatgttgtt	420
tcttctctat	caggagagga	ttgttgtGga	gtgtgaactt	gcttttgctc	tcgagcattc	480
aaggactgac	aagggcattg	tgcatctatg	ttacgatgtt	ggagatttta	atcgatataa	540
cggt						

(2) INFORMATION FOR SEQ ID NO:3419:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..96

(D) OTHER INFORMATION: / Ceres Seq. ID 1576800

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3419:

Ile	Phe	Gln	Pro	Lys	Val	Pro	Ser	His	Cys	Ser	Leu	Cys	Pro	Ser	Val	
1				5					10						15	
His	Asn	Leu	Leu	His	Asp	Arg	Thr	Ser	Arg	Ala	Asp	Pro	Ser	Pro	Ser	
			20					25					30			
Pro	Ala	Pro	Gly	Ser	Ser	Gly	Gly	Gly	Gly	Glu	Asp	Asp	His	Thr	Gly	
			35				40					45				
Ala	Leu	Leu	His	Leu	Arg	Gln	Gly	Asp	Trp	Glu	Gln	Val	Gly	Pro	Leu	
			50			55					60					
Pro	Arg	Pro	Pro	Pro	Gly	Arg	Leu	Leu	Gly	Arg	Gly	Cys	Ser	Gly	Cys	
65					70					75					80	
Phe	Gly	Ile	Val	Pro	Leu	Leu	Leu	Gln	Ala	Asn	Ala	His	Asp	Pro	Cys	
				85					90					95		

(2) INFORMATION FOR SEQ ID NO:3420:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..114

(D) OTHER INFORMATION: / Ceres Seq. ID 1576801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3420:

Ser	Ser	Ser	Pro	Lys	Phe	His	Pro	Ile	Ala	Arg	Ser	Val	Pro	Pro	Phe	
1				5					10						15	
Thr	Thr	Ser	Ser	Thr	Thr	Glu	Arg	Ala	Glu	Gln	Thr	Leu	Pro	Pro	His	
			20					25					30			
Gln	Leu	Arg	Val	Pro	Ala	Ala	Ala	Ala	Ala	Lys	Met	Ile	Ile	Pro	Val	
			35				40					45				
Arg	Cys	Phe	Thr	Cys	Gly	Lys	Val	Ile	Gly	Asn	Lys	Trp	Asp	Leu	Tyr	
			50			55				60						
Leu	Asp	Leu	Leu	Gln	Ala	Asp	Tyr	Ser	Glu	Gly	Asp	Ala	Leu	Asp	Ala	
65				70					75					80		

Leu Glu Leu Phe Arg Tyr Cys Cys Arg Arg Met Leu Met Thr His Val  
85 90 95  
Asp Leu Ile Glu Lys Leu Leu Asn Tyr Asn Thr Leu Glu Lys Thr Glu  
100 105 110  
Thr Ser

(2) INFORMATION FOR SEQ ID NO:3421:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..71
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576802

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3421:

Met Ile Ile Pro Val Arg Cys Phe Thr Cys Gly Lys Val Ile Gly Asn  
1 5 10 15  
Lys Trp Asp Leu Tyr Leu Asp Leu Leu Gln Ala Asp Tyr Ser Glu Gly  
20 25 30  
Asp Ala Leu Asp Ala Leu Glu Leu Phe Arg Tyr Cys Cys Arg Arg Met  
35 40 45  
Leu Met Thr His Val Asp Leu Ile Glu Lys Leu Leu Asn Tyr Asn Thr  
50 55 60  
Leu Glu Lys Thr Glu Thr Ser  
65 70

(2) INFORMATION FOR SEQ ID NO:3422:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 748 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..748
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576803

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3422:

aacttaacca ctactccgca tctactgacg ccgccgccgc cgccgccgcg ctctctccgt 60  
cggactagtc agagcatccg tcatggcgaa gaacccaag gtgttcttcg acatcctcat 120  
cggcaagtcc aaggccgggc gggtcgtgat ggagctcttc gccgacaagg tgcccaagac 180  
ggccgagaac ttccgctgcc tgtgcacggg cgagaagggc ctgggstccg cggggaagcc 240  
gctgcactac aagggtcgg ccttccaccg cgtcatcccg ggcttcatgt gccagggcgg 300  
cgacttcacc cggggcaacg gcacgggcgg cgagtccatc tacggcgcca gggtcgccga 360  
cgagaacttc aagCtgcgcc acacgggacc cggcgtgctc tccatggcca acgcggggcc 420  
cgacaccaac ggctcccagt tcttcatctg caccgcgcag acgccctggc ttgacggcaa 480  
gcacgtcgtc ttccggcaag tcgtcgawgk ctacgccgtc gtggacaaga tggaggctgt 540  
cggttctcag tcaggtgcc cggccgagag cgtacgcata gaggactgcg gccagcttgc 600  
cgacgactga gggcctcgt gtgtccgatt gtaaccaa atgaatgatcaa taaatttctt 660  
tctttcattc ttttgtttct gtggagatgg ataccggcct gtagttaatt aaccaatata 720  
aactatggat ggatggggcg gtgatttg

(2) INFORMATION FOR SEQ ID NO:3423:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..157  
(D) OTHER INFORMATION: / Ceres Seq. ID 1576804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3423:

Asn Leu Thr Thr Thr Pro His Leu Leu Thr Pro Pro Pro Pro Pro Pro  
1 5 10 15  
Arg Ser Leu Arg Arg Thr Ser Gln Ser Ile Arg His Gly Glu Glu Pro  
20 25 30  
Gln Gly Val Leu Arg His Pro His Arg Gln Val Gln Gly Arg Ala Gly  
35 40 45  
Arg Asp Gly Ala Leu Arg Arg Gln Gly Ala Gln Asp Gly Arg Glu Leu  
50 55 60  
Pro Leu Pro Val His Gly Arg Glu Gly Pro Gly Xaa Arg Gly Glu Ala  
65 70 75 80  
Ala Ala Leu Gln Gly Leu Gly Leu Pro Pro Arg His Pro Gly Leu His  
85 90 95  
Val Pro Gly Arg Arg Leu His Pro Gly Gln Arg His Gly Arg Arg Val  
100 105 110  
His Leu Arg Arg Gln Val Arg Arg Glu Leu Gln Ala Ala Pro His  
115 120 125  
Gly Thr Arg Arg Ala Leu His Gly Gln Arg Gly Ala Arg His Gln Arg  
130 135 140  
Leu Pro Val Leu His Leu His Arg Ala Asp Ala Leu Ala  
145 150 155

(2) INFORMATION FOR SEQ ID NO:3424:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 175 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..175  
(D) OTHER INFORMATION: / Ceres Seq. ID 1576805

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3424:

Met Ala Lys Asn Pro Lys Val Phe Phe Asp Ile Leu Ile Gly Lys Ser  
1 5 10 15  
Lys Ala Gly Arg Val Val Met Glu Leu Phe Ala Asp Lys Val Pro Lys  
20 25 30  
Thr Ala Glu Asn Phe Arg Cys Leu Cys Thr Gly Glu Lys Gly Leu Xaa  
35 40 45  
Ser Ala Gly Lys Pro Leu His Tyr Lys Gly Ser Ala Phe His Arg Val  
50 55 60  
Ile Pro Gly Phe Met Cys Gln Gly Gly Asp Phe Thr Arg Gly Asn Gly  
65 70 75 80  
Thr Gly Gly Glu Ser Ile Tyr Gly Ala Arg Phe Ala Asp Glu Asn Phe  
85 90 95  
Lys Leu Arg His Thr Gly Pro Gly Val Leu Ser Met Ala Asn Ala Gly  
100 105 110  
Pro Asp Thr Asn Gly Ser Gln Phe Phe Ile Cys Thr Ala Gln Thr Pro  
115 120 125  
Trp Leu Asp Gly Lys His Val Val Phe Gly Lys Val Val Xaa Xaa Tyr  
130 135 140  
Ala Val Val Asp Lys Met Glu Ala Val Gly Ser Gln Ser Gly Ala Thr  
145 150 155 160  
Ala Glu Ser Val Arg Ile Glu Asp Cys Gly Gln Leu Ala Asp Asp  
165 170 175

(2) INFORMATION FOR SEQ ID NO:3425:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 amino acids

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- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..153
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1576806
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3425:

Met Glu Leu Phe Ala Asp Lys Val Pro Lys Thr Ala Glu Asn Phe Arg  
1 5 10 15  
Cys Leu Cys Thr Gly Glu Lys Gly Leu Xaa Ser Ala Gly Lys Pro Leu  
20 25 30  
His Tyr Lys Gly Ser Ala Phe His Arg Val Ile Pro Gly Phe Met Cys  
35 40 45  
Gln Gly Gly Asp Phe Thr Arg Gly Asn Gly Thr Gly Gly Glu Ser Ile  
50 55 60  
Tyr Gly Ala Arg Phe Ala Asp Glu Asn Phe Lys Leu Arg His Thr Gly  
65 70 75 80  
Pro Gly Val Leu Ser Met Ala Asn Ala Gly Pro Asp Thr Asn Gly Ser  
85 90 95  
Gln Phe Phe Ile Cys Thr Ala Gln Thr Pro Trp Leu Asp Gly Lys His  
100 105 110  
Val Val Phe Gly Lys Val Val Xaa Xaa Tyr Ala Val Val Asp Lys Met  
115 120 125  
Glu Ala Val Gly Ser Gln Ser Gly Ala Thr Ala Glu Ser Val Arg Ile  
130 135 140  
Glu Asp Cys Gly Gln Leu Ala Asp Asp  
145 150

- (2) INFORMATION FOR SEQ ID NO:3426:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 642 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..642
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1576807
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3426:

caattcatcc agacaagtca tatctagcta tagctctccc ttgagaagca tttgarggag 60  
gagccatgtc tgaggagaag caccaccacc acctgtttca ccaccgcaag ccagaggagg 120  
agggcgccctc cggcgagggtc gactacgaga agaaggagaa gcaccacaag cacatggaga 180  
agctcggcga gctcggcgcc atcgccgccg gcgcgtacgc cctgcacgag aagcacaagg 240  
ccaagaagga ccagagaaac gagcacgggc accgggtcaa ggaggagggtg gccgcgctcg 300  
ccgcggtggg ctccgcgggc ttcgctttcc acgagcacca cgagaagaag gacgccaaga 360  
agcacgcccc caactgatcc gtcgcggttg ctgttccatc tgtttttcca gcctcgtctt 420  
cgtctactgt gtgccggcca ggccttgatt tgggctaccg atatttgcat ggacgtagga 480  
actgtgttgg tcggctctcg gcgttcTttg tatcaagatc aaatcaggcc ttgaataagt 540  
gtgtgtgcat atatcttttt ttttaatttt tatctctttt ttttttgtat cgagagatgt 600  
cctgaataat gtgaatttac gtgtgtttat ataaacgaat tt

- (2) INFORMATION FOR SEQ ID NO:3427:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 103 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide



(B) LOCATION: 1..103

(D) OTHER INFORMATION: / Ceres Seq. ID 1576808

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3427:

Met Ser Glu Glu Lys His His His His Leu Phe His His Arg Lys Pro  
1 5 10 15  
Glu Glu Glu Gly Ala Ser Gly Glu Val Asp Tyr Glu Lys Lys Glu Lys  
20 25 30  
His His Lys His Met Glu Lys Leu Gly Glu Leu Gly Ala Ile Ala Ala  
35 40 45  
Gly Ala Tyr Ala Leu His Glu Lys His Lys Ala Lys Lys Asp Pro Glu  
50 55 60  
Asn Glu His Gly His Arg Val Lys Glu Glu Val Ala Ala Val Ala Ala  
65 70 75 80  
Val Gly Ser Ala Gly Phe Ala Phe His Glu His His Glu Lys Lys Asp  
85 90 95  
Ala Lys Lys His Ala His Asn  
100

(2) INFORMATION FOR SEQ ID NO:3428:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 67 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..67

(D) OTHER INFORMATION: / Ceres Seq. ID 1576809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3428:

Met Glu Lys Leu Gly Glu Leu Gly Ala Ile Ala Ala Gly Ala Tyr Ala  
1 5 10 15  
Leu His Glu Lys His Lys Ala Lys Lys Asp Pro Glu Asn Glu His Gly  
20 25 30  
His Arg Val Lys Glu Glu Val Ala Ala Val Ala Ala Val Gly Ser Ala  
35 40 45  
Gly Phe Ala Phe His Glu His His Glu Lys Lys Asp Ala Lys Lys His  
50 55 60  
Ala His Asn  
65

(2) INFORMATION FOR SEQ ID NO:3429:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 722 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..722

(D) OTHER INFORMATION: / Ceres Seq. ID 1576816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3429:

acacaagtca tccgagaagc aagcacaagc accgcaccga acgagcagcg agcgtgttga 60  
ggcaggcagt cagtggcagt gggagtagga gacaaggcta ccgagatgaa gggcctcttg 120  
ttgctcgtcc tcgccctggt cgcgtccgct gcatgcctcg tggccgtNcg cggcgcGggc 180  
gagtgcGggg cgacgccgcc ggacaggatg gcgctgaagc tggcgccgtg Cscgtccgcg 240  
gcgcagaacc ccagctcggc gccgtccaac ggctgctgca cggcggtgca caccatcggg 300  
aagcagagcc ccagtgccct ctgcgccgtc atgctgtcca agaccgcca gaagtccggg 360  
atcaagccc aggtggccat caccatcccc aagcgtgca acctcgtcga ccgccccgtc 420  
ggctacaagt gcggagatta cactctgcca tgastgcgcg agagctgctt gagcacatgt 480  
gcatgatccg tgtcggagtt agcacgacgt ccgcaggaag tgacggtgac gtgtcagtgt 540  
atgtgtgcgt tggttaataaa cgtcgcggca ctccgcactt gttgtgatta ccatacatgt 600

ggaagtccag tatgatatga gtgtctcaca gtcttcaaaa gaaatatggg tcgtatcgta 660  
tgtaagtgtc agggttccag agatgctgtc ctgcatcctc gaaataaaac ttgtcttctt 720  
gg

(2) INFORMATION FOR SEQ ID NO:3430:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..194
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576817

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3430:

Thr Ser His Pro Arg Ser Lys His Lys His Arg Thr Glu Arg Ala Ala  
1 5 10 15  
Ser Val Leu Arg Gln Ala Val Ser Gly Ser Gly Ser Arg Arg Gln Gly  
20 25 30  
Tyr Arg Asp Glu Gly Pro Leu Val Ala Arg Pro Arg Pro Gly Arg Val  
35 40 45  
Arg Cys Met Pro Arg Gly Arg Xaa Arg Arg Gly Arg Val Arg Gly Asp  
50 55 60  
Ala Ala Gly Gln Asp Gly Ala Glu Ala Gly Ala Val Xaa Val Arg Gly  
65 70 75 80  
Ala Glu Pro Gln Leu Gly Ala Val Gln Arg Leu Leu His Gly Gly Ala  
85 90 95  
His His Arg Glu Ala Glu Pro Pro Val Pro Leu Arg Arg His Ala Val  
100 105 110  
Gln Asp Arg Gln Glu Val Arg Asp Gln Ala Arg Gly Gly His His His  
115 120 125  
Pro Gln Ala Leu Gln Pro Arg Arg Pro Pro Arg Arg Leu Gln Val Arg  
130 135 140  
Arg Leu His Ser Ala Met Xaa Ala Arg Glu Leu Leu Glu His Met Cys  
145 150 155 160  
Met Ile Arg Val Gly Val Ser Thr Thr Ser Ala Gly Ser Asp Gly Asp  
165 170 175  
Val Ser Val Tyr Val Cys Val Gly Asn Lys Arg Arg Gly Thr Pro His  
180 185 190  
Leu Leu

(2) INFORMATION FOR SEQ ID NO:3431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..115
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576818

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3431:

Met Lys Gly Leu Leu Leu Val Leu Ala Leu Val Ala Ser Ala Ala  
1 5 10 15  
Cys Leu Val Ala Xaa Arg Gly Ala Gly Glu Cys Gly Ala Thr Pro Pro  
20 25 30  
Asp Arg Met Ala Leu Lys Leu Ala Pro Cys Xaa Ser Ala Ala Gln Asn  
35 40 45  
Pro Ser Ser Ala Pro Ser Asn Gly Cys Cys Thr Ala Val His Thr Ile  
50 55 60

Gly Lys Gln Ser Pro Gln Cys Leu Cys Ala Val Met Leu Ser Lys Thr  
65 70 75 80  
Ala Lys Lys Ser Gly Ile Lys Pro Glu Val Ala Ile Thr Ile Pro Lys  
85 90 95  
Arg Cys Asn Leu Val Asp Arg Pro Val Gly Tyr Lys Cys Gly Asp Tyr  
100 105 110  
Thr Leu Pro  
115

(2) INFORMATION FOR SEQ ID NO:3432:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 144 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..144

(D) OTHER INFORMATION: / Ceres Seq. ID 1576819

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3432:

Met Pro Arg Gly Arg Xaa Arg Arg Gly Arg Val Arg Gly Asp Ala Ala  
1 5 10 15  
Gly Gln Asp Gly Ala Glu Ala Gly Ala Val Xaa Val Arg Gly Ala Glu  
20 25 30  
Pro Gln Leu Gly Ala Val Gln Arg Leu Leu His Gly Gly Ala His His  
35 40 45  
Arg Glu Ala Glu Pro Pro Val Pro Leu Arg Arg His Ala Val Gln Asp  
50 55 60  
Arg Gln Glu Val Arg Asp Gln Ala Arg Gly Gly His His His Pro Gln  
65 70 75 80  
Ala Leu Gln Pro Arg Arg Pro Pro Arg Arg Leu Gln Val Arg Arg Leu  
85 90 95  
His Ser Ala Met Xaa Ala Arg Glu Leu Leu Glu His Met Cys Met Ile  
100 105 110  
Arg Val Gly Val Ser Thr Thr Ser Ala Gly Ser Asp Gly Asp Val Ser  
115 120 125  
Val Tyr Val Cys Val Gly Asn Lys Arg Arg Gly Thr Pro His Leu Leu  
130 135 140

(2) INFORMATION FOR SEQ ID NO:3433:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 702 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..702

(D) OTHER INFORMATION: / Ceres Seq. ID 1576842

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3433:

ttcagttggc agttgcgact tgcgagtggc tccaacaagg caacacaatc caccggcacc 60  
aaccacagcg gcgcccaccg gcgaccgcta ccccttccc cggagagcga tggcgacgga 120  
gctgacggcg gcgcaactgc cgcgtacgac ggcaccgacc cgtccaagcc catctacgtc 180  
tccgtccggg gcaaggtcta cgacgtcaacc tccggccgCc ggctttctaag gccNccggcg 240  
gcgcctacgc cgtcttcgcg ggcccgcgagg Ccagccgcgc cctcggcaag atgtccaagg 300  
acgaggccga cgtctccggg gacctctccg ggctcaccga caaggagctc ggcgtcctcg 360  
ccgactggga gaccaagttc caGggccaag taccocgctg tcgcccgact cgccgccgac 420  
gcctgaactc ggcagtctcg gtgtaaattt actctgtcct gcctcttgcg gtgttcagtg 480  
ttgtgcttgc ttgcttgttg ctagtgtgctt tgctaSccca ataatctgaa tGggaaggac 540

gtatgtgatg tgcctgctga atagctcgag ctccctagtc ttgcatacac tgctgtgcta 600  
ccacatgaca tgatgtactc gtgtgtgctt tgggtgttgt gtaattccat gaccatgatc 660  
agtaatctga ataaaaaata ttggagatgt gcttgcttcc tg

(2) INFORMATION FOR SEQ ID NO:3434:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..141
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576843

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3434:

Phe	Ser	Trp	Gln	Leu	Arg	Leu	Ala	Ser	Gly	Ser	Asn	Lys	Ala	Thr	Gln	
1			5						10					15		
Ser	Thr	Gly	Thr	Asn	Pro	Ala	Arg	Arg	His	Arg	Arg	Pro	Val	Pro	Pro	
		20						25					30			
Ser	Pro	Glu	Ser	Asp	Gly	Asp	Gly	Ala	Asp	Gly	Gly	Ala	Leu	Arg	Ala	
		35				40						45				
Tyr	Asp	Gly	Thr	Asp	Pro	Ser	Lys	Pro	Ile	Tyr	Val	Ser	Val	Arg	Gly	
	50					55					60					
Lys	Val	Tyr	Asp	Val	Thr	Ser	Gly	Arg	Arg	Leu	Leu	Arg	Xaa	Pro	Ala	
65					70					75				80		
Ala	Pro	Thr	Pro	Ser	Ser	Arg	Ala	Ala	Arg	Pro	Ala	Ala	Pro	Ser	Ala	
				85					90					95		
Arg	Cys	Pro	Arg	Thr	Arg	Pro	Thr	Ser	Pro	Gly	Thr	Ser	Pro	Gly	Ser	
		100						105					110			
Pro	Thr	Arg	Ser	Ser	Ala	Ser	Ser	Pro	Thr	Gly	Arg	Pro	Ser	Ser	Arg	
		115					120					125				
Ala	Lys	Tyr	Pro	Val	Val	Ala	Arg	Leu	Ala	Ala	Asp	Ala				
	130					135					140					

(2) INFORMATION FOR SEQ ID NO:3435:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..175
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576844

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3435:

Ser	Val	Gly	Ser	Cys	Asp	Leu	Arg	Val	Ala	Pro	Thr	Arg	Gln	His	Asn	
1				5					10					15		
Pro	Pro	Ala	Pro	Thr	Gln	Arg	Gly	Ala	Thr	Gly	Asp	Pro	Tyr	Pro	Leu	
		20						25					30			
Pro	Arg	Arg	Ala	Met	Ala	Thr	Glu	Leu	Thr	Ala	Ala	His	Cys	Ala	Arg	
		35					40					45				
Thr	Thr	Ala	Pro	Thr	Arg	Pro	Ser	Pro	Ser	Thr	Ser	Pro	Ser	Gly	Ala	
	50					55					60					
Arg	Ser	Thr	Thr	Ser	Pro	Pro	Ala	Ala	Gly	Phe	Tyr	Gly	Xaa	Arg	Arg	
65					70					75				80		
Arg	Leu	Arg	Arg	Leu	Arg	Gly	Pro	Arg	Gly	Gln	Pro	Arg	Pro	Arg	Gln	
				85					90					95		
Asp	Val	Gln	Gly	Arg	Gly	Arg	Arg	Leu	Arg	Gly	Pro	Leu	Arg	Ala	His	
		100						105				110				
Arg	Gln	Gly	Ala	Arg	Arg	Pro	Arg	Arg	Leu	Gly	Asp	Gln	Val	Pro	Gly	
		115					120					125				

Pro Ser Thr Pro Ser Ser Pro Asp Ser Pro Pro Thr Pro Glu Leu Gly  
130 135 140  
Ser Leu Gly Val Asn Leu Leu Cys Pro Ala Ser Cys Gly Val Gln Cys  
145 150 155 160  
Cys Ala Cys Leu Leu Val Ala Ser Cys Phe Ala Xaa Pro Ile Ile  
165 170 175

(2) INFORMATION FOR SEQ ID NO:3436:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..139

(D) OTHER INFORMATION: / Ceres Seq. ID 1576845

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3436:

Met Ala Thr Glu Leu Thr Ala Ala His Cys Ala Arg Thr Thr Ala Pro  
1 5 10 15  
Thr Arg Pro Ser Pro Ser Thr Ser Pro Ser Gly Ala Arg Ser Thr Thr  
20 25 30  
Ser Pro Pro Ala Ala Gly Phe Tyr Gly Xaa Arg Arg Arg Leu Arg Arg  
35 40 45  
Leu Arg Gly Pro Arg Gly Gln Pro Arg Pro Arg Gln Asp Val Gln Gly  
50 55 60  
Arg Gly Arg Arg Leu Arg Gly Pro Leu Arg Ala His Arg Gln Gly Ala  
65 70 75 80  
Arg Arg Pro Arg Arg Leu Gly Asp Gln Val Pro Gly Pro Ser Thr Pro  
85 90 95  
Ser Ser Pro Asp Ser Pro Pro Thr Pro Glu Leu Gly Ser Leu Gly Val  
100 105 110  
Asn Leu Leu Cys Pro Ala Ser Cys Gly Val Gln Cys Cys Ala Cys Leu  
115 120 125  
Leu Val Ala Ser Cys Phe Ala Xaa Pro Ile Ile  
130 135

(2) INFORMATION FOR SEQ ID NO:3437:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 828 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..828

(D) OTHER INFORMATION: / Ceres Seq. ID 1576855

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3437:

acggttggtc cacctcctcc tgctcctctg gcctctgagg tgctcctcc cgggtcccag 60  
tcccggccat gtcgtcgccg ctggaggatg tcagcgtggg catggaggag gaggatcagc 120  
ggcccctgaa ccgggccctg ctccaccgga ggcgccaccac caacgcctcc cagggtggcca 180  
tggtcggtc caatccctgc cctatcgaga gcctcgacta cgagatgata gagaacgagc 240  
tggtcgacca gaactggagg acgaggcgca aggcggacca ggtgcggtac gtggtgctca 300  
agtggacctt ctgCttcgcc atcggcatcc tcaccgggat cgtcggttc ttcacacacc 360  
tcgccgtcga gaacgtcgcg ggcttcaagc accaggccgt ttccgCccct catggactcc 420  
gccagctact ggacggcggt ctgggtgttc gccggctgca acctggcgct cctgctgctg 480  
gcgtcgacca tcacggcggt cttgtcgccg gcggccggcg ggtcggaat cccggaggtc 540  
aaggcctacc tcaacggcgt cgacgcgcc aacatcttct cgctcgcgac cctcgctgtc 600  
aagggtcgcc gtgtgtgttc cgttcccatt ctctgccct cgccgnygt ttcgcttgc 660  
gcagtgcaca tgctcccctc accatttcct ggtgccastg cgcaaattga ttaccatcca 720  
cactaatata atgtaacaag ggcattcatt cctccatcca actgcatgat ctacgagaaa 780

ggaaagcaac cagcaagtaa ataaacaatc ataattagac ttttctkg

(2) INFORMATION FOR SEQ ID NO:3438:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 244 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..244

(D) OTHER INFORMATION: / Ceres Seq. ID 1576856

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3438:

Arg Leu Val His Leu Leu Leu Leu Leu Trp Pro Leu Arg Cys Leu Leu  
1 5 10 15  
Pro Val Pro Ser Pro Gly His Val Val Ala Ala Gly Gly Cys Gln Arg  
20 25 30  
Gly His Gly Gly Gly Gly Ser Ala Ala Pro Glu Pro Gly Pro Ala Pro  
35 40 45  
Pro Glu Arg His His Gln Arg Leu Pro Gly Gly His Gly Arg Leu Gln  
50 55 60  
Ser Leu Pro Tyr Arg Glu Pro Arg Leu Arg Asp Asp Arg Glu Arg Ala  
65 70 75 80  
Val Arg Pro Glu Leu Glu Asp Glu Ala Gln Gly Gly Pro Gly Ala Val  
85 90 95  
Arg Gly Ala Gln Val Asp Leu Leu Leu Arg His Arg His Pro His Arg  
100 105 110  
Asp Arg Arg Leu Leu His Gln Pro Arg Arg Arg Glu Arg Arg Gly Leu  
115 120 125  
Gln Ala Pro Gly Arg Phe Arg Pro Ser Trp Thr Pro Pro Ala Thr Gly  
130 135 140  
Arg Arg Ser Gly Cys Ser Pro Ala Ala Thr Trp Arg Ser Cys Cys Trp  
145 150 155 160  
Arg Arg Pro Ser Arg Arg Ser Cys Arg Arg Arg Pro Ala Gly Arg Glu  
165 170 175  
Ser Arg Arg Ser Arg Pro Thr Ser Thr Ala Ser Thr Arg Pro Thr Ser  
180 185 190  
Ser Arg Cys Gly Pro Ser Leu Ser Arg Cys Ala Val Cys Val Pro Phe  
195 200 205  
Pro Ser Ser Cys Pro Arg Xaa Xaa Phe Arg Leu Leu Gln Cys Thr Cys  
210 215 220  
Ser Pro His His Phe Leu Val Pro Xaa Arg Lys Trp Ile Thr Ile His  
225 230 235 240  
Thr Asn Ile Met

(2) INFORMATION FOR SEQ ID NO:3439:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 242 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..242

(D) OTHER INFORMATION: / Ceres Seq. ID 1576857

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3439:

Gly Trp Ser Thr Ser Ser Cys Ser Ser Gly Leu Cys Gly Ala Ser Ser  
1 5 10 15  
Arg Ser Arg Val Pro Ala Met Ser Ser Pro Leu Glu Asp Val Ser Val  
20 25 30

Gly Met Glu Glu Glu Asp Gln Arg Pro Leu Asn Arg Ala Leu Leu His  
35 40 45  
Arg Ser Ala Thr Thr Asn Ala Ser Gln Val Ala Met Val Gly Ser Asn  
50 55 60  
Pro Cys Pro Ile Glu Ser Leu Asp Tyr Glu Met Ile Glu Asn Glu Leu  
65 70 75 80  
Phe Asp Gln Asn Trp Arg Thr Arg Arg Lys Ala Asp Gln Val Arg Tyr  
85 90 95  
Val Val Leu Lys Trp Thr Phe Cys Phe Ala Ile Gly Ile Leu Thr Gly  
100 105 110  
Ile Val Gly Phe Phe Ile Asn Leu Ala Val Glu Asn Val Ala Gly Phe  
115 120 125  
Lys His Gln Ala Val Ser Ala Pro His Gly Leu Arg Gln Leu Leu Asp  
130 135 140  
Gly Val Leu Gly Val Arg Arg Leu Gln Pro Gly Ala Pro Ala Ala Gly  
145 150 155 160  
Val Val His His Gly Val Leu Val Ala Gly Gly Arg Arg Val Gly Asn  
165 170 175  
Pro Gly Gly Gln Gly Leu Pro Gln Arg Arg Arg Arg Ala Gln His Leu  
180 185 190  
Leu Ala Ala Asp Pro Arg Cys Gln Gly Ala Pro Cys Val Phe Arg Ser  
195 200 205  
His Pro Pro Ala Leu Ala Xaa Ala Phe Ala Cys Cys Ser Ala His Ala  
210 215 220  
Pro Leu Thr Ile Ser Trp Cys Xaa Cys Ala Asn Gly Leu Pro Ser Thr  
225 230 235 240  
Leu Ile

(2) INFORMATION FOR SEQ ID NO:3440:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 220 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..220

(D) OTHER INFORMATION: / Ceres Seq. ID 1576858

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3440:

Met Ser Ser Pro Leu Glu Asp Val Ser Val Gly Met Glu Glu Glu Asp  
1 5 10 15  
Gln Arg Pro Leu Asn Arg Ala Leu Leu His Arg Ser Ala Thr Thr Asn  
20 25 30  
Ala Ser Gln Val Ala Met Val Gly Ser Asn Pro Cys Pro Ile Glu Ser  
35 40 45  
Leu Asp Tyr Glu Met Ile Glu Asn Glu Leu Phe Asp Gln Asn Trp Arg  
50 55 60  
Thr Arg Arg Lys Ala Asp Gln Val Arg Tyr Val Val Leu Lys Trp Thr  
65 70 75 80  
Phe Cys Phe Ala Ile Gly Ile Leu Thr Gly Ile Val Gly Phe Phe Ile  
85 90 95  
Asn Leu Ala Val Glu Asn Val Ala Gly Phe Lys His Gln Ala Val Ser  
100 105 110  
Ala Pro His Gly Leu Arg Gln Leu Leu Asp Gly Val Leu Gly Val Arg  
115 120 125  
Arg Leu Gln Pro Gly Ala Pro Ala Ala Gly Val Val His His Gly Val  
130 135 140  
Leu Val Ala Gly Gly Arg Arg Val Gly Asn Pro Gly Gly Gln Gly Leu  
145 150 155 160  
Pro Gln Arg Arg Arg Arg Ala Gln His Leu Leu Ala Ala Asp Pro Arg

165 170 175  
Cys Gln Gly Ala Pro Cys Val Phe Arg Ser His Pro Pro Ala Leu Ala  
180 185 190  
Xaa Ala Phe Ala Cys Cys Ser Ala His Ala Pro Leu Thr Ile Ser Trp  
195 200 205  
Cys Xaa Cys Ala Asn Gly Leu Pro Ser Thr Leu Ile  
210 215 220

(2) INFORMATION FOR SEQ ID NO:3441:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 955 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..955  
(D) OTHER INFORMATION: / Ceres Seq. ID 1576876

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3441:

aagcgtcagg gcctctcgat cgctcatcag tcgccagagg agtagttgat cgaggtgagt 60  
gaggttgaaa agcaggcggc gaacaaaggc accatcgta tggacggcgg atactacggc 120  
ggccgcgata agcgctacac cngcgggtac tacggcggcg gtggcatcgc gacgccgggg 180  
tacgctccgg cggtcccgtc cgggatgtcg caggtgaaca tcgadggcha cgggtgcngg 240  
cdggcrtgc cgccgcagcc gaccgtgaag gtgtactgcc gcgccaaccc caactacgcc 300  
atgarcgtcc gckacgggaa ggtrgtgctg gcgcccgcga accccaagga cgagtaccag 360  
cactggatca aggacatgcn gtggagcacg agcatcaagg acgakaagg ttaccggcg 420  
ttcgcrctgg tgaacaargc gaccggggag gccatcaagR cactcgctGg gggcagtc 480  
acccgggtgcg cctgggtgcc tacaacccgg actttttgga cgagtcgggtg ctgtggacgg 540  
agagccgcga cgtcggcaac ggcttccgct gcgtccgcat ggtcaacaac atctacctca 600  
acttcgacgc cctccacggc gacaagtggc acggcggcgt ccgtgacggc accgacgtcg 660  
tgctctggaa gtgggtgcgag ggcgacaacc agcgtggaa gatccagccc tactactgaa 720  
ccaacggatg atatgacat cgcgcccatc gatcgtgcac atgcatgcat acgtactagc 780  
agaataacag gggctcttat tcccgaggcg tcttttgcac gcatgccagc agttgcatag 840  
ataaagcagg agcgagacaa aggggtgttca tgtatatgtc agctgtatca ctgtatgtat 900  
gtgccattgt gccttgtaat aatacatata ataataaagt tgctcggagt gtatt

(2) INFORMATION FOR SEQ ID NO:3442:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..246  
(D) OTHER INFORMATION: / Ceres Seq. ID 1576877

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3442:

Met Asp Gly Gly Tyr Gly Gly Arg Asp Gln Arg Tyr Xaa Xaa Gly  
1 5 10 15  
Tyr Tyr Gly Gly Gly Gly Ile Ala Thr Pro Gly Tyr Ala Pro Ala Val  
20 25 30  
Pro Tyr Gly Met Ser Gln Val Asn Ile Xaa Gly Xaa Gly Cys Xaa Xaa  
35 40 45  
Xaa Leu Pro Pro Gln Pro Thr Val Lys Val Tyr Cys Arg Ala Asn Pro  
50 55 60  
Asn Tyr Ala Met Xaa Val Arg Xaa Gly Lys Xaa Val Leu Ala Pro Ala  
65 70 75 80  
Asn Pro Lys Asp Glu Tyr Gln His Trp Ile Lys Asp Met Xaa Trp Ser  
85 90 95  
Thr Ser Ile Lys Asp Xaa Glu Gly Tyr Pro Ala Phe Xaa Leu Val Asn  
100 105 110



Xaa Ala Thr Gly Glu Ala Ile Lys Xaa Leu Ala Gly Gly Ser Pro Thr  
115 120 125  
Arg Cys Ala Trp Cys Pro Thr Thr Arg Thr Phe Trp Thr Ser Arg Cys  
130 135 140  
Cys Gly Arg Arg Ala Ala Thr Ser Ala Thr Ala Ser Ala Ala Ser Ala  
145 150 155 160  
Trp Ser Thr Thr Ser Thr Ser Thr Ser Thr Pro Ser Thr Ala Thr Ser  
165 170 175  
Gly Thr Ala Ala Ser Val Thr Ala Pro Thr Ser Cys Ser Gly Ser Gly  
180 185 190  
Ala Arg Ala Thr Thr Ser Ala Gly Arg Ser Ser Pro Thr Thr Glu Pro  
195 200 205  
Thr Asp Asp Met Thr Ile Ala Pro Ile Asp Arg Ala His Ala Cys Ile  
210 215 220  
Arg Thr Ser Arg Ile Thr Gly Val Leu Ser Pro Glu Ala Ser Phe Ala  
225 230 235 240  
Cys Met Pro Ala Val Ala  
245

(2) INFORMATION FOR SEQ ID NO:3443:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 211 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..211

(D) OTHER INFORMATION: / Ceres Seq. ID 1576878

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3443:

Met Ser Gln Val Asn Ile Xaa Gly Xaa Gly Cys Xaa Xaa Xaa Leu Pro  
1 5 10 15  
Pro Gln Pro Thr Val Lys Val Tyr Cys Arg Ala Asn Pro Asn Tyr Ala  
20 25 30  
Met Xaa Val Arg Xaa Gly Lys Xaa Val Leu Ala Pro Ala Asn Pro Lys  
35 40 45  
Asp Glu Tyr Gln His Trp Ile Lys Asp Met Xaa Trp Ser Thr Ser Ile  
50 55 60  
Lys Asp Xaa Glu Gly Tyr Pro Ala Phe Xaa Leu Val Asn Xaa Ala Thr  
65 70 75 80  
Gly Glu Ala Ile Lys Xaa Leu Ala Gly Gly Ser Pro Thr Arg Cys Ala  
85 90 95  
Trp Cys Pro Thr Thr Arg Thr Phe Trp Thr Ser Arg Cys Cys Gly Arg  
100 105 110  
Arg Ala Ala Thr Ser Ala Thr Ala Ser Ala Ala Ser Ala Trp Ser Thr  
115 120 125  
Thr Ser Thr Ser Thr Ser Thr Pro Ser Thr Ala Thr Ser Gly Thr Ala  
130 135 140  
Ala Ser Val Thr Ala Pro Thr Ser Cys Ser Gly Ser Gly Ala Arg Ala  
145 150 155 160  
Thr Thr Ser Ala Gly Arg Ser Ser Pro Thr Thr Glu Pro Thr Asp Asp  
165 170 175  
Met Thr Ile Ala Pro Ile Asp Arg Ala His Ala Cys Ile Arg Thr Ser  
180 185 190  
Arg Ile Thr Gly Val Leu Ser Pro Glu Ala Ser Phe Ala Cys Met Pro  
195 200 205  
Ala Val Ala  
210

(2) INFORMATION FOR SEQ ID NO:3444:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 179 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..179
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1576879
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3444:

Met Xaa Val Arg Xaa Gly Lys Xaa Val Leu Ala Pro Ala Asn Pro Lys  
1 5 10 15  
Asp Glu Tyr Gln His Trp Ile Lys Asp Met Xaa Trp Ser Thr Ser Ile  
20 25 30  
Lys Asp Xaa Glu Gly Tyr Pro Ala Phe Xaa Leu Val Asn Xaa Ala Thr  
35 40 45  
Gly Glu Ala Ile Lys Xaa Leu Ala Gly Gly Ser Pro Thr Arg Cys Ala  
50 55 60  
Trp Cys Pro Thr Thr Arg Thr Phe Trp Thr Ser Arg Cys Cys Gly Arg  
65 70 75 80  
Arg Ala Ala Thr Ser Ala Thr Ala Ser Ala Ser Ala Trp Ser Thr  
85 90 95  
Thr Ser Thr Ser Thr Ser Thr Pro Ser Thr Ala Thr Ser Gly Thr Ala  
100 105 110  
Ala Ser Val Thr Ala Pro Thr Ser Cys Ser Gly Ser Gly Ala Arg Ala  
115 120 125  
Thr Thr Ser Ala Gly Arg Ser Ser Pro Thr Thr Glu Pro Thr Asp Asp  
130 135 140  
Met Thr Ile Ala Pro Ile Asp Arg Ala His Ala Cys Ile Arg Thr Ser  
145 150 155 160  
Arg Ile Thr Gly Val Leu Ser Pro Glu Ala Ser Phe Ala Cys Met Pro  
165 170 175  
Ala Val Ala

- (2) INFORMATION FOR SEQ ID NO:3445:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 727 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..727
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1576888
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3445:

cttgctcgct gcgcgcgcgc ctccgacatc gtcccttctgt cccacgagc aaccgataat 60  
ccgcggcggt tgagatgttg gtttatcagg atctctatc tggcgacgag ctctgtcggt 120  
attCcatcA acctacaagg agctcgagaa cGggcgctct gtgggaggtc gagggaaagt 180  
gggtcaccca aggtctgtt gatgtggaca ttggtgccaa tccatccgcc gaggggtggtg 240  
aggacgaaag cgttgatgac acagctgtga aggtggttga tattgttgac acattccgtc 300  
tacaggagca acctcctttt gacaagaaat catttgtgtc ttacatcaaa aaatacatca 360  
agaatctcac tgctgtgttg gagccagaga aagcggatga gttcaaaaag ggtgtcgagg 420  
gtgcaaccaa gtttctcctt agcaagctga aggacctcca attttttGgt tgggtgagtc 480  
atgaaggatg atgcgtctgt ggtattcgcc tattacaagg atggtgccac taatccgaca 540  
ttcctctatt tctctcatgg tcttaaggag atcaagtgtc aggcgtgcgg cgaaattagt 600  
taccatggtt gggtactatc tatgtactat tattatatcc aaaactatag ttgtcctggc 660  
tgaattgaac tcaaaagggt ttgtttgaga aaaaattgtc ccaagattgg attgcttgtt 720  
aaagccc

- (2) INFORMATION FOR SEQ ID NO:3446:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 89 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..89
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1576889

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3446:

Leu Ala Arg Cys Ala Ala Ala Ser Asp Ile Val Pro Ser Ser Pro Arg  
1 5 10 15  
Ala Thr Asp Asn Pro Pro Ala Leu Arg Cys Trp Phe Ile Arg Ile Ser  
20 25 30  
Tyr Leu Ala Thr Ser Ser Cys Arg Ile Pro Phe Asn Leu Gln Gly Ala  
35 40 45  
Arg Glu Arg Ala Ser Cys Gly Arg Ser Arg Glu Ser Gly Ser Pro Lys  
50 55 60  
Val Leu Leu Met Trp Thr Leu Val Pro Ile His Pro Pro Arg Val Val  
65 70 75 80  
Arg Thr Lys Ala Leu Met Thr Gln Leu  
85

(2) INFORMATION FOR SEQ ID NO:3447:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 133 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..133
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1576890

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3447:

Met Leu Val Tyr Gln Asp Leu Leu Ser Gly Asp Glu Leu Leu Ser Asp  
1 5 10 15  
Ser Ile Gln Pro Thr Arg Ser Ser Arg Thr Gly Val Leu Trp Glu Val  
20 25 30  
Glu Gly Lys Trp Val Thr Gln Gly Pro Val Asp Val Asp Ile Gly Ala  
35 40 45  
Asn Pro Ser Ala Glu Gly Gly Glu Asp Glu Ser Val Asp Asp Thr Ala  
50 55 60  
Val Lys Val Val Asp Ile Val Asp Thr Phe Arg Leu Gln Glu Gln Pro  
65 70 75 80  
Pro Phe Asp Lys Lys Ser Phe Val Ser Tyr Ile Lys Lys Tyr Ile Lys  
85 90 95  
Asn Leu Thr Ala Val Leu Glu Pro Glu Lys Ala Asp Glu Phe Lys Lys  
100 105 110  
Gly Val Glu Gly Ala Thr Lys Phe Leu Leu Ser Lys Leu Lys Asp Leu  
115 120 125  
Gln Phe Phe Gly Trp  
130

(2) INFORMATION FOR SEQ ID NO:3448:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 66 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..66

(D) OTHER INFORMATION: / Ceres Seq. ID 1576891

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3448:

Met Met Arg Leu Trp Tyr Ser Pro Ile Thr Arg Met Val Pro Leu Ile  
1 5 10 15  
Arg His Ser Ser Ile Ser Leu Met Val Leu Arg Arg Ser Ser Ala Arg  
20 25 30  
Arg Ala Ala Lys Leu Val Thr His Val Gly Tyr Tyr Leu Cys Thr Ile  
35 40 45  
Ile Ile Ser Lys Thr Ile Val Val Leu Ala Glu Leu Asn Ser Lys Gly  
50 55 60  
Phe Val  
65

(2) INFORMATION FOR SEQ ID NO:3449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 663 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..663

(D) OTHER INFORMATION: / Ceres Seq. ID 1576896

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3449:

aaacaccgcc gaagaancca gccaacctt cagcacccgc atttcccaag ggaaccatac 60  
cagagcggca gaggcttccc ctccgctccc cagtcccacc cgcaccctag ccctcagcaa 120  
accctaaccg ctcgctcgcca tgaaggacac ctcgttcaag gccaccggCg ccaagcgcaa 180  
gaaggtcggc ggcGccaagc gcgggctcac ccccttcttc gcgttttttg ctgagtttag 240  
gccgcagtac ctggagaagc accctgagct caagggcgta aaggaggtga gcaaggcggc 300  
tggggagaag tggcgctcta tgtcggtatga ggagaaggcg aagtatggca gtagcaagaa 360  
gcaggatggc aaagcaagca agaaggagaa cactagctcc aagaaggcca aagctgatat 420  
tcgggagggg gatgaagcag aaggttctaa caagtcaaaa tctgaggttg aggatgatga 480  
gcaggatggt aatgaggatg aggatgagta aatagtacga tggggaacag cagctttgca 540  
tttgagtgtt tgctgcttta cttatttttc tatatgctgt tccttttgat gttatatgct 600  
gtaaggaaaa tctgtacatg atggtacctt aggggtatggc atgctggagt tcccctttaa 660  
ccc

(2) INFORMATION FOR SEQ ID NO:3450:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..77

(D) OTHER INFORMATION: / Ceres Seq. ID 1576897

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3450:

Lys His Arg Arg Arg Xaa Gln Pro Asn Leu His Ala Pro His Phe Pro  
1 5 10 15  
Arg Glu Pro Tyr Gln Ser Gly Arg Ala Phe Pro Ser Ala Pro Gln Ser  
20 25 30  
His Pro His Pro Ser Pro Gln Gln Thr Leu Thr Ala Arg His Glu  
35 40 45  
Gly His Leu Val Gln Gly His Arg Arg Gln Ala Gln Glu Gly Arg Arg  
50 55 60  
Arg Gln Ala Arg Ala His Pro Leu Leu Arg Val Phe Gly  
65 70 75

(2) INFORMATION FOR SEQ ID NO:3451:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids

- (B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..123  
(D) OTHER INFORMATION: / Ceres Seq. ID 1576898  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3451:

Met Lys Asp Thr Ser Phe Lys Ala Thr Gly Ala Lys Arg Lys Lys Val  
1 5 10 15  
Gly Gly Ala Lys Arg Gly Leu Thr Pro Phe Phe Ala Phe Leu Ala Glu  
20 25 30  
Phe Arg Pro Gln Tyr Leu Glu Lys His Pro Glu Leu Lys Gly Val Lys  
35 40 45  
Glu Val Ser Lys Ala Ala Gly Glu Lys Trp Arg Ser Met Ser Asp Glu  
50 55 60  
Glu Lys Ala Lys Tyr Gly Ser Ser Lys Lys Gln Asp Gly Lys Ala Ser  
65 70 75 80  
Lys Lys Glu Asn Thr Ser Ser Lys Lys Ala Lys Ala Asp Ile Arg Glu  
85 90 95  
Gly Asp Glu Ala Glu Gly Ser Asn Lys Ser Lys Ser Glu Val Glu Asp  
100 105 110  
Asp Glu Gln Asp Gly Asn Glu Asp Glu Asp Glu  
115 120

(2) INFORMATION FOR SEQ ID NO:3452:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 63 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..63  
(D) OTHER INFORMATION: / Ceres Seq. ID 1576899

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3452:

Met Ser Asp Glu Lys Lys Ala Lys Tyr Gly Ser Ser Lys Lys Gln Asp  
1 5 10 15  
Gly Lys Ala Ser Lys Lys Glu Asn Thr Ser Ser Lys Lys Ala Lys Ala  
20 25 30  
Asp Ile Arg Glu Gly Asp Glu Ala Glu Gly Ser Asn Lys Ser Lys Ser  
35 40 45  
Glu Val Glu Asp Asp Glu Gln Asp Gly Asn Glu Asp Glu Asp Glu  
50 55 60

(2) INFORMATION FOR SEQ ID NO:3453:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 829 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..829  
(D) OTHER INFORMATION: / Ceres Seq. ID 1576923

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3453:

aaactctttt cttcaccaga cgtccagacc tgctcacggc ctcccaaact cgcgcgccgc 60  
cctgcttcca gtctcccctg gcaatctcgc ccttgcaaac cctagccgct gccatggcat 120  
atctagctcc cgcgaccgcc gcctcttccc tccgcacccc catctacgta gccgcctctt 180  
cccggcgccg ttcttttttc cctgcccgcg tcaaagccat cgccagttct gcacatccca 240

```
tctctctctc cctccgcatg gccgcctccg ccgcccgttct cttcgcgcgc acctccccgg 300
cactcgcgtg caccctctcc gttcctccgc ccccgcctcac tctcttgaca gtcacgggtgt 360
cccacgacga cgccatccta gacgcctccc gactcttcga gaagctgata atcgagactg 420
cctgchtcgA scgcgtcggc cgcgcggacg aagcgcgctc gcgcctgtcc acagccggat 480
gtggagagaG ctacgcccgc ctccatagccg ctcaggttct gttcgtggac gggaagttgg 540
acgaggcgat cgcagcattc gaggagcttg cgcgggagga ccccgccgac tatcgccctc 600
tgttctgcca gggcgtgctg tacctcgccc ttggaaggga ggcggaatca gagtccatgc 660
tcgagcgatg ccgcgaggtc ggcgcgacg cgctaactgt agatccgtca ctgatgataa 720
cgccgaccgt ggagacggaa ttcgatggg agaagccgga gccggcgaag gtttgacctg 780
taactctgca gcgatgatc tcagaataag gtaacactgg catttttgt
```

(2) INFORMATION FOR SEQ ID NO:3454:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..270

(D) OTHER INFORMATION: / Ceres Seq. ID 1576924

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3454:

```
Asn Ser Phe Leu His Gln Thr Ser Arg Pro Ala His Gly Leu Pro Asn
1      5      10      15
Ser Ala Ala Ala Leu Leu Pro Val Ser Pro Gly Asn Leu Arg Leu Ala
20      25      30
Asn Pro Ser Arg Cys His Gly Ile Ser Ser Ser Arg Asp Arg Arg Leu
35      40      45
Phe Pro Pro His Pro His Leu Arg Ser Arg Leu Phe Pro Ala Pro Phe
50      55      60
Leu Ser Pro Cys Arg Arg Gln Ser His Arg Gln Phe Cys Thr Ser His
65      70      75      80
Pro Leu Leu Pro Pro His Gly Arg Leu Arg Arg Arg Ser Leu Arg Arg
85      90      95
His Leu Pro Gly Thr Arg Val His Pro Leu Arg Ser Ser Ala Pro Ala
100     105     110
His Ser Ser Asp Ser His Gly Val Pro Arg Arg Arg His Pro Arg Arg
115     120     125
Leu Pro Thr Leu Arg Glu Ala Asp Asn Arg Asp Cys Leu Xaa Arg Xaa
130     135     140
Arg Arg Pro Arg Gly Arg Ser Ala Leu Ala Pro Val His Ser Arg Met
145     150     155     160
Trp Arg Glu Leu Arg Pro Pro Pro Ser Arg Ser Gly Ser Val Arg Gly
165     170     175
Arg Glu Val Gly Arg Gly Asp Arg Ser Ile Arg Gly Ala Cys Ala Gly
180     185     190
Gly Pro Arg Arg Leu Ser Pro Ser Val Leu Pro Gly Arg Ala Val Pro
195     200     205
Arg Pro Trp Lys Gly Gly Gly Ile Arg Val His Ala Arg Ala Met Pro
210     215     220
Arg Gly Arg Arg Arg Arg Ala Asn Arg Arg Ser Val Thr Asp Asp Asn
225     230     235     240
Ala Asp Arg Gly Asp Gly Ile Arg Trp Gly Glu Ala Gly Ala Gly Glu
245     250     255
Gly Leu Thr Cys Asn Ser Ala Ala Asp Asp Leu Arg Ile Arg
260     265     270
```

(2) INFORMATION FOR SEQ ID NO:3455:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

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- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..257  
(D) OTHER INFORMATION: / Ceres Seq. ID 1576925  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3455:

Thr Leu Phe Phe Thr Arg Arg Pro Asp Leu Leu Thr Ala Ser Gln Thr  
1                   5                   10                   15  
Pro Pro Pro Pro Cys Phe Gln Ser Pro Leu Ala Ile Ser Ala Leu Gln  
                  20                   25                   30  
Thr Leu Ala Ala Ala Met Ala Tyr Leu Ala Pro Ala Thr Ala Ala Ser  
                  35                   40                   45  
Ser Leu Arg Thr Pro Ile Tyr Val Ala Ala Ser Ser Arg Arg Arg Ser  
50                   55                   60  
Phe Leu Pro Ala Ala Val Lys Ala Ile Ala Ser Ser Ala His Pro Ile  
65                   70                   75                   80  
Leu Ser Ser Leu Arg Met Ala Ala Ser Ala Ala Val Leu Phe Ala Ala  
                  85                   90                   95  
Thr Ser Pro Ala Leu Ala Cys Thr Pro Ser Val Pro Pro Pro Leu  
                  100                   105                   110  
Thr Pro Leu Thr Val Thr Val Ser His Asp Asp Ala Ile Leu Asp Ala  
115                   120                   125  
Ser Arg Leu Phe Glu Lys Leu Ile Ile Glu Thr Ala Cys Xaa Xaa Arg  
130                   135                   140  
Val Gly Arg Ala Asp Glu Ala Arg Ser Arg Leu Ser Thr Ala Gly Cys  
145                   150                   155                   160  
Gly Glu Ser Tyr Ala Arg Leu Leu Ala Ala Gln Val Leu Phe Val Asp  
                  165                   170                   175  
Gly Lys Leu Asp Glu Ala Ile Ala Ala Phe Glu Glu Leu Ala Arg Glu  
                  180                   185                   190  
Asp Pro Ala Asp Tyr Arg Pro Leu Phe Cys Gln Gly Val Leu Tyr Leu  
195                   200                   205  
Ala Leu Gly Arg Glu Ala Glu Ser Glu Ser Met Leu Glu Arg Cys Arg  
210                   215                   220  
Glu Val Gly Gly Asp Ala Leu Ile Val Asp Pro Ser Leu Met Ile Thr  
225                   230                   235                   240  
Pro Thr Val Glu Thr Glu Phe Asp Gly Glu Lys Pro Glu Pro Ala Lys  
                  245                   250                   255  
Val

- (2) INFORMATION FOR SEQ ID NO:3456:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 220 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..220  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1576926  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3456:

Met Ala Tyr Leu Ala Pro Ala Thr Ala Ser Ser Leu Arg Thr Pro  
1                   5                   10                   15  
Ile Tyr Val Ala Ala Ser Ser Arg Arg Arg Ser Phe Leu Pro Ala Ala  
                  20                   25                   30  
Val Lys Ala Ile Ala Ser Ser Ala His Pro Ile Leu Ser Ser Leu Arg  
35                   40                   45  
Met Ala Ala Ser Ala Ala Val Leu Phe Ala Ala Thr Ser Pro Ala Leu  
50                   55                   60

Ala Cys Thr Pro Ser Val Pro Pro Pro Pro Leu Thr Pro Leu Thr Val  
65 70 75 80  
Thr Val Ser His Asp Asp Ala Ile Leu Asp Ala Ser Arg Leu Phe Glu  
85 90 95  
Lys Leu Ile Ile Glu Thr Ala Cys Xaa Xaa Arg Val Gly Arg Ala Asp  
100 105 110  
Glu Ala Arg Ser Arg Leu Ser Thr Ala Gly Cys Gly Glu Ser Tyr Ala  
115 120 125  
Arg Leu Leu Ala Ala Gln Val Leu Phe Val Asp Gly Lys Leu Asp Glu  
130 135 140  
Ala Ile Ala Ala Phe Glu Leu Ala Arg Glu Asp Pro Ala Asp Tyr  
145 150 155 160  
Arg Pro Leu Phe Cys Gln Gly Val Leu Tyr Leu Ala Leu Gly Arg Glu  
165 170 175  
Ala Glu Ser Glu Ser Met Leu Glu Arg Cys Arg Glu Val Gly Gly Asp  
180 185 190  
Ala Leu Ile Val Asp Pro Ser Leu Met Ile Thr Pro Thr Val Glu Thr  
195 200 205  
Glu Phe Asp Gly Glu Lys Pro Glu Pro Ala Lys Val  
210 215 220

(2) INFORMATION FOR SEQ ID NO:3457:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 600 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..600
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576935

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3457:

gagtgtctcg gtagcttctt cccattcac attcggccat tctccaccgt ccaaccaacc	60
accggcgcg gcacaaggga agcgaagagg aatcaacgag atgtctgcga ccacggcggc	120
ggtgcccttc tggcgggcg cgggatgac ctacatcggc tactccaaca tctGcgctgc	180
gctggtacgg aactgcctca aggagccctt caagtccaag gccgcgtccc gcgagaaggt	240
ccatttctcc atctccaagt ggacggatgg caaacaggag aagcccactg tccgcacaga	300
atccgatgaa taaagctctg gtgccatagt ggcatagtcc ttgctacaga tgatttgaag	360
tggtgttgca agtttccgga acatgctatt tagctggctt gattttatag tcaatgctga	420
ataataaata ctttttacga caattgtctt tttcgttgct aattgcactc gccctacctg	480
aatcagtcac gtgaacatca tggaatgctt cagttttgta caaactaaat ttgttgtgct	540
gtccgacaga ttctatgtct ggtccttaaa aataaaggaa taatgaatgt agtgttttcg	600

(2) INFORMATION FOR SEQ ID NO:3458:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..102
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576936

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3458:

Glu Cys Leu Gly Ser Phe Phe Pro Ile His Ile Arg Pro Phe Ser Thr	
1 5 10 15	
Val Gln Pro Thr Thr Gly Gly Gly Thr Arg Glu Ala Lys Arg Asn Gln	
20 25 30	
Arg Asp Val Cys Asp His Gly Gly Gly Ala Leu Leu Ala Gly Gly Arg	
35 40 45	



Asp Asp Leu His Arg Leu Leu Gln His Leu Arg Cys Ala Gly Thr Glu  
50 55 60  
Leu Pro Gln Gly Ala Leu Gln Val Gln Gly Arg Val Pro Arg Glu Gly  
65 70 75 80  
Pro Phe Leu His Leu Gln Val Asp Gly Trp Gln Thr Gly Glu Ala His  
85 90 95  
Cys Pro His Arg Ile Arg  
100

(2) INFORMATION FOR SEQ ID NO:3459:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 103 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..103

(D) OTHER INFORMATION: / Ceres Seq. ID 1576937

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3459:

Ser Val Ser Val Ala Ser Ser Pro Phe Thr Phe Gly His Ser Pro Pro  
1 5 10 15  
Ser Asn Gln Pro Pro Ala Ala Ala Gln Gly Lys Arg Arg Gly Ile Asn  
20 25 30  
Ala Met Ser Ala Thr Thr Ala Ala Val Pro Phe Trp Arg Ala Ala Gly  
35 40 45  
Met Thr Tyr Ile Gly Tyr Ser Asn Ile Cys Ala Ala Leu Val Arg Asn  
50 55 60  
Cys Leu Lys Glu Pro Phe Lys Ser Lys Ala Ala Ser Arg Glu Lys Val  
65 70 75 80  
His Phe Ser Ile Ser Lys Trp Thr Asp Gly Lys Gln Glu Lys Pro Thr  
85 90 95  
Val Arg Thr Glu Ser Asp Glu  
100

(2) INFORMATION FOR SEQ ID NO:3460:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..70

(D) OTHER INFORMATION: / Ceres Seq. ID 1576938

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3460:

Met Ser Ala Thr Thr Ala Ala Val Pro Phe Trp Arg Ala Ala Gly Met  
1 5 10 15  
Thr Tyr Ile Gly Tyr Ser Asn Ile Cys Ala Ala Leu Val Arg Asn Cys  
20 25 30  
Leu Lys Glu Pro Phe Lys Ser Lys Ala Ala Ser Arg Glu Lys Val His  
35 40 45  
Phe Ser Ile Ser Lys Trp Thr Asp Gly Lys Gln Glu Lys Pro Thr Val  
50 55 60  
Arg Thr Glu Ser Asp Glu  
65 70

(2) INFORMATION FOR SEQ ID NO:3461:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 815 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

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- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..815  
(D) OTHER INFORMATION: / Ceres Seq. ID 1576943

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3461:

```
agctctcccc ctctagcctc acctgcccta tacacagcca ctactgtcga tcgattgaat      60
ttgaacccac caggatcagg attaggatta cagcatgtcg gcgtccccgg agttgtacag      120
gcccgcggaa gscgcgcctt ctgcgcgtcc tgcgccacgc agccgctcgt gttcgcgggc      180
gacgactact gctgcaggac gccgacgggc agcgggatct gctacctgag ggagcccacc      240
acgtgccccg ccgcgccccg gaagccgcgc ccgcggcccc gtcctgtgca ggaagcgcc      300
cttccaagcg gcggatcagc agcttgctga ggcgggcccc gtccctgtta tcagcatccg      360
cctcgacgag ctggagcgcc tcttccgccc ctgtccgcgc ccgaccacca ccaccaccga      420
caagcggcgc cgctccggct ccggccccag cccagatcc gccacgaaac atggtgctca      480
gctgcagCtg cgcaGcatNg aattgaattg ggtagcgta acgtagcttg cacgcaccaa      540
ccaaccactC cccttttttag tttttgctgc tgcattctgtc tgcttcttgt tgctgcaaca      600
agcaaagcgc aagcgggtggc gcttcttttt atttatttat ttatttatta cggagtactt      660
gcttccgttc tcaaataatt gtcatttgat agttcatttc aaaaatttga caaataaaaa      720
agaacgacga agcaagcagt acccacctgt gtaaatcaaa tcaaataatgc aaagttaccg      780
ccatagcaat aaaatcaccc gtgtaaatca gatcg
```

(2) INFORMATION FOR SEQ ID NO:3462:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 109 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..109  
(D) OTHER INFORMATION: / Ceres Seq. ID 1576944

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3462:

```
Ser Ser Pro Pro Leu Ala Ser Pro Ala Leu Tyr Thr Ala Thr Thr Val
1          5          10          15
Asp Arg Leu Asn Leu Asn Pro Pro Gly Ser Gly Leu Gly Leu Gln His
20          25          30
Val Gly Val Pro Gly Val Val Gln Ala Arg Gly Xaa Pro Ala Phe Ser
35          40          45
Pro Ser Cys Ala Thr Gln Pro Leu Val Phe Ala Gly Asp Asp Tyr Cys
50          55          60
Cys Arg Thr Pro Thr Gly Ser Gly Ile Cys Tyr Leu Arg Glu Pro Thr
65          70          75          80
Thr Cys Pro Pro Ala Pro Arg Lys Pro Pro Pro Pro Pro His Val
85          90          95
Gln Glu Ala Pro Leu Pro Ser Gly Gly Ser Ala Ala Cys
100         105
```

(2) INFORMATION FOR SEQ ID NO:3463:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 167 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..167  
(D) OTHER INFORMATION: / Ceres Seq. ID 1576945

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3463:

```
Leu Ser Pro Ser Ser Leu Thr Cys Pro Ile His Ser His Tyr Cys Arg
1          5          10          15
```

Ser Ile Glu Phe Glu Pro Thr Arg Ile Arg Ile Arg Ile Thr Ala Cys  
20 25 30  
Arg Arg Pro Arg Ser Cys Thr Gly Pro Arg Lys Xaa Gly Leu Leu Ala  
35 40 45  
Val Leu Arg His Ala Ala Ala Arg Val Arg Arg Arg Arg Leu Leu Leu  
50 55 60  
Gln Asp Ala Asp Gly Gln Arg Asp Leu Leu Pro Glu Gly Ala His His  
65 70 75 80  
Val Pro Ala Arg Ala Pro Glu Ala Ala Ala Ala Ala Pro Cys Ala  
85 90 95  
Gly Ser Ala Ser Ser Lys Arg Arg Ile Ser Ser Leu Leu Arg Arg Ala  
100 105 110  
Pro Ser Leu Leu Ser Ala Ser Ala Ser Thr Ser Trp Ser Ala Ser Ser  
115 120 125  
Ala Pro Val Arg Arg Arg Pro Pro Pro Pro Pro Thr Ser Gly Ala Ala  
130 135 140  
Pro Ala Pro Ala Pro Ala Pro Asp Pro Pro Arg Asn Met Val Leu Ser  
145 150 155 160  
Cys Ser Cys Ala Ala Xaa Asn  
165

(2) INFORMATION FOR SEQ ID NO:3464:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 958 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..958
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576950

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3464:

angtctcagc	acccgatccg	agtaaccgct	gccgatctct	cctcgtcatt	tcgtcgtcgt	60
ctccatctcg	cttttgatcg	actcagaaaa	ttccccacca	aaatctcctc	cccctgaagt	120
cccgaagctc	gcggaagscc	gagatgtacc	atccccacgag	aggcggcgctc	cgcggcggca	180
gagatcaatt	caaatgggac	gatgtgaagg	ttgacaagca	tcggggagaat	taccttggtc	240
atagtgttaa	ggctccggtt	ggtagatggc	agaaaggaaa	ggatctttac	tggtatactc	300
gggataagaa	atccgacacg	gaagatgctc	ttaagggaaga	aatcaggaga	gtgaaggaag	360
aggaggaaca	ggctatgcgt	gaggctcttg	gcttagctcc	taagcgcaGc	aatcgaactc	420
agggtaatcg	cttgataag	catgaatatg	ctgagctgat	taagagagga	tcaactgcgg	480
aggacttggg	agcagggcac	gctgaagcag	cacaagtgc	gggtctagga	ttgtacaagg	540
cccctcgcg	tgaggttga	tcaagttctt	tgagccttga	ccctcaaattg	gagcctgagc	600
aggctgaacc	cctactagca	cccaagcagg	aggatgattt	ggaagataat	aggaagggga	660
aaaggccacg	tgaacgtgac	gagaagagag	gggagaagga	gcggaaacga	gacaggcatg	720
gtgatgga	ggagaggagg	cgggacaagc	acgagaggag	gcacgacttg	gaggacagat	780
caaagcggca	ccgcaaagac	aagcagaaga	ggaggcacga	ttccgattct	gattgataac	840
ggcctg	cgctcctgt	atgactactg	tatactgcga	aatttcaa	ccatggagcc	900
gctttt	ggtt	gatgtatgcc	tacgctttta	attatgtttg	ccctaata	gatttaagg

(2) INFORMATION FOR SEQ ID NO:3465:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..230
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576951

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3465:

Met Tyr His Pro Thr Arg Gly Gly Val Arg Gly Gly Arg Asp Gln Phe

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1 5 10 15  
Lys Trp Asp Asp Val Lys Val Asp Lys His Arg Glu Asn Tyr Leu Gly  
20 25 30  
His Ser Val Lys Ala Pro Val Gly Arg Trp Gln Lys Gly Lys Asp Leu  
35 40 45  
Tyr Trp Tyr Thr Arg Asp Lys Lys Ser Asp Thr Glu Asp Ala Leu Lys  
50 55 60  
Glu Glu Ile Arg Arg Val Lys Glu Glu Glu Glu Gln Ala Met Arg Glu  
65 70 75 80  
Ala Leu Gly Leu Ala Pro Lys Arg Ser Asn Arg Thr Gln Gly Asn Arg  
85 90 95  
Leu Asp Lys His Glu Tyr Ala Glu Leu Ile Lys Arg Gly Ser Thr Ala  
100 105 110  
Glu Asp Leu Gly Ala Gly His Ala Glu Ala Ala Gln Val Gln Gly Leu  
115 120 125  
Gly Leu Tyr Lys Ala Pro Arg Asp Glu Gly Gly Ser Ser Ser Leu Ser  
130 135 140  
Leu Asp Pro Gln Met Glu Pro Glu Gln Ala Glu Pro Leu Leu Ala Pro  
145 150 155 160  
Lys Gln Glu Asp Asp Leu Glu Asp Asn Arg Lys Gly Lys Arg Pro Arg  
165 170 175  
Glu Arg Asp Glu Lys Arg Gly Glu Lys Glu Arg Lys Arg Asp Arg His  
180 185 190  
Gly Asp Gly Lys Glu Arg Arg Arg Asp Lys His Glu Arg Arg His Asp  
195 200 205  
Leu Glu Asp Arg Ser Lys Arg His Arg Lys Asp Lys Gln Lys Arg Arg  
210 215 220  
His Asp Ser Asp Ser Asp  
225 230

(2) INFORMATION FOR SEQ ID NO:3466:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..153
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576952

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3466:

Met Arg Glu Ala Leu Gly Leu Ala Pro Lys Arg Ser Asn Arg Thr Gln  
1 5 10 15  
Gly Asn Arg Leu Asp Lys His Glu Tyr Ala Glu Leu Ile Lys Arg Gly  
20 25 30  
Ser Thr Ala Glu Asp Leu Gly Ala Gly His Ala Glu Ala Ala Gln Val  
35 40 45  
Gln Gly Leu Gly Leu Tyr Lys Ala Pro Arg Asp Glu Gly Gly Ser Ser  
50 55 60  
Ser Leu Ser Leu Asp Pro Gln Met Glu Pro Glu Gln Ala Glu Pro Leu  
65 70 75 80  
Leu Ala Pro Lys Gln Glu Asp Asp Leu Glu Asp Asn Arg Lys Gly Lys  
85 90 95  
Arg Pro Arg Glu Arg Asp Glu Lys Arg Gly Glu Lys Glu Arg Lys Arg  
100 105 110  
Asp Arg His Gly Asp Gly Lys Glu Arg Arg Arg Asp Lys His Glu Arg  
115 120 125  
Arg His Asp Leu Glu Asp Arg Ser Lys Arg His Arg Lys Asp Lys Gln  
130 135 140  
Lys Arg Arg His Asp Ser Asp Ser Asp  
145 150

(2) INFORMATION FOR SEQ ID NO:3467:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 618 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..618
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576959

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3467:

gccgcaaaac gcaggtgcat gcgtcgtcgc caagccccc aa ggccagtctg agtgtgcggt	60
cgattcgcgtt gtgctgcagc taggggtttag aggtttttctg ggcgcnagagC Gggadgcggc	120
ggcggctatg gctgcggcgg aggaggagat cgcgggtgaag gagccgctgg atctgatacg	180
cctcagcctc gacgagcgca tctacgtcaa gctccgatcc gaccgcgagC tgcgcggcaa	240
gctccatgcg tatgatcaac atttaaacad gatacttgga gatgttgaag aggtcgtgac	300
aactgttgag atagatgatg aaacatatga agaaattgtg cgcaccacga aacgcactat	360
cccctttctt tttgtccgag gtgatggtgt catattggtt tctccacccc ttcgtacggc	420
atgaagtttg aagttagatc atgctggttg ttaattatga taactggtgt atttgccac	480
ttgatggcgt tgcattggagt gGtatgttat gggcctagcc gctacttttt ctgatgggat	540
gtaggtttta catgtgatac aatcgtgtaa acaactgctt gtgcttgga tctctgtcgg	600
atctcagggg tttctccc	

(2) INFORMATION FOR SEQ ID NO:3468:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..140
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3468:

Pro	Gln	Asn	Ala	Gly	Ala	Cys	Val	Val	Ala	Lys	Pro	Gln	Gly	Gln	Ser
1				5						10				15	
Glu	Cys	Ala	Phe	Asp	Ser	Leu	Val	Leu	Gln	Leu	Gly	Phe	Arg	Gly	Phe
			20					25				30			
Leu	Gly	Xaa	Glu	Arg	Xaa	Ala	Ala	Ala	Ala	Met	Ala	Ala	Ala	Glu	Glu
		35				40				45					
Glu	Ile	Ala	Val	Lys	Glu	Pro	Leu	Asp	Leu	Ile	Arg	Leu	Ser	Leu	Asp
		50				55				60					
Glu	Arg	Ile	Tyr	Val	Lys	Leu	Arg	Ser	Asp	Arg	Glu	Leu	Arg	Gly	Lys
65					70				75					80	
Leu	His	Ala	Tyr	Asp	Gln	His	Leu	Asn	Met	Ile	Leu	Gly	Asp	Val	Glu
			85					90						95	
Glu	Val	Val	Thr	Thr	Val	Glu	Ile	Asp	Asp	Glu	Thr	Tyr	Glu	Glu	Ile
			100					105					110		
Val	Arg	Thr	Thr	Lys	Arg	Thr	Ile	Pro	Phe	Leu	Phe	Val	Arg	Gly	Asp
		115				120						125			
Gly	Val	Ile	Leu	Val	Ser	Pro	Pro	Leu	Arg	Thr	Ala				
		130				135					140				

(2) INFORMATION FOR SEQ ID NO:3469:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..98  
(D) OTHER INFORMATION: / Ceres Seq. ID 1576961

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3469:

Met Ala Ala Ala Glu Glu Glu Ile Ala Val Lys Glu Pro Leu Asp Leu  
1 5 10 15  
Ile Arg Leu Ser Leu Asp Glu Arg Ile Tyr Val Lys Leu Arg Ser Asp  
20 25 30  
Arg Glu Leu Arg Gly Lys Leu His Ala Tyr Asp Gln His Leu Asn Met  
35 40 45  
Ile Leu Gly Asp Val Glu Glu Val Val Thr Thr Val Glu Ile Asp Asp  
50 55 60  
Glu Thr Tyr Glu Glu Ile Val Arg Thr Thr Lys Arg Thr Ile Pro Phe  
65 70 75 80  
Leu Phe Val Arg Gly Asp Gly Val Ile Leu Val Ser Pro Pro Leu Arg  
85 90 95  
Thr Ala

(2) INFORMATION FOR SEQ ID NO:3470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 960 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..960  
(D) OTHER INFORMATION: / Ceres Seq. ID 1576970

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3470:

accaccacca ccaagccagc aggtgctgcg atacattgca cacaacaaca accccagctc 60  
tgccccagcc cgccacagag agttcccgca tctccctctg gtctgggtcac aggagttccg 120  
agacctctcc aatggcggtt aagatctacg ttgtgtacta ttccatgtat gggcatgttg 180  
gcaaaactagc tgaagagatc aagaaaggtg ccttatctgt tgaaggtgtt gaggctaaaa 240  
tatggcaggt ccctgaaatt ctctctgaag aagtgccttg aaagatgggc gcgcccccta 300  
agcccgcacgt gccagtcac acaccgcaga acttgacagag gctgacggta tcctctttgg 360  
gttcccagaca aggttcggaa tgatggcagc tcagatgaag gcgttcttcg atgccaccgg 420  
tgggctcttg agggagcaga gcctcgctgg caaGcctgcc ggcattgtct tcagcactgg 480  
aaccaggggt ggtggccaag agactacacc gctgacggcg attaccagtg tgacgcacca 540  
cggcatgggtg ttgtgtgccg tgggctacac ttcggcgcc aagctgttcg catggaccag 600  
gtccagggtg gcagccccta cggcgccggc acgttcgncg ccgacggctc gaggtggccg 660  
agcgaggtgg agctggagca cgccttcac caggggaaat acttcgcggg catcgccaag 720  
aagytcaagg gctctgcttg atctgcacat acccctctgt cagatatcat aaaacattta 780  
cagattcgtc ataccogtca ccgtcaatag attggctctgt gttctctcgt ggtgcctcga 840  
tgctatgtag ttcatggta ctgctgccgt atgaatttcg atgattgctc tggtgacttg 900  
gtttgtaatt tggagttgga ctatcgttgt ttctgccgca taaatttcga tgatttggtc 960

(2) INFORMATION FOR SEQ ID NO:3471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..126  
(D) OTHER INFORMATION: / Ceres Seq. ID 1576971

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3471:

His His His Gln Ala Ser Arg Cys Cys Asp Thr Leu His Thr Thr Thr  
1 5 10 15

Thr Pro Ala Leu Pro Gln Pro Ala His Arg Ser Ser Arg Ile Ser Leu  
20 25 30  
Trp Ser Gly His Arg Ser Ser Glu Thr Ser Pro Met Ala Val Lys Ile  
35 40 45  
Tyr Val Val Tyr Tyr Ser Met Tyr Gly His Val Gly Lys Leu Ala Glu  
50 55 60  
Glu Ile Lys Lys Gly Ala Leu Ser Val Glu Gly Val Glu Ala Lys Ile  
65 70 75 80  
Trp Gln Val Pro Glu Ile Leu Ser Glu Glu Val Leu Gly Lys Met Gly  
85 90 95  
Ala Pro Pro Lys Pro Asp Val Pro Val Ile Thr Pro Gln Asn Leu Gln  
100 105 110  
Arg Leu Thr Val Ser Ser Leu Gly Ser Arg Gln Gly Ser Glu  
115 120 125

(2) INFORMATION FOR SEQ ID NO:3472:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 130 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..130

(D) OTHER INFORMATION: / Ceres Seq. ID 1576972

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3472:

Met Met Ala Ala Gln Met Lys Ala Phe Phe Asp Ala Thr Gly Gly Leu  
1 5 10 15  
Trp Arg Glu Gln Ser Leu Ala Gly Lys Pro Ala Gly Met Phe Phe Ser  
20 25 30  
Thr Gly Thr Gln Gly Gly Gly Gln Glu Thr Thr Pro Leu Thr Ala Ile  
35 40 45  
Thr Gln Leu Thr His His Gly Met Val Phe Val Pro Val Gly Tyr Thr  
50 55 60  
Ser Ala Pro Ser Cys Ser Ala Trp Thr Arg Ser Arg Val Ala Ala Pro  
65 70 75 80  
Thr Ala Pro Ala Arg Ser Xaa Pro Thr Ala Arg Gly Gly Arg Ala Arg  
85 90 95  
Trp Ser Trp Ser Thr Pro Ser Thr Arg Gly Asn Thr Ser Arg Ala Ser  
100 105 110  
Pro Arg Xaa Ser Arg Ala Leu Leu Asp Leu His Ile Pro Leu Cys Gln  
115 120 125  
Ile Ser  
130

(2) INFORMATION FOR SEQ ID NO:3473:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 129 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..129

(D) OTHER INFORMATION: / Ceres Seq. ID 1576973

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3473:

Met Ala Ala Gln Met Lys Ala Phe Phe Asp Ala Thr Gly Gly Leu Trp  
1 5 10 15  
Arg Glu Gln Ser Leu Ala Gly Lys Pro Ala Gly Met Phe Phe Ser Thr  
20 25 30  
Gly Thr Gln Gly Gly Gly Gln Glu Thr Thr Pro Leu Thr Ala Ile Thr

	35				40					45					
Gln	Leu	Thr	His	His	Gly	Met	Val	Phe	Val	Pro	Val	Gly	Tyr	Thr	Ser
50						55					60				
Ala	Pro	Ser	Cys	Ser	Ala	Trp	Thr	Arg	Ser	Arg	Val	Ala	Ala	Pro	Thr
65					70					75					80
Ala	Pro	Ala	Arg	Ser	Xaa	Pro	Thr	Ala	Arg	Gly	Gly	Arg	Ala	Arg	Trp
				85					90					95	
Ser	Trp	Ser	Thr	Pro	Ser	Thr	Arg	Gly	Asn	Thr	Ser	Arg	Ala	Ser	Pro
			100					105					110		
Arg	Xaa	Ser	Arg	Ala	Leu	Leu	Asp	Leu	His	Ile	Pro	Leu	Cys	Gln	Ile
			115				120					125			
Ser															

(2) INFORMATION FOR SEQ ID NO:3474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 877 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..877
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576996

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3474:

gtcatcaciaa	actcactaca	cgatcggtta	tagcgagcta	acagaagctc	tatcaagtag	60
tgtgtaggcc	atggccggag	ccctcgtctt	cgtcgctgtt	ctcctcgcgc	caagcgctcg	120
cgctacgacg	gctaccacgc	tgaccatcca	caacctctgc	ccccacccgg	tgtggccgct	180
ggtagccccg	agctcgggct	tccctcccat	ctccaccaac	accgcgcggc	tgggccccaa	240
cgcgctgctc	tccctctcct	tcccgcccac	cttctgggac	ggcgcgctcg	ccgcgcgcac	300
gggctgcgac	gcccgcgcgt	ccggctgctg	gacggggacc	acgcgcgcgc	ccaccgtcgt	360
gcaggtcacc	gtccacgacg	gcgggaacct	ggaccaggcc	acctacagcg	tgtctctcgt	420
cgacggcttc	aacgtgcccc	tggtggtcag	cccgcagccc	gtcggcggcg	ggcagtgccc	480
ggcgtctcgg	tgccccatca	acctcaactg	cgactgcctc	ccccagaacc	gcaccgccga	540
nggngnctcy	gtgccgcggc	ccgcgcggag	acttcaagaa	ccggtgcccc	ytaccaggga	600
ccacgcccac	cgacgtcgag	cccgtgaccg	cagagctgcc	gcgccccggg	ggagctcaag	660
gtcatcttct	gccaggcgac	catcgtcaca	tgccggcgcg	aagcagagcg	caccgtcctc	720
gccgacagct	agacagatcg	agccgtccag	ctccattcgc	ctccaggtcc	gctgaatcct	780
tacagtaatt	gtcatgcttt	cttttgctcc	atgtgtttgt	tagctttggc	ttcgacgcgc	840
gtgtactccg	gtggttttat	tttagaaatc	agcagtg			

(2) INFORMATION FOR SEQ ID NO:3475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..234
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576997

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3475:

Met	Ala	Gly	Ala	Leu	Val	Phe	Val	Ala	Val	Leu	Leu	Ala	Ala	Ser	Val
1				5					10					15	
Gly	Ala	Thr	Thr	Ala	Thr	Thr	Leu	Thr	Ile	His	Asn	Leu	Cys	Pro	His
			20				25					30			
Pro	Val	Trp	Pro	Leu	Val	Thr	Pro	Ser	Ser	Gly	Phe	Pro	Ser	Ile	Ser
		35				40				45					
Thr	Asn	Thr	Ala	Arg	Leu	Gly	Pro	Asn	Ala	Leu	Leu	Ser	Leu	Ser	Phe
	50				55				60						
Pro	Pro	Thr	Phe	Trp	Ala	Gly	Arg	Val	Ala	Ala	Arg	Thr	Gly	Cys	Asp



(2) INFORMATION FOR SEO ID NO:3476:

(A) LENGTH: 893 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

MOLECULE TYPE: DNA (g

## (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..893

(D) OTHER INFORMATION: / Ceres Seq. ID 1576998

(xi) SEQUENCE DESCRIPTION: SEO ID NO:3476:

aaaaacccaa	gcacagcagc	aggtagaccg	ctgcagcaaa	accgcncccc	accgctwccc	60
cgtwmcccac	cccgaccgac	tgtctcccct	ccccgcacc	agcctcaagg	catcgccggc	120
gccgcaacat	cgctgaggaa	gcccgcaccc	ctgcccgat	cogatggcca	acagcaacct	180
cccgcgcg	atcatcaagg	agactcagcg	gctgctcagc	gagccaagcac	cggggatcag	240
cgcgtcgccc	tcggaGgaga	acatgcgcta	cttcaacgtt	atgatccttG	gggcccggcgc	300
agtcgccta	tgaaggtgga	gtttttaagc	ttgaactctt	tttaacctatg	gaatatccaa	360
tggctgcccc	aaaggttagg	tctctgacaa	agatctatca	tcccaactatc	gacaagcttg	420
gtaggatatg	cctcgacatt	ctcaaggaca	aatggagccc	agcacttcag	attcgaaacag	480
ttcttttgag	tatacaggct	ctactgagtg	cgccaaatcc	agacgaccct	ctttcggata	540
acattgcaaa	gcactggaaa	gccaatgagg	tagaagctgt	tgaaacagct	aaggagtgga	600
ctcgctgta	tgcgagcgg	gcatgagaac	gcagtgatgt	tcttgatgta	ataaccatc	660
atacttcagt	cctcatctat	tgccatttgt	ttgataaaaa	ataggctgga	gatattttgcc	720
atggaatgaa	gtctctacat	gactatcact	ctgaattggt	tggttgtaca	cctgtggctg	780
gttcccttta	ccttggggca	cccttgacaa	atcagtatct	gtggtagaac	tgtctgatac	840
tgtaatatat	ttgttacttc	atgtagaaga	gcttctcaac	ttgtccattatt	gtc	

(2) INFORMATION FOR SEQ ID NO:3477:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..128

(D) OTHER INFORMATION: / Ceres Seq. ID 1576999

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3477:

Lys Asn Pro Ser Thr Ala Ala Gly Arg Pro Leu Gln Gln Asn Arg Xaa

1 5 10 15  
Pro Pro Xaa Pro Arg Xaa Pro Pro Arg Pro Thr Ala Pro Pro Pro Pro  
20 25 30  
His Gln Pro Gln Gly Ile Ala Gly Ala Ala Thr Ser Leu Arg Lys Pro  
35 40 45  
Ala Pro Leu Pro Gly Ser Asp Gly Gln Gln Gln Pro Pro Ala Ala Asp  
50 55 60  
His Gln Gly Asp Ser Ala Ala Ala Gln Arg Ala Ser Thr Gly Asp Gln  
65 70 75 80  
Arg Val Ala Leu Gly Gly Glu His Ala Leu Leu Gln Arg Tyr Asp Pro  
85 90 95  
Trp Gly Arg Arg Ser Arg Pro Met Lys Val Glu Phe Leu Ser Leu Asn  
100 105 110  
Ser Phe Tyr Leu Arg Asn Ile Gln Trp Leu Pro Gln Arg Leu Gly Leu  
115 120 125

(2) INFORMATION FOR SEQ ID NO:3478:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..88

(D) OTHER INFORMATION: / Ceres Seq. ID 1577000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3478:

Met Ala Ala Pro Lys Val Arg Ser Leu Thr Lys Ile Tyr His Pro Asn  
1 5 10 15  
Ile Asp Lys Leu Gly Arg Ile Cys Leu Asp Ile Leu Lys Asp Lys Trp  
20 25 30  
Ser Pro Ala Leu Gln Ile Arg Thr Val Leu Leu Ser Ile Gln Ala Leu  
35 40 45  
Leu Ser Ala Pro Asn Pro Asp Asp Pro Leu Ser Asp Asn Ile Ala Lys  
50 55 60  
His Trp Lys Ala Asn Glu Val Glu Ala Val Glu Thr Ala Lys Glu Trp  
65 70 75 80  
Thr Arg Leu Tyr Ala Ser Gly Ala  
85

(2) INFORMATION FOR SEQ ID NO:3479:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 636 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..636

(D) OTHER INFORMATION: / Ceres Seq. ID 1577001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3479:

accaccaggc accagcatag atctcgttct cgccactatt attctgcaca gcaacgcac 60  
aagccttcta gaaccatctc gccgccgcca caccacaacc cgtcgaagcg aaGcaagcaa 120  
tggccggagt cggatcgaag gccctcgccg ttgccgcgt tctggcggcc gtctccctct 180  
cggtgccgc cgcggccgag gcgcggcgcc ccagcccgt cNtccgCgc cgtcgcggck 240  
tcgtcgccct tcgccgcgc cctcgtcgcc tcgcgcgcg ccttctctct cgccgcgctc 300  
cgccactgag ccgatggggc ctcgtcgctg caggctacct agcagtactt ccgccgctgc 360  
tgccgccgcc gcctagatct atttattgga gtgctatcca gtagtactag tagtagtgag 420  
atttcttcgg tgctgtcggt tcgtcgtcgc attttggctg gatctggttt ccttggtgca 480

gggaggggttt ctataccatg tgcgcggtg Gggttggtg atctcatccc cccttgtaga 540  
tagtactctg ctatctcgtc gtgatcgtga gtggtgattc tgtctggttg atatttgcta 600  
ctgatattgg tccatttga gatatgcgtt gctgct

(2) INFORMATION FOR SEQ ID NO:3480:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..102
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577002

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3480:

Thr Thr Arg His Gln His Arg Ser Arg Ser Arg His Tyr Tyr Ser Ala  
1 5 10 15  
Gln Gln Arg Ile Lys Pro Ser Arg Thr Ile Ser Pro Pro Pro His His  
20 25 30  
Asn Pro Ser Lys Arg Ser Lys Gln Trp Pro Glu Ser Asp Arg Arg Pro  
35 40 45  
Ser Pro Leu Pro Pro Phe Trp Arg Pro Ser Pro Ser Arg Trp Pro Pro  
50 55 60  
Arg Pro Arg Arg Arg Arg Pro Ala Pro Xaa Ser Ala Ala Val Ala Xaa  
65 70 75 80  
Ser Ser Pro Phe Ala Ala Ala Leu Val Ala Ser Ala Ala Ala Phe Leu  
85 90 95  
Phe Ala Ala Val Arg His  
100

(2) INFORMATION FOR SEQ ID NO:3481:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..124
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577003

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3481:

Pro Pro Gly Thr Ser Ile Asp Leu Val Leu Ala Thr Ile Ile Leu His  
1 5 10 15  
Ser Asn Ala Ser Ser Leu Leu Glu Pro Ser Arg Arg Arg His Thr Thr  
20 25 30  
Thr Arg Arg Ser Glu Ala Ser Asn Gly Arg Ser Arg Ile Glu Gly Pro  
35 40 45  
Arg Arg Cys Arg Arg Ser Gly Gly Arg Leu Pro Leu Gly Gly Arg Arg  
50 55 60  
Gly Arg Gly Ala Gly Ala Gln Pro Arg Xaa Pro Pro Pro Ser Arg Xaa  
65 70 75 80  
Arg Arg Pro Ser Pro Arg Pro Ser Ser Pro Pro Pro Pro Ser Ser  
85 90 95  
Ser Pro Pro Ser Ala Thr Glu Pro Met Gly Pro Arg Ala Cys Arg Leu  
100 105 110  
Pro Ser Ser Thr Ser Ala Ala Ala Ala Ala Ala  
115 120

(2) INFORMATION FOR SEQ ID NO:3482:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..94  
(D) OTHER INFORMATION: / Ceres Seq. ID 1577004

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3482:

Met Ala Gly Val Gly Ser Lys Ala Leu Ala Val Ala Ala Val Leu Ala  
1 5 10 15  
Ala Val Ser Leu Ser Val Ala Ala Ala Glu Ala Pro Ala Pro Ser  
20 25 30  
Pro Val Xaa Arg Arg Arg Arg Gly Xaa Val Ala Leu Arg Arg Gly Pro  
35 40 45  
Arg Arg Leu Arg Arg Arg Leu Pro Leu Arg Arg Arg Pro Pro Leu Ser  
50 55 60  
Arg Trp Gly Leu Val Pro Ala Gly Tyr Leu Ala Val Leu Pro Pro Leu  
65 70 75 80  
Leu Pro Pro Pro Pro Arg Ser Ile Tyr Trp Ser Ala Ile Gln  
85 90

(2) INFORMATION FOR SEQ ID NO:3483:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 722 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..722  
(D) OTHER INFORMATION: / Ceres Seq. ID 1577048

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3483:

ccggaaactg gtaccatccg ccgmcgcagc catccgcttg ttctcttcgg ttcagttctc 60  
gagtttccag gatgaaggta atagctgcct atctgcttgc tgttctgggt ggaaacactt 120  
ccccgactgc tgatgatgtt aagagcatto tggaatcagt tgggtgctgaa gctgatgaag 180  
aaaaactaga gttcctgctc acagaactca aagacaagga cataacagaa gtgattgcag 240  
ctggaaggga aaggttatcc tctgtgcctt caggtggttg tgcaattgac atgggagctc 300  
cagcagctgt agctggcgtt ggcgcaGcac ctgctGgaag aggcaaagaa ggaagaaaag 360  
gttgaagaga aggaagagtc tgatgragat atggggttca gcttgttcga ttaaaacagc 420  
actaccagtt tacagtttct tcgcgaatgg tctcataata ttggccggtt tccacaaaat 480  
aagattgtcA atagctacta cgtacttatg ctattctgca tgtgatgtac gagtgtgcat 540  
cttcaagaat ctttaagttg aatggtcggt ggtcccataa taatattggt aacaatgtaa 600  
attgtatgtc ctgtacgtac tttggtatcg cgacatctca gtgtgcatct tcaaggatca 660  
taagttgaat gttatcatta aggtcagttt gggttcagata aatataattg ctagttatag 720  
cc

(2) INFORMATION FOR SEQ ID NO:3484:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 120 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..120  
(D) OTHER INFORMATION: / Ceres Seq. ID 1577049

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3484:

Gly Asn Trp Tyr His Pro Pro Xaa Gln Pro Ser Ala Cys Ser Leu Arg  
1 5 10 15  
Phe Ser Ser Arg Val Ser Arg Met Lys Val Ile Ala Ala Tyr Leu Leu  
20 25 30

Ala Val Leu Gly Gly Asn Thr Ser Pro Thr Ala Asp Asp Val Lys Ser  
35 40 45  
Ile Leu Glu Ser Val Gly Ala Glu Ala Asp Glu Glu Lys Leu Glu Phe  
50 55 60  
Leu Leu Thr Glu Leu Lys Asp Lys Asp Ile Thr Glu Val Ile Ala Ala  
65 70 75 80  
Gly Arg Glu Arg Leu Ser Ser Val Pro Ser Gly Gly Gly Ala Ile Asp  
85 90 95  
Met Gly Ala Pro Ala Ala Val Ala Gly Gly Gly Ala Ala Pro Ala Gly  
100 105 110  
Arg Gly Lys Glu Gly Arg Lys Gly  
115 120

(2) INFORMATION FOR SEQ ID NO:3485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..97
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577050

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3485:

Met Lys Val Ile Ala Ala Tyr Leu Leu Ala Val Leu Gly Gly Asn Thr  
1 5 10 15  
Ser Pro Thr Ala Asp Asp Val Lys Ser Ile Leu Glu Ser Val Gly Ala  
20 25 30  
Glu Ala Asp Glu Glu Lys Leu Glu Phe Leu Leu Thr Glu Leu Lys Asp  
35 40 45  
Lys Asp Ile Thr Glu Val Ile Ala Ala Gly Arg Glu Arg Leu Ser Ser  
50 55 60  
Val Pro Ser Gly Gly Gly Ala Ile Asp Met Gly Ala Pro Ala Ala Val  
65 70 75 80  
Ala Gly Gly Gly Ala Ala Pro Ala Gly Arg Gly Lys Glu Gly Arg Lys  
85 90 95  
Gly

(2) INFORMATION FOR SEQ ID NO:3486:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..831
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577058

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3486:

acccctcatc	ttcctctcct	tccctcccaa	cctcggtcac	cagtccatcg	atcctcgaat	60
cgctcgcttg	cactgcactg	caaggtacat	acgccatgaa	gctgagcatg	cctttcttcg	120
gctcgcttcc	ctcctcctcc	ggcaagaaga	ggaaggggtc	aaagaccggc	ggctcctctt	180
ccttcgtctc	caccgcgtcg	tgctcctcgt	cgacagagtg	cgcatcgccg	tcagccgtca	240
cgacgacgcc	acgcaccgtc	ctccaatccc	agcgtccgc	ccccaacccg	aaGcctccgg	300
cggNtagtag	cgcgcgcgtg	gacgcgggag	gacctggagg	tggcGctgcg	ccgggtggtc	360
cgcagcgagg	acgagctggc	cgcggtgctg	gccgaggcgg	aggccNgccG	Ggctcgcgcc	420
cgagcaggcc	gcgtccgcGg	aggcggaggga	cgaggccgag	ctCgcgcacg	cgttcgcggt	480
gttcgacgcg	gacggcgacg	gcaggatctc	cgcgaggagg	tccgcgccgt	gctcgccgcg	540
ctcggcgacg	ccgcctgctc	cgtcgaggac	tgccgcgcga	tgatcgggcg	cgtcgacggc	600
gatggcgacg	gcttcgtctg	cttccacgac	ttctcgcgca	tgatgatgca	gggggcgtga	660

ttctggcgctc gtcgtgcctg gctgggttgt gtcggtctcc gcgtgtttct tctgttgcaa 720  
aatctctcta cctgtatgtg gacctgtttt ttcggtgtca tctactcgta tcatctccgt 780  
cgtgcgagat gaatgaaccc aaaagagatc tatatatattt catcttttcc g

(2) INFORMATION FOR SEQ ID NO:3487:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..276
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577059

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3487:

Pro	Ser	Ser	Ser	Ser	Pro	Ser	Leu	Pro	Thr	Ser	Val	Thr	Ser	Pro	Ser
1				5				10						15	
Ile	Leu	Glu	Ser	Leu	Ala	Cys	Thr	Ala	Leu	Gln	Gly	Thr	Tyr	Ala	Met
		20						25					30		
Lys	Leu	Ser	Met	Pro	Phe	Phe	Gly	Ser	Ser	Ser	Ser	Ser	Ser	Gly	Lys
		35					40					45			
Lys	Arg	Lys	Gly	Ser	Lys	Thr	Gly	Gly	Ser	Ser	Ser	Phe	Val	Ser	Thr
	50					55					60				
Ala	Ser	Ser	Ser	Ser	Ser	Asp	Glu	Cys	Ala	Ser	Pro	Ser	Ala	Val	Thr
65					70				75					80	
Thr	Thr	Pro	Arg	Thr	Val	Leu	Gln	Ser	Gln	Pro	Ser	Ala	Pro	Asn	Pro
			85					90						95	
Lys	Pro	Pro	Ala	Xaa	Ser	Ser	Arg	Arg	Arg	Asp	Ala	Gly	Gly	Pro	Gly
			100					105					110		
Gly	Gly	Ala	Ala	Pro	Gly	Gly	Pro	Gln	Arg	Gly	Arg	Ala	Gly	Arg	Gly
		115					120					125			
Ala	Gly	Arg	Gly	Gly	Gly	Xaa	Pro	Gly	Ser	Arg	Pro	Ser	Arg	Pro	Arg
	130					135					140				
Pro	Arg	Arg	Arg	Arg	Thr	Arg	Pro	Ser	Ser	Ala	Thr	Arg	Ser	Arg	Cys
145					150					155				160	
Ser	Thr	Arg	Thr	Ala	Thr	Ala	Gly	Ser	Pro	Arg	Arg	Xaa	Pro	Arg	Arg
			165					170					175		
Ala	Arg	Arg	Ala	Arg	Arg	Arg	Arg	Leu	Leu	Arg	Arg	Gly	Leu	Pro	Pro
			180					185					190		
His	Asp	Arg	Pro	Arg	Arg	Arg	Arg	Trp	Arg	Arg	Leu	Arg	Leu	Leu	Pro
	195						200				205				
Arg	Leu	Leu	Ala	His	Asp	Asp	Ala	Gly	Gly	Val	Ile	Leu	Ala	Ser	Ser
	210				215					220					
Cys	Leu	Ala	Gly	Leu	Cys	Arg	Ser	Pro	Arg	Val	Ser	Ser	Val	Ala	Lys
225					230					235				240	
Ser	Leu	Tyr	Leu	Tyr	Val	Asp	Leu	Phe	Phe	Arg	Cys	His	Leu	Leu	Val
			245					250					255		
Ser	Ser	Pro	Ser	Cys	Glu	Met	Asn	Glu	Pro	Lys	Arg	Asp	Leu	Tyr	Ile
			260					265					270		
Phe	Ile	Phe	Ser												
			275												

(2) INFORMATION FOR SEQ ID NO:3488:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..245

(D) OTHER INFORMATION: / Ceres Seq. ID 1577060

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3488:

Met Lys Leu Ser Met Pro Phe Phe Gly Ser Ser Ser Ser Ser Gly  
1 5 10 15  
Lys Lys Arg Lys Gly Ser Lys Thr Gly Gly Ser Ser Ser Phe Val Ser  
20 25 30  
Thr Ala Ser Ser Ser Ser Ser Asp Glu Cys Ala Ser Pro Ser Ala Val  
35 40 45  
Thr Thr Thr Pro Arg Thr Val Leu Gln Ser Gln Pro Ser Ala Pro Asn  
50 55 60  
Pro Lys Pro Pro Ala Xaa Ser Ser Arg Arg Arg Asp Ala Gly Gly Pro  
65 70 75 80  
Gly Gly Gly Ala Ala Pro Gly Gly Pro Gln Arg Gly Arg Ala Gly Arg  
85 90 95  
Gly Ala Gly Arg Gly Gly Gly Xaa Pro Gly Ser Arg Pro Ser Arg Pro  
100 105 110  
Arg Pro Arg Arg Arg Arg Thr Arg Pro Ser Ser Ala Thr Arg Ser Arg  
115 120 125  
Cys Ser Thr Arg Thr Ala Thr Ala Gly Ser Pro Arg Arg Xaa Pro Arg  
130 135 140  
Arg Ala Arg Arg Ala Arg Arg Arg Arg Leu Leu Arg Arg Gly Leu Pro  
145 150 155 160  
Pro His Asp Arg Pro Arg Arg Arg Arg Trp Arg Arg Leu Arg Leu Leu  
165 170 175  
Pro Arg Leu Leu Ala His Asp Asp Ala Gly Gly Val Ile Leu Ala Ser  
180 185 190  
Ser Cys Leu Ala Gly Leu Cys Arg Ser Pro Arg Val Ser Ser Val Ala  
195 200 205  
Lys Ser Leu Tyr Leu Tyr Val Asp Leu Phe Phe Arg Cys His Leu Leu  
210 215 220  
Val Ser Ser Pro Ser Cys Glu Met Asn Glu Pro Lys Arg Asp Leu Tyr  
225 230 235 240  
Ile Phe Ile Phe Ser  
245

(2) INFORMATION FOR SEQ ID NO:3489:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 241 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..241

(D) OTHER INFORMATION: / Ceres Seq. ID 1577061

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3489:

Met Pro Phe Phe Gly Ser Ser Ser Ser Ser Ser Gly Lys Lys Arg Lys  
1 5 10 15  
Gly Ser Lys Thr Gly Gly Ser Ser Ser Phe Val Ser Thr Ala Ser Ser  
20 25 30  
Ser Ser Ser Asp Glu Cys Ala Ser Pro Ser Ala Val Thr Thr Thr Pro  
35 40 45  
Arg Thr Val Leu Gln Ser Gln Pro Ser Ala Pro Asn Pro Lys Pro Pro  
50 55 60  
Ala Xaa Ser Ser Arg Arg Arg Asp Ala Gly Gly Pro Gly Gly Gly Ala  
65 70 75 80  
Ala Pro Gly Gly Pro Gln Arg Gly Arg Ala Gly Arg Gly Ala Gly Arg  
85 90 95  
Gly Gly Gly Xaa Pro Gly Ser Arg Pro Ser Arg Pro Arg Pro Arg Arg  
100 105 110  
Arg Arg Thr Arg Pro Ser Ser Ala Thr Arg Ser Arg Cys Ser Thr Arg

	115		120		125										
Thr	Ala	Thr	Ala	Gly	Ser	Pro	Arg	Arg	Xaa	Pro	Arg	Arg	Ala	Arg	Arg
130						135				140					
Ala	Arg	Arg	Arg	Arg	Leu	Leu	Arg	Arg	Gly	Leu	Pro	Pro	His	Asp	Arg
145					150					155					160
Pro	Arg	Arg	Arg	Arg	Trp	Arg	Arg	Leu	Arg	Leu	Leu	Pro	Arg	Leu	Leu
				165					170					175	
Ala	His	Asp	Asp	Ala	Gly	Gly	Val	Ile	Leu	Ala	Ser	Ser	Cys	Leu	Ala
			180					185					190		
Gly	Leu	Cys	Arg	Ser	Pro	Arg	Val	Ser	Ser	Val	Ala	Lys	Ser	Leu	Tyr
		195					200					205			
Leu	Tyr	Val	Asp	Leu	Phe	Phe	Arg	Cys	His	Leu	Leu	Val	Ser	Ser	Pro
	210					215				220					
Ser	Cys	Glu	Met	Asn	Glu	Pro	Lys	Arg	Asp	Leu	Tyr	Ile	Phe	Ile	Phe
225					230					235					240
Ser															

(2) INFORMATION FOR SEQ ID NO:3490:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 876 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..876

(D) OTHER INFORMATION: / Ceres Seq. ID 1577062

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3490:

tccaactctg	cgccgcaatc	cactcaagaa	ggttagccct	cgtgggtctcg	gatttgata	60
atcctccgcc	gaggtatgaa	acaggangcg	gccaccagca	tagtggtgac	ccaggaggac	120
gtcctgcacc	actacaagga	gcctccaccc	cgmcgcgagg	acgatycgcc	agcactggct	180
gcgtcgctgt	cgttgccgtc	gtcactgtcg	gaggacaatg	gcgacgccat	gccgcagcca	240
tcttcatacg	cggtcttgcc	gcgcggggat	ggcgagctgg	tgtctgcgga	ggagctgctg	300
ctgAgtgccg	ccgtcaaat	tgcCccatgg	tggaccacgg	cgtgtaccgc	tccggNattc	360
ccggacgcct	ccaacttgcc	gtttcttgag	acgctccgac	tccgctccgt	cctgtgcctg	420
tgcccggagc	catacccgga	ggctaactctg	gagttcctcc	gtgcccacgg	gatcaagctc	480
ttccagttcg	gaatcgacgg	ctccaaggaa	ccatttgatga	acataccaga	agatagaatc	540
cgtgaagctc	tagaagtcac	cctagatgca	agcaaccatc	cggttcttat	tcactgcaag	600
cgaggaaagc	atcgaaccgg	ctgtgtgggt	ggatgcttta	ggaaattgca	acgctgggtg	660
ctaacttcaa	tatttgacga	ataccagcgt	tttgctgctg	ccaaaacaag	agtttctgac	720
tacggttcat	ggagctatct	gatgtatcga	gcataaagca	tttagcattt	gagtcgtctg	780
tatgatagta	acattgggtgc	atgataacaa	ctcaataactg	gttccattac	ggtgtcatct	840
ttttcattta	agaaaaaaaa	tcattttctaa	aaatgc			

(2) INFORMATION FOR SEQ ID NO:3491:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..128

(D) OTHER INFORMATION: / Ceres Seq. ID 1577063

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3491:

Gln	Leu	Cys	Ala	Ala	Ile	His	Ser	Arg	Arg	Leu	Ala	Leu	Val	Val	Ser
1			5					10					15		
Asp	Leu	Asp	Asn	Pro	Pro	Pro	Arg	Tyr	Glu	Thr	Gly	Xaa	Gly	His	Gln
			20				25					30			
His	Ser	Gly	Asp	Pro	Gly	Gly	Arg	Pro	Ala	Pro	Leu	Gln	Gly	Ala	Ser



(2) INFORMATION FOR SEQ ID NO:3492:

(A) LENGTH: 226 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..226

(D) OTHER INFORMATION: / Ceres Seq. ID 1577064

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 175 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..175

(D) OTHER INFORMATION: / Ceres Seq. ID 1577065

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3493:

Met Pro Gln Pro Ser Ser Tyr Ala Val Leu Pro Arg Arg Asp Gly Glu  
1 5 10 15  
Leu Val Ser Ala Glu Glu Leu Leu Leu Ser Ala Ala Ala Gln Leu Arg  
20 25 30  
Pro Trp Trp Thr Thr Ala Cys Thr Ala Pro Xaa Phe Pro Asp Ala Ser  
35 40 45  
Asn Leu Pro Phe Leu Glu Thr Leu Arg Leu Arg Ser Val Leu Cys Leu  
50 55 60  
Cys Pro Glu Pro Tyr Pro Glu Ala Asn Leu Glu Phe Leu Arg Ala His  
65 70 75 80  
Gly Ile Lys Leu Phe Gln Phe Gly Ile Asp Gly Ser Lys Glu Pro Phe  
85 90 95  
Val Asn Ile Pro Glu Asp Arg Ile Arg Glu Ala Leu Glu Val Ile Leu  
100 105 110  
Asp Ala Ser Asn His Pro Val Leu Ile His Cys Lys Arg Gly Lys His  
115 120 125  
Arg Thr Gly Cys Val Val Gly Cys Phe Arg Lys Leu Gln Arg Trp Cys  
130 135 140  
Leu Thr Ser Ile Phe Asp Glu Tyr Gln Arg Phe Ala Ala Ala Lys Thr  
145 150 155 160  
Arg Val Ser Asp Tyr Gly Ser Trp Ser Tyr Leu Met Tyr Arg Ala  
165 170 175

(2) INFORMATION FOR SEQ ID NO:3494:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 630 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..630

(D) OTHER INFORMATION: / Ceres Seq. ID 1577073

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3494:

aaaattaaag gaaaacggtg gactagaaac ttccaaatcg aacggcacac aaaaatcaca 60  
acccggaaag ggaccagcag cgcaaagggtg agcgagcttt ccttcggaac tctctcgtgc 120  
tcacctcAat ccgtccgaca gatccacacg aatcctctga ttcagagcag ggtggtggca 180  
ttgatcagac gcctgccatg gctgatcagt tcgaggattc ggccaacaat gtgatcattg 240  
aggaggtgaa caagggcctg aacccaggaa tgggtggttct gcttgtggtt gcaagcttcc 300  
tgctgatctt ctttgtgggg aactatgcgc tgtatgtgta tgcgcagaag acgctcccgc 360  
caaagaagaa gaagccggtg tcgaagaaga agctgaagaa ggaaaagctg aagcaggggg 420  
tctctgcgcc gggagagtaa acggccatgc tgccgatcct cccgtccaga gctcctattc 480  
acatgattat tagagaaaaa aattatatat atataaccaga tggagccgta gtgtDtgagg 540  
tAactttgtt ctgtagatgc tctgtcttta atggtacatc tgtattggag actttgagac 600  
cttgtttcag caactgatga atcttagccc

(2) INFORMATION FOR SEQ ID NO:3495:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..77

(D) OTHER INFORMATION: / Ceres Seq. ID 1577074

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3495:

Lys Ile Lys Gly Lys Arg Trp Thr Arg Asn Phe Gln Ile Glu Arg His  
1 5 10 15  
Thr Lys Ile Thr Thr Arg Lys Gly Thr Ser Ser Ala Lys Val Ser Glu  
20 25 30  
Leu Ser Phe Gly Thr Leu Ser Cys Ser Pro Gln Ser Val Arg Gln Ile  
35 40 45  
His Thr Asn Pro Leu Ile Gln Ser Arg Val Leu Ala Leu Ile Arg Arg  
50 55 60  
Leu Pro Trp Leu Ile Ser Ser Arg Ile Arg Arg Thr Met  
65 70 75

(2) INFORMATION FOR SEQ ID NO:3496:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..80

(D) OTHER INFORMATION: / Ceres Seq. ID 1577075

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3496:

Met Ala Asp Gln Phe Glu Asp Ser Ala Asn Asn Val Ile Ile Glu Glu  
1 5 10 15  
Val Asn Lys Gly Leu Asn Pro Gly Met Val Val Leu Leu Val Val Ala  
20 25 30  
Ser Phe Leu Leu Ile Phe Phe Val Gly Asn Tyr Ala Leu Tyr Val Tyr  
35 40 45  
Ala Gln Lys Thr Leu Pro Pro Lys Lys Lys Lys Pro Val Ser Lys Lys  
50 55 60  
Lys Leu Lys Lys Glu Lys Leu Lys Gln Gly Val Ser Ala Pro Gly Glu  
65 70 75 80

(2) INFORMATION FOR SEQ ID NO:3497:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..56

(D) OTHER INFORMATION: / Ceres Seq. ID 1577076

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3497:

Met Leu Pro Ile Leu Pro Ser Arg Ala Pro Ile His Met Ile Ile Arg  
1 5 10 15  
Glu Lys Asn Tyr Ile Tyr Ile Pro Asp Gly Ala Val Val Xaa Gly Val  
20 25 30  
Thr Leu Phe Cys Arg Cys Ser Val Phe Asn Gly Thr Ser Val Leu Glu  
35 40 45  
Thr Leu Arg Pro Cys Phe Ser Asn  
50 55

(2) INFORMATION FOR SEQ ID NO:3498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 885 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..885  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1577089

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3498:

atccgagtcc	acccaactaa	tcacgcccaa	tcagaacaga	ctcggtcgct	tcaccactcc	60
actcgccgca	ggcgccgggc	gccgcccagg	ggatcgaggc	aagatgttct	tccacatcgt	120
gctggagcgg	aacatgcagc	tgcacccacg	acacttcggg	ccgcacctcc	gcgacaagct	180
cgtttccaag	ctcatcaagg	acgtcgaggg	cacctgcagc	gggcggcacg	ggttcgttgt	240
ggcgatcacg	ggtgtggagg	acatcggcaa	ggggctcatc	cggaaggca	cgggatacgt	300
caccttcccc	gycaagtacc	agtgcgttgt	ctttagacct	ttcaagggcg	agatcctcga	360
agctgtcgtc	accatggtga	acaagatggg	cttctttgcg	gaggctgggc	cgggtgcagat	420
cttcgtgtcc	aaccatttga	ttccagacga	tatggagttc	caatcaRgga	gatgtgccga	480
actacacaac	ttctgatgga	tcggtgaaaa	ttcaaaaaga	gagtgagggtg	cggctgaaga	540
ttattGggta	ctcgtgtcga	tgctacagaa	attttttgca	ttggcacAat	Aaaaggatga	600
ttttctgggt	gktatcacg	atcctggtgc	gscagtgtaa	atggtctaag	aagcgagatt	660
gtactccatt	gttctgactt	ctgagtacta	tcgcagacgt	gtgtaatcgc	tggtcggtta	720
aaactgcaat	ggctgtactg	actgcggaac	ttgttgagaa	tgatgtgact	aggaccttgt	780
ttagggcctg	tttggttctt	tagtatggcc	ctgattggca	caactgctgt	ttattgaaaa	840
aacagcttat	ctgataagct	ggtgaaaaat	agcttctgct	tgttg		

(2) INFORMATION FOR SEQ ID NO:3499:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 164 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..164  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1577090

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3499:

Ser	Glu	Ser	Thr	Gln	Leu	Ile	Thr	Pro	Asn	Gln	Asn	Arg	Leu	Gly	Arg
1				5					10					15	
Phe	Thr	Thr	Pro	Leu	Ala	Ala	Gly	Ala	Gly	Arg	Arg	Arg	Gly	Asp	Arg
			20					25					30		
Ser	Lys	Met	Phe	Phe	His	Ile	Val	Leu	Glu	Arg	Asn	Met	Gln	Leu	His
		35					40					45			
Pro	Arg	His	Phe	Gly	Pro	His	Leu	Arg	Asp	Lys	Leu	Val	Ser	Lys	Leu
		50				55					60				
Ile	Lys	Asp	Val	Glu	Gly	Thr	Cys	Ser	Gly	Arg	His	Gly	Phe	Val	Val
65				70					75					80	
Ala	Ile	Thr	Gly	Val	Glu	Asp	Ile	Gly	Lys	Gly	Leu	Ile	Arg	Glu	Gly
			85					90						95	
Thr	Gly	Tyr	Val	Thr	Phe	Pro	Xaa	Lys	Tyr	Gln	Cys	Val	Val	Phe	Arg
			100					105					110		
Pro	Phe	Lys	Gly	Glu	Ile	Leu	Glu	Ala	Val	Val	Thr	Met	Val	Asn	Lys
		115					120					125			
Met	Gly	Phe	Phe	Ala	Glu	Ala	Gly	Pro	Val	Gln	Ile	Phe	Val	Ser	Asn
		130				135					140				
His	Leu	Ile	Pro	Asp	Asp	Met	Glu	Phe	Gln	Ser	Xaa	Arg	Cys	Ala	Glu
145				150					155					160	
Leu	His	Asn	Phe												

(2) INFORMATION FOR SEQ ID NO:3500:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 130 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..130  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1577091  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3500:

Met Phe Phe His Ile Val Leu Glu Arg Asn Met Gln Leu His Pro Arg  
1                  5                  10                  15  
His Phe Gly Pro His Leu Arg Asp Lys Leu Val Ser Lys Leu Ile Lys  
                  20                  25                  30  
Asp Val Glu Gly Thr Cys Ser Gly Arg His Gly Phe Val Val Ala Ile  
                  35                  40                  45  
Thr Gly Val Glu Asp Ile Gly Lys Gly Leu Ile Arg Glu Gly Thr Gly  
                  50                  55                  60  
Tyr Val Thr Phe Pro Xaa Lys Tyr Gln Cys Val Val Phe Arg Pro Phe  
65                  70                  75                  80  
Lys Gly Glu Ile Leu Glu Ala Val Val Thr Met Val Asn Lys Met Gly  
                  85                  90                  95  
Phe Phe Ala Glu Ala Gly Pro Val Gln Ile Phe Val Ser Asn His Leu  
                  100                  105                  110  
Ile Pro Asp Asp Met Glu Phe Gln Ser Xaa Arg Cys Ala Glu Leu His  
                  115                  120                  125  
Asn Phe  
130

(2) INFORMATION FOR SEQ ID NO:3501:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 120 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
    (B) LOCATION: 1..120  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1577092

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3501:

Met Gln Leu His Pro Arg His Phe Gly Pro His Leu Arg Asp Lys Leu  
1                  5                  10                  15  
Val Ser Lys Leu Ile Lys Asp Val Glu Gly Thr Cys Ser Gly Arg His  
                  20                  25                  30  
Gly Phe Val Val Ala Ile Thr Gly Val Glu Asp Ile Gly Lys Gly Leu  
                  35                  40                  45  
Ile Arg Glu Gly Thr Gly Tyr Val Thr Phe Pro Xaa Lys Tyr Gln Cys  
50                  55                  60  
Val Val Phe Arg Pro Phe Lys Gly Glu Ile Leu Glu Ala Val Val Thr  
65                  70                  75                  80  
Met Val Asn Lys Met Gly Phe Phe Ala Glu Ala Gly Pro Val Gln Ile  
                  85                  90                  95  
Phe Val Ser Asn His Leu Ile Pro Asp Asp Met Glu Phe Gln Ser Xaa  
                  100                  105                  110  
Arg Cys Ala Glu Leu His Asn Phe  
115                  120

(2) INFORMATION FOR SEQ ID NO:3502:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 776 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(B) LOCATION: 1..776

(D) OTHER INFORMATION: / Ceres Seq. ID 1577122

gggcaactcg	aagaagccgc	gtgcgttata	ctttgagcag	tttgggcgct	gagcaagtcc	60
agtgagarar	ggagarcgc	gagaggatgg	ctgggatggc	atcgctgcag	ggcgccatGg	120
cgtcgctctc	catctccGcg	ctaggcgcg	cgacggcgag	cagcagcagc	ttctggggca	180
accggctcgc	cacctactcc	gcgccgcagc	ctggggtaag	gtttatggtc	aagatatgcc	240
caattgaatt	gagacttaag	agatgggagc	gaaagaagt	taaaccaaac	agtcttctcg	300
tgctgcacaa	gagtcattgt	aggatcgggg	acacgggtaca	ggttattgca	ggcgtgaga	360
aaggaaaggt	tggagaagtc	acacgccttt	tcaagcacia	cagcacggtg	atcgtgaagg	420
acctgaactt	gaagtogaag	cacaagaaa	gcacagacga	tgaacccggg	gaaatcgtca	480
tgattgaagg	ccccattcat	agctcaaatt	tgatgctcta	ctctaaggag	aagagtgtgg	540
taagcagggt	tggccacaaa	ttcctggagg	acgggaccaa	ggtccgatac	ctggtcaaga	600
ccggtgaagt	aatcgacagt	gttgagaagt	gggtaaaggt	ttttaaggaa	ggaaattcgg	660
agtaacagtt	ttagcatgaa	aacctgcaaa	atgctctgaa	cgctrmcgcg	ctttgcatgt	720
tgaattgagc	ctgtttatcc	ctctatgttg	tattttacgc	caatttttcc	cctgtg	

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..192

(D) OTHER INFORMATION: / Ceres Seq. ID 1577123

Met 1	Ala	Gly	Met 5	Ala	Ser	Leu	Gln	Gly	Ala 10	Met	Ala	Ser	Leu 15	Ser	Ile
Ser	Ala	Leu	Gly 20	Ala	Ala	Thr	Ala	Ser 25	Ser	Ser	Ser	Phe	Trp 30	Gly	Asn
Arg	Leu	Ala 35	Thr	Tyr	Ser	Ala	Pro 40	Gln	Pro	Gly	Val	Arg 45	Phe	Met	Val
Lys	Ile 50	Cys	Pro	Ile	Glu	Met 55	Arg	Leu	Lys	Arg	Trp 60	Glu	Arg	Lys	Lys
Cys 65	Lys	Pro	Asn	Ser	Leu 70	Pro	Val	Leu	His	Lys 75	Met	His	Val	Arg	Ile 80
Gly	Asp	Thr	Val	Gln 85	Val	Ile	Ala	Gly	Arg 90	Glu	Lys	Gly	Lys	Val 95	Gly
Glu	Val	Thr	Arg 100	Leu	Phe	Lys	His	Asn 105	Ser	Thr	Val	Ile	Val 110	Lys	Asp
Leu	Asn	Leu 115	Lys	Ser	Lys	His	Lys 120	Lys	Gly	Thr	Asp	Asp 125	Glu	Pro	Gly
Glu	Ile 130	Val	Met	Ile	Glu	Gly 135	Pro	Ile	His	Ser	Ser 140	Asn	Val	Met	Leu
Tyr 145	Ser	Lys	Glu	Lys	Ser 150	Val	Val	Ser	Arg	Val 155	Gly	His	Lys	Phe	Leu 160
Glu	Asp	Gly	Thr	Lys 165	Val	Arg	Tyr	Leu	Val 170	Lys	Thr	Gly	Glu	Val 175	Ile
Asp	Ser	Val	Glu 180	Lys	Trp	Val	Lys	Val 185	Phe	Lys	Glu	Gly	Asn 190	Ser	Glu

(2) INFORMATION FOR SEQ ID NO:3504:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 189 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..189

(D) OTHER INFORMATION: / Ceres Seq. ID 1577124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3504:

Met Ala Ser Leu Gln Gly Ala Met Ala Ser Leu Ser Ile Ser Ala Leu  
1 5 10 15  
Gly Ala Ala Thr Ala Ser Ser Ser Ser Phe Trp Gly Asn Arg Leu Ala  
20 25 30  
Thr Tyr Ser Ala Pro Gln Pro Gly Val Arg Phe Met Val Lys Ile Cys  
35 40 45  
Pro Ile Glu Met Arg Leu Lys Arg Trp Glu Arg Lys Lys Cys Lys Pro  
50 55 60  
Asn Ser Leu Pro Val Leu His Lys Met His Val Arg Ile Gly Asp Thr  
65 70 75 80  
Val Gln Val Ile Ala Gly Arg Glu Lys Gly Lys Val Gly Glu Val Thr  
85 90 95  
Arg Leu Phe Lys His Asn Ser Thr Val Ile Val Lys Asp Leu Asn Leu  
100 105 110  
Lys Ser Lys His Lys Lys Gly Thr Asp Asp Glu Pro Gly Glu Ile Val  
115 120 125  
Met Ile Glu Gly Pro Ile His Ser Ser Asn Val Met Leu Tyr Ser Lys  
130 135 140  
Glu Lys Ser Val Val Ser Arg Val Gly His Lys Phe Leu Glu Asp Gly  
145 150 155 160  
Thr Lys Val Arg Tyr Leu Val Lys Thr Gly Glu Val Ile Asp Ser Val  
165 170 175  
Glu Lys Trp Val Lys Val Phe Lys Glu Gly Asn Ser Glu  
180 185

(2) INFORMATION FOR SEQ ID NO:3505:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 182 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..182

(D) OTHER INFORMATION: / Ceres Seq. ID 1577125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3505:

Met Ala Ser Leu Ser Ile Ser Ala Leu Gly Ala Ala Thr Ala Ser Ser  
1 5 10 15  
Ser Ser Phe Trp Gly Asn Arg Leu Ala Thr Tyr Ser Ala Pro Gln Pro  
20 25 30  
Gly Val Arg Phe Met Val Lys Ile Cys Pro Ile Glu Met Arg Leu Lys  
35 40 45  
Arg Trp Glu Arg Lys Lys Cys Lys Pro Asn Ser Leu Pro Val Leu His  
50 55 60  
Lys Met His Val Arg Ile Gly Asp Thr Val Gln Val Ile Ala Gly Arg  
65 70 75 80  
Glu Lys Gly Lys Val Gly Glu Val Thr Arg Leu Phe Lys His Asn Ser  
85 90 95  
Thr Val Ile Val Lys Asp Leu Asn Leu Lys Ser Lys His Lys Lys Gly  
100 105 110  
Thr Asp Asp Glu Pro Gly Glu Ile Val Met Ile Glu Gly Pro Ile His  
115 120 125  
Ser Ser Asn Val Met Leu Tyr Ser Lys Glu Lys Ser Val Val Ser Arg  
130 135 140  
Val Gly His Lys Phe Leu Glu Asp Gly Thr Lys Val Arg Tyr Leu Val

(2) INFORMATION FOR SEQ ID NO:3506:

(A) LENGTH: 814 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) NAME/KEY: -

(B) LOCATION: 1..814

(D) OTHER INFORMATION: / Ceres Seq. ID 1577130

agtgtaaacc	agcccaccc	cctccccgtc	tctctctcc	ccccatgcgc	tgttttggtc	60
tgtattgggt	tgtgcgcggg	ggacaggacg	cctcctgcgc	cgaccgttcc	gttcgtgttt	120
gtgcctgcct	gtgccttcgg	ttgttccctc	gagcgacggc	gagtcggcga	ccgaggggga	180
ccacagacgc	attagctggg	tgaactcttt	caaaaggggc	aggtgcgc	gtttgaatgg	240
ctgctacaaa	gcttcagggc	ttttggaacc	accctgctgg	ccccaaaacc	attcattttc	300
ggcgcccaac	attcaaatgg	ggatatcagca	ttgccaacat	agccgacttt	gcaaaagccgc	360
ctgaaaagat	atcttaccct	cagcaagttg	ctgttgcatg	cactggaatc	atttggtaa	420
ggtacagctt	ggttatcaca	ccgaaaaaact	ggaacctttt	cagtgttaac	gttgcaatgg	480
cgggtacagg	cctgtatcag	ctttcacgga	agattagsca	agattacNtt	gtctggtgag	540
aaggatgNct	gNctccacaa	ctgNcaagaa	tagataatga	caacacacaa	agaataactg	600
attgagaagt	ctgnccggct	agggatctta	ctcttgattt	ttctgggnca	ggncaaggat	660
atgtctcgat	ccaggacggg	tcatgtttgt	tttctgttgc	ttctgaaatc	atgagncagg	720
ttaatgtgaa	aatctcctgc	caaaaaaaga	agcccatgaa	gtaatatattt	gtgcattttt	780
gtgggaaaaa	agtcatgncc	aggacatgat	tctgt			

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..64

(D) OTHER INFORMATION: / Ceres Seq. ID 1577131

Ser	Val	Asn	Gln	Pro	Thr	Leu	Leu	Pro	Val	Ser	Ser	Pro	Ser	Pro	Cys
1				5					10					15	
Ala	Val	Leu	Phe	Cys	Ile	Gly	Leu	Cys	Ala	Gly	Asp	Arg	Thr	Pro	Pro
			20					25					30		
Ala	Pro	Thr	Val	Pro	Phe	Val	Phe	Val	Pro	Ala	Cys	Ala	Phe	Gly	Cys
			35				40					45			
Ser	Ser	Glu	Arg	Arg	Arg	Val	Gly	Asp	Arg	Gly	Gly	Pro	Gln	Thr	His
	50					55					60				

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:



- (A) NAME/KEY: peptide  
(B) LOCATION: 1..100  
(D) OTHER INFORMATION: / Ceres Seq. ID 1577132

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3508:

```
Met Ala Ala Thr Lys Leu Gln Ala Phe Trp Asn His Pro Ala Gly Pro
1      5      10      15
Lys Thr Ile His Phe Trp Ala Pro Thr Phe Lys Trp Gly Ile Ser Ile
      20      25      30
Ala Asn Ile Ala Asp Phe Ala Lys Pro Pro Glu Lys Ile Ser Tyr Pro
      35      40      45
Gln Gln Val Ala Val Ala Cys Thr Gly Ile Ile Trp Ser Arg Tyr Ser
      50      55      60
Leu Val Ile Thr Pro Lys Asn Trp Asn Leu Phe Ser Val Asn Val Ala
      65      70      75      80
Met Ala Gly Thr Gly Leu Tyr Gln Leu Ser Arg Lys Ile Xaa Gln Asp
      85      90      95
Tyr Xaa Val Trp
      100
```

(2) INFORMATION FOR SEQ ID NO:3509:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 764 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..764  
(D) OTHER INFORMATION: / Ceres Seq. ID 1577133

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3509:

```
gaaatacccg ccgtacagc ctactgctgg acatctaagg gccacactga aaaaaccctt      60
gcgcgcgtga gctgagtgccc cttcccttct ctcgtgcgct ccgcctccgc cttcagttta      120
gcctccaagc aggggcgcgc cgcggggtat tctgtccgtc gttgaggata gagagtcact      180
tgcaccgggg gagcggagat gaagccgggt gtggggatcg tgggtgctgaa caagatgcag      240
aagtcgggtg tgggtgcatt ggaccgcctc ttccacaacC Aaaggtatac Aaaccgctac      300
gtcaagcgca cHctCccaag ttcatggcac acgacgatga caacacctgc aacattggcg      360
aCccgggtta ggctggatcc Tttctaggcc cttgagcaga cacaagcact gggttgttgc      420
tgaaattctc cgcagagcta aggtgtacgt tccaccagct gcaacagcgt ccagtgaacg      480
tggtagcaaa tctcaacaag ctgggtgtgc taocaaatga tccatctgaa gttactcaga      540
acaagatgca gtcacggctt gtttttcttt cgtgtatgt ttgtttcctt gtggaatgtg      600
gttgccatgt ttagcatggg agaaaaaata gcaagcagcc agcatctttg cttaattact      660
gttgttcttc tgtggtgtcc ttogtttaac ggtactagcc attaaggatg tagttaccag      720
attcaacaag accaatggat tcatattgta ttggttcaact tccg
```

(2) INFORMATION FOR SEQ ID NO:3510:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..62  
(D) OTHER INFORMATION: / Ceres Seq. ID 1577134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3510:

```
Met Lys Pro Val Val Gly Ile Val Val Ser Asn Lys Met Gln Lys Ser
1      5      10      15
Val Val Val Ala Leu Asp Arg Leu Phe His Asn Gln Arg Tyr Thr Asn
      20      25      30
Arg Tyr Val Lys Arg Xaa Leu Pro Ser Ser Trp His Thr Thr Met Thr
      35      40      45
```

Thr Pro Ala Thr Leu Ala Thr Arg Val Arg Leu Asp Pro Phe  
50 55 60

(2) INFORMATION FOR SEQ ID NO:3511:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..50

(D) OTHER INFORMATION: / Ceres Seq. ID 1577135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3511:

Met Gln Lys Ser Val Val Val Ala Leu Asp Arg Leu Phe His Asn Gln  
1 5 10 15  
Arg Tyr Thr Asn Arg Tyr Val Lys Arg Xaa Leu Pro Ser Ser Trp His  
20 25 30  
Thr Thr Met Thr Thr Pro Ala Thr Leu Ala Thr Arg Val Arg Leu Asp  
35 40 45  
Pro Phe  
50

(2) INFORMATION FOR SEQ ID NO:3512:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..62

(D) OTHER INFORMATION: / Ceres Seq. ID 1577136

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3512:

Met Ile His Leu Lys Leu Leu Arg Thr Arg Cys Ser His Gly Leu Phe  
1 5 10 15  
Phe Phe Arg Cys Met Phe Val Ser Leu Trp Asn Val Val Ala Met Phe  
20 25 30  
Ser Met Gly Glu Lys Ile Ala Ser Ser Gln His Leu Cys Leu Ile Thr  
35 40 45  
Val Val Leu Leu Trp Cys Pro Ser Phe Asn Gly Thr Ser His  
50 55 60

(2) INFORMATION FOR SEQ ID NO:3513:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 698 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..698

(D) OTHER INFORMATION: / Ceres Seq. ID 1577137

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3513:

tgcataatg tccggcgggt aattcatttt gctagctttct cctaacgata cgccgggtggt	60
tcttaattca atgcgtttat acgtgtagct ggagaagctg gccgagatgc tgcacgagcc	120
gccgcagggc aagtactacg gcggcaatgc ggacgacgtg cgctcgggcg gcgtcggcgg	180
cacgaaggag gaggaggagt Cccacagacg cctgcgcgcg ggccgcgctc tactcgtccg	240
agtgcgctgg cggtggcagg ttcacgcgc acttccttggc ggacgacgac gtgggagcag	300
ccctcttccg gccgccgtcg tctccgcagc cgaccgctgg ctactcacg tcgtcggggc	360
cgccggagca ccagccgttc cagttccact ccggctactg ctggccgtcg tcgtcggcgg	420

aGcagacctg cagcggctcg caatggtggg agttcgagtc cctcagcgag tgacgtacga 480  
tgatcacaag cggccggggg tcaactcggtt ccaagcacac gtaagggccg ggccaatacg 540  
agttcgttcg tagcgggtctc gtcactcgtc agctagccct gcagagcaac ggtgtatgca 600  
tagcttcagt agatcgaagt ccaggtccag gactgcccatt caagcagttt cttcttctcg 660  
ccatcgatca tcgatcatgc atgcaaaaga tttttttt

(2) INFORMATION FOR SEQ ID NO:3514:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..148

(D) OTHER INFORMATION: / Ceres Seq. ID 1577138

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3514:

Met Leu His Glu Pro Pro Gln Gly Lys Tyr Tyr Gly Gly Asn Ala Asp  
1 5 10 15  
Asp Val Arg Ser Gly Gly Val Gly Gly Thr Lys Glu Glu Glu Glu Ser  
20 25 30  
His Arg Arg Leu Arg Arg Gly Arg Ala Leu Leu Val Arg Val Arg Trp  
35 40 45  
Arg Trp Gln Val His Arg Ala Leu Leu Gly Gly Arg Arg Arg Gly Ser  
50 55 60  
Ser Pro Leu Pro Ala Ala Val Val Ser Ala Ala Asp Arg Trp Leu Thr  
65 70 75 80  
His Val Val Gly Ala Ala Gly Ala Pro Ala Val Pro Val Pro Leu Arg  
85 90 95  
Leu Leu Leu Ala Val Val Val Gly Gly Ala Asp Leu Gln Arg Leu Ala  
100 105 110  
Met Val Gly Val Arg Val Pro Gln Arg Val Thr Tyr Asp Asp His Lys  
115 120 125  
Arg Pro Gly Val Thr Arg Phe Gln Ala His Val Arg Ala Gly Pro Ile  
130 135 140  
Arg Val Arg Ser  
145

(2) INFORMATION FOR SEQ ID NO:3515:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..108

(D) OTHER INFORMATION: / Ceres Seq. ID 1577139

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3515:

Met Arg Thr Thr Cys Ala Arg Ala Ala Ser Ala Ala Arg Arg Arg Arg  
1 5 10 15  
Arg Ser Pro Thr Asp Ala Cys Ala Gly Ala Ala Leu Tyr Ser Ser Glu  
20 25 30  
Cys Ala Gly Gly Gly Arg Phe Ile Ala His Phe Leu Ala Asp Asp Asp  
35 40 45  
Val Gly Ala Ala Leu Phe Arg Pro Pro Ser Ser Pro Gln Pro Thr Ala  
50 55 60  
Gly Leu Leu Thr Ser Ser Gly Pro Pro Glu His Gln Pro Phe Gln Phe  
65 70 75 80  
His Ser Gly Tyr Cys Trp Pro Ser Ser Ser Ala Glu Gln Thr Cys Ser  
85 90 95

Gly Ser Gln Trp Trp Glu Phe Glu Ser Leu Ser Glu  
100 105

(2) INFORMATION FOR SEQ ID NO:3516:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 570 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..570
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577146

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3516:

aaagaattag tgggagtgc aactgaagtt gtgtatgaga aatgcccac cgaagctatg	60
attgaaactg gggggttttc ctatgcggtg gtggttggtg gagaggttcc atatgccgaa	120
ttgacaggag atagaactga ccttagtatt cgttttaatg gctctgacct tatcatccgt	180
gttgcaagta aaatccctac cctagtgtat gttatatctg gaaggccatt aattattgag	240
tcacaagttt tggaaaagat agaagctcta gtcgctgcct ggctgcctgg aagtgagggc	300
atgggaatta ccgattgcct ctttgagat catgattttg tgggcacatt gcctgtgaca	360
tgggtgaagt ctgttgatca attgcctata gatctggag actctaacta tgaccgcgta	420
ttccctgttg gatattgggt aaaaatgttt cgaagcgata atgattcaac ataactttat	480
tattttattg gtacatttga atctttgtga tgttaaatac tctgtattta ttggctattg	540
gGaaactaaa atgaaataat atattgttgt	

(2) INFORMATION FOR SEQ ID NO:3517:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..157
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577147

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3517:

Lys	Glu	Leu	Val	Gly	Val	Gln	Thr	Glu	Val	Tyr	Glu	Lys	Cys	Pro
1			5					10					15	
Thr	Glu	Ala	Met	Ile	Glu	Thr	Gly	Gly	Phe	Ser	Tyr	Ala	Val	Val
		20					25					30		
Val	Gly	Glu	Val	Pro	Tyr	Ala	Glu	Leu	Thr	Gly	Asp	Arg	Thr	Asp
		35					40				45			
Ser	Ile	Pro	Phe	Asn	Gly	Ser	Asp	Leu	Ile	Ile	Arg	Val	Ala	Ser
		50				55					60			Lys
Ile	Pro	Thr	Leu	Val	Ile	Val	Ile	Ser	Gly	Arg	Pro	Leu	Ile	Ile
		65			70				75					80
Ser	Gln	Val	Leu	Glu	Lys	Ile	Glu	Ala	Leu	Val	Ala	Ala	Trp	Leu
			85					90					95	Pro
Gly	Ser	Glu	Gly	Met	Gly	Ile	Thr	Asp	Cys	Leu	Phe	Gly	Asp	His
			100				105					110		Asp
Phe	Val	Gly	Thr	Leu	Pro	Val	Thr	Trp	Cys	Lys	Ser	Val	Asp	Gln
		115				120						125		Leu
Pro	Ile	Asp	Ala	Gly	Asp	Ser	Asn	Tyr	Asp	Pro	Leu	Phe	Pro	Val
		130				135					140			Gly
Tyr	Gly	Leu	Lys	Met	Phe	Arg	Ser	Asp	Asn	Asp	Ser	Thr		
		145			150					155				

(2) INFORMATION FOR SEQ ID NO:3518:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..138  
(D) OTHER INFORMATION: / Ceres Seq. ID 1577148

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3518:

Met Ile Glu Thr Gly Gly Phe Ser Tyr Ala Val Val Val Val Gly Glu  
1                  5                  10                  15  
Val Pro Tyr Ala Glu Leu Thr Gly Asp Arg Thr Asp Leu Ser Ile Pro  
                  20                  25                  30  
Phe Asn Gly Ser Asp Leu Ile Ile Arg Val Ala Ser Lys Ile Pro Thr  
                  35                  40                  45  
Leu Val Ile Val Ile Ser Gly Arg Pro Leu Ile Ile Glu Ser Gln Val  
                  50                  55                  60  
Leu Glu Lys Ile Glu Ala Leu Val Ala Ala Trp Leu Pro Gly Ser Glu  
65                  70                  75                  80  
Gly Met Gly Ile Thr Asp Cys Leu Phe Gly Asp His Asp Phe Val Gly  
                  85                  90                  95  
Thr Leu Pro Val Thr Trp Cys Lys Ser Val Asp Gln Leu Pro Ile Asp  
                  100                 105                 110  
Ala Gly Asp Ser Asn Tyr Asp Pro Leu Phe Pro Val Gly Tyr Gly Leu  
                 115                 120                 125  
Lys Met Phe Arg Ser Asp Asn Asp Ser Thr  
                 130                 135

(2) INFORMATION FOR SEQ ID NO:3519:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 1047 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..1047  
(D) OTHER INFORMATION: / Ceres Seq. ID 1577163

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3519:

agccacaccc ggacacccca cacaggcacg aggcaaccag ccacgcgagc ggcgaaactg          60  
cgggagccaa tcagaacctc cagcgatgca atgatcgccg tcgcatcgtc cttcccctcg         120  
cgcgccacag cggctccgtt cggctcgggg acaactgccac cgccgtctac gcggcgcasa         180  
cgtcctcccg ccacccgcgc gtctcggcgc tcggtggagg cctcgaagga gagccgggga         240  
agatactgga tccgcgcgcc acgccgttcc agatcctcgg cctcgacgcc gccgcgggct         300  
actccgcgcg cgaactcaag gccgcttttc gcgccggggt taaggaattc catcctgatg         360  
tttgcaagga cccagaaaaat gcagatttaa taatgaggcg agtgatcgag gcctatcaga         420  
tggtatctgg caaccaagaa atgatgtttg aaaggaacaa tggtgaccca tttgatgaac         480  
ctgagtgtga agctcgtgac atatttgtca atgaacttct atgcattggc actggatgtc         540  
catattcttg tgttaaaagg gcaCctcatg tattttcatt ttcagatgat actggtacag         600  
ctcgtgcaat atctcaaggt aatggagaag atgatcttgt tcagctcgct gttgggcagt         660  
gtccaagaaa gtgcatatac tatgtgacgc cttgccaaac cactattttg gaggatgttc         720  
ttgctagtgt gttgatggtg cttacgatc ttgctgaagc agcagttctg gattccctcc         780  
tttcaaaagc gaagtctgag aataacaggt ataagaagcc ccaaagagga gcaaaatcat         840  
cctccgatta tgttgattgg atgtgatctg atcccagagc acaaagagga tgccagattc         900  
agccgaaggc agttcggtag atttatgctg gtttgccctat tctccttggt cagttgcccc         960  
atagtttata aaatggaata cgtttacgtg gacagactgc tttgtttgtg gtatacgggt         1020  
atgatttcta taatatttct ttctgcc

(2) INFORMATION FOR SEQ ID NO:3520:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 287 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..287

(D) OTHER INFORMATION: / Ceres Seq. ID 1577164

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3520:

Pro	His	Pro	Asp	Thr	Pro	His	Arg	His	Glu	Ala	Thr	Ser	His	Ala	Ser	
1				5					10					15		
Gly	Glu	Thr	Ala	Gly	Ala	Asn	Gln	Asn	Leu	Gln	Arg	Cys	Asn	Asp	Arg	
			20					25					30			
Arg	Arg	Ile	Val	Leu	Pro	Leu	Ala	Arg	Pro	Arg	Gly	Ser	Val	Arg	Leu	
			35				40					45				
Gly	Asp	Thr	Ala	Thr	Ala	Val	Tyr	Ala	Ala	Xaa	Thr	Ser	Leu	Arg	His	
	50					55					60					
Pro	Arg	Val	Ser	Ala	Leu	Gly	Gly	Gly	Leu	Glu	Gly	Glu	Pro	Gly	Lys	
65					70					75					80	
Ile	Leu	Asp	Pro	Arg	Ala	Thr	Pro	Phe	Gln	Ile	Leu	Gly	Leu	Asp	Ala	
				85					90					95		
Ala	Ala	Gly	Tyr	Ser	Ala	Ala	Glu	Leu	Lys	Ala	Ala	Phe	Arg	Ala	Arg	
			100					105					110			
Val	Lys	Glu	Phe	His	Pro	Asp	Val	Cys	Lys	Asp	Pro	Glu	Asn	Ala	Asp	
		115					120					125				
Leu	Ile	Met	Arg	Arg	Val	Ile	Glu	Ala	Tyr	Gln	Met	Leu	Ser	Gly	Asn	
	130					135					140					
Gln	Glu	Met	Met	Phe	Glu	Arg	Asn	Asn	Val	Asp	Pro	Phe	Asp	Glu	Pro	
145					150					155					160	
Glu	Cys	Glu	Ala	Arg	Asp	Ile	Phe	Val	Asn	Glu	Leu	Leu	Cys	Ile	Gly	
				165					170					175		
Thr	Gly	Cys	Pro	Tyr	Ser	Cys	Val	Lys	Arg	Ala	Pro	His	Val	Phe	Ser	
			180					185					190			
Phe	Ser	Asp	Asp	Thr	Gly	Thr	Ala	Arg	Ala	Ile	Ser	Gln	Gly	Asn	Gly	
		195					200					205				
Glu	Asp	Asp	Leu	Val	Gln	Leu	Ala	Val	Gly	Gln	Cys	Pro	Arg	Lys	Cys	
	210					215					220					
Ile	Tyr	Tyr	Val	Thr	Pro	Cys	Gln	His	Thr	Ile	Leu	Glu	Asp	Val	Leu	
225					230					235					240	
Ala	Ser	Val	Leu	Met	Val	Pro	Tyr	Asp	Leu	Ala	Glu	Ala	Ala	Val	Leu	
				245					250					255		
Asp	Ser	Leu	Leu	Ser	Lys	Ala	Lys	Phe	Glu	Asn	Asn	Arg	Tyr	Lys	Lys	
		260						265					270			
Pro	Gln	Arg	Gly	Ala	Lys	Ser	Ser	Ser	Asp	Tyr	Val	Asp	Trp	Met		
	275						280						285			

(2) INFORMATION FOR SEQ ID NO:3521:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 157 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..157

(D) OTHER INFORMATION: / Ceres Seq. ID 1577165

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3521:

Met	Arg	Arg	Val	Ile	Glu	Ala	Tyr	Gln	Met	Leu	Ser	Gly	Asn	Gln	Glu	
1				5					10					15		
Met	Met	Phe	Glu	Arg	Asn	Asn	Val	Asp	Pro	Phe	Asp	Glu	Pro	Glu	Cys	
			20					25					30			
Glu	Ala	Arg	Asp	Ile	Phe	Val	Asn	Glu	Leu	Leu	Cys	Ile	Gly	Thr	Gly	
		35					40					45				
Cys	Pro	Tyr	Ser	Cys	Val	Lys	Arg	Ala	Pro	His	Val	Phe	Ser	Phe	Ser	

50 55 60  
Asp Asp Thr Gly Thr Ala Arg Ala Ile Ser Gln Gly Asn Gly Glu Asp  
65 70 75 80  
Asp Leu Val Gln Leu Ala Val Gly Gln Cys Pro Arg Lys Cys Ile Tyr  
85 90 95  
Tyr Val Thr Pro Cys Gln His Thr Ile Leu Glu Asp Val Leu Ala Ser  
100 105 110  
Val Leu Met Val Pro Tyr Asp Leu Ala Glu Ala Ala Val Leu Asp Ser  
115 120 125  
Leu Leu Ser Lys Ala Lys Phe Glu Asn Asn Arg Tyr Lys Lys Pro Gln  
130 135 140  
Arg Gly Ala Lys Ser Ser Asp Tyr Val Asp Trp Met  
145 150 155

(2) INFORMATION FOR SEQ ID NO:3522:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..148
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577166

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3522:

Met Leu Ser Gly Asn Gln Glu Met Met Phe Glu Arg Asn Asn Val Asp  
1 5 10 15  
Pro Phe Asp Glu Pro Glu Cys Glu Ala Arg Asp Ile Phe Val Asn Glu  
20 25 30  
Leu Leu Cys Ile Gly Thr Gly Cys Pro Tyr Ser Cys Val Lys Arg Ala  
35 40 45  
Pro His Val Phe Ser Phe Ser Asp Asp Thr Gly Thr Ala Arg Ala Ile  
50 55 60  
Ser Gln Gly Asn Gly Glu Asp Asp Leu Val Gln Leu Ala Val Gly Gln  
65 70 75 80  
Cys Pro Arg Lys Cys Ile Tyr Tyr Val Thr Pro Cys Gln His Thr Ile  
85 90 95  
Leu Glu Asp Val Leu Ala Ser Val Leu Met Val Pro Tyr Asp Leu Ala  
100 105 110  
Glu Ala Ala Val Leu Asp Ser Leu Leu Ser Lys Ala Lys Phe Glu Asn  
115 120 125  
Asn Arg Tyr Lys Lys Pro Gln Arg Gly Ala Lys Ser Ser Ser Asp Tyr  
130 135 140  
Val Asp Trp Met  
145

(2) INFORMATION FOR SEQ ID NO:3523:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..832
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577167

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3523:

attttcgtca cccctgacgc tcgacgcctc tctctctctc cdccccacc cgtccatcgc 60  
ccctccctcc ggtctgcgct ccacagcct caccctgcg cccccgccga ttgcgctcgc 120  
cctttgttg aaggaacgat ggagcagacc ttcatcatga tcaagcccga cggcgtccag 180  
cggggcctga tcggggacat catcagtcgc ttcgagaaga aagggttcta cctcaagggg 240

atgaagttca tgaacgtgga gaggtccttc ggcagCCag cactacgctg acctttccga 300  
caagcctttc ttYCCCCgg gttggtggag tacatcattt cgggccccgt ggtggcgatg 360  
gtgtgggagg ggaaggacgt cgtgttgact ggccgcaGga tcattggggc caccaggcct 420  
tgggaggcag cccccgtac cattcgtggg gactacgccg tggaagtcgg caggaatgtc 480  
atccatggaa gcgactccgt ggagaacggg aagaaggaga tcgctctctg gttccctgaa 540  
ggtgtggcac agtgggaagag caaccttcat ccctggatct acgaggcttg agcagttgag 600  
cttgatgcc ttgcctgctc catggaaacc agagttttgt ttgagtatta tctgttggt 660  
ctggctgaag agtcataatt tagcgtctctg tgtgttacac cagagttaag tctgcctgaa 720  
cttatgtggc atttgtttga gtttctgcct tcgtgccttg ttttctaatt taccgtggt 780  
gtgaaccggc caatgtgatc tgaaataaaa cattgcgtgc caagtttgtg tc

(2) INFORMATION FOR SEQ ID NO:3524:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..96

(D) OTHER INFORMATION: / Ceres Seq. ID 1577168

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3524:

Ile Phe Val Thr Pro Asp Ala Arg Arg Leu Ser Ser Ser Xaa Pro Pro  
1 5 10 15  
Pro Val His Arg Pro Ser Leu Arg Ser Ala Leu Pro Gln Pro His Pro  
20 25 30  
Cys Ala Pro Ala Asp Ser Arg Arg Pro Leu Leu Glu Gly Thr Met Glu  
35 40 45  
Gln Thr Phe Ile Met Ile Lys Pro Asp Gly Val Gln Arg Gly Leu Ile  
50 55 60  
Gly Asp Ile Ile Ser Arg Phe Glu Lys Lys Gly Phe Tyr Leu Lys Gly  
65 70 75 80  
Met Lys Phe Met Asn Val Glu Arg Ser Phe Ala Gln Pro Ala Leu Arg  
85 90 95

(2) INFORMATION FOR SEQ ID NO:3525:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..77

(D) OTHER INFORMATION: / Ceres Seq. ID 1577169

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3525:

Met Val Trp Glu Gly Lys Asp Val Val Leu Thr Gly Arg Arg Ile Ile  
1 5 10 15  
Gly Ala Thr Arg Pro Trp Glu Ala Ala Pro Gly Thr Ile Arg Gly Asp  
20 25 30  
Tyr Ala Val Glu Val Gly Arg Asn Val Ile His Gly Ser Asp Ser Val  
35 40 45  
Glu Asn Gly Lys Lys Glu Ile Ala Leu Trp Phe Pro Glu Gly Val Ala  
50 55 60  
Gln Trp Lys Ser Asn Leu His Pro Trp Ile Tyr Glu Ala  
65 70 75

(2) INFORMATION FOR SEQ ID NO:3526:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids



(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..77  
(D) OTHER INFORMATION: / Ceres Seq. ID 1577170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3526:

```
Met Ser Ser Met Glu Ala Thr Pro Trp Arg Thr Gly Arg Arg Arg Ser
1          5          10          15
Leu Ser Gly Ser Leu Lys Val Trp His Ser Gly Arg Ala Thr Phe Ile
20          25          30
Pro Gly Ser Thr Arg Leu Glu Gln Leu Ser Leu Asp Ala Leu Pro Ala
35          40          45
Pro Trp Lys Pro Glu Phe Cys Leu Ser Ile Ile Cys Trp Leu Trp Leu
50          55          60
Lys Ser His Asn Leu Ala Leu Cys Val Leu His Gln Ser
65          70          75
```

(2) INFORMATION FOR SEQ ID NO:3527:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 866 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..866  
(D) OTHER INFORMATION: / Ceres Seq. ID 1577175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3527:

```
gtttctctcct cctggctcct ggggtctcatc tcttcccttc gcttcgcaag gccacaacagg      60
aactccacca cgcacggccg caccgcacc cgcacccgct ctctgctgcc atggcgctcgt      120
ccttcgtcgc gctcaccggt atgttcgggt tcaccgcagc cctgtgctgc ctccagctcc      180
tcggcgcgga caccacggcc acgaccacga cccagagcgg tctcgcgcg ctaggcgcgg      240
cctccctggt cccggcggtc ctggscgccc tgacgctgac cccgctgcty gcgttcgcgc      300
gcgtgcacgC ccgtGccggg gcggaggggg cgctcgtgtc gggccttgcc aaggcgacc      360
tcctcgcggg gacgggtggct ctcgtcgcgg cgcccggtgg gcagctcggc gccgacggc      420
acctcgaccg cggncgcagc acgtcgcgog cctgaacgtg aagtgaagca agaagcaatc      480
ccccctcct tcttctcctg actataaaaa taacctgcgc caagcgtcgg cgtgtcgtcg      540
ctggaggcgt ctggacgacc ggaccactgc taggtcctc gctctgctcg atccgttcgg      600
agctcagcgc gtctgggctt tctgatggcg gcggcgctct aaggagaagg gggtgattaa      660
tgtttggcgt gcccccggtg ccgtgcgggt aaaaaggagg atacttttat tttgttttcc      720
tccgtatatg ttggcctagt sttgcgttc tggatttgtg gtaagctcac tgtctatgta      780
atcccactgg gactgggatt tcagtttgc ttttcacctc ctggacggtc ttgtaaatat      840
atatatatat atactgtgtt tcagtt
```

(2) INFORMATION FOR SEQ ID NO:3528:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 154 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..154  
(D) OTHER INFORMATION: / Ceres Seq. ID 1577176

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3528:

```
Phe Ser Pro Pro Gly Ser Trp Val Ser Ser Pro Pro Phe Ala Ser Gln
1          5          10          15
Gly Gln Gln Gly Thr Pro Pro Arg Thr Ala Ala Pro Ala Pro Ala Pro
```

20 25 30  
Ala Leu Cys Cys His Gly Val Val Leu Arg Arg Ala His Arg Tyr Val  
35 40 45  
Arg Leu His Arg Ser Pro Val Leu Pro Pro Ala Pro Arg Arg Gly His  
50 55 60  
His Gly His Asp His Asp Pro Glu Arg Ser Arg Ala Pro Gly Arg Gly  
65 70 75 80  
Leu Pro Gly Pro Gly Gly Pro Xaa Arg Pro Asp Ala Asp Pro Ala Ala  
85 90 95  
Xaa Val Arg Ala Arg Ala Arg Pro Cys Arg Gly Gly Gly Gly Ala Arg  
100 105 110  
Val Gly Pro Cys Gln Gly Asp Pro Pro Arg Gly Asp Gly Gly Ser Arg  
115 120 125  
Arg Gly Gly Arg Gly Ala Ala Arg Arg Arg Arg Ala Pro Arg Pro Arg  
130 135 140  
Xaa Asp Asp Val Ala Arg Leu Asn Val Lys  
145 150

(2) INFORMATION FOR SEQ ID NO:3529:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..150

(D) OTHER INFORMATION: / Ceres Seq. ID 1577177

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3529:

Ser Leu Leu Leu Ala Pro Gly Ser His Leu Leu Pro Ser Leu Arg Lys  
1 5 10 15  
Ala Asn Lys Glu Leu His His Ala Arg Pro His Pro His Pro His Pro  
20 25 30  
Leu Ser Ala Ala Met Ala Ser Ser Phe Val Ala Leu Thr Val Met Phe  
35 40 45  
Gly Phe Thr Ala Ala Leu Cys Cys Leu Gln Leu Leu Gly Ala Asp Thr  
50 55 60  
Thr Ala Thr Thr Thr Thr Gln Ser Gly Leu Ala Arg Leu Ala Ala Ala  
65 70 75 80  
Ser Leu Val Pro Ala Val Leu Xaa Ala Leu Thr Leu Thr Pro Leu Xaa  
85 90 95  
Ala Phe Ala Arg Val His Ala Arg Ala Gly Ala Glu Gly Ala Leu Val  
100 105 110  
Ser Gly Leu Ala Lys Ala Thr Leu Ala Gly Thr Val Ala Leu Val  
115 120 125  
Ala Ala Ala Val Val Gln Leu Gly Ala Asp Gly His Leu Asp Arg Xaa  
130 135 140  
Pro Thr Thr Ser Arg Ala  
145 150

(2) INFORMATION FOR SEQ ID NO:3530:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..114

(D) OTHER INFORMATION: / Ceres Seq. ID 1577178

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3530:

11/11/2011 11:11:11

Met Ala Ser Ser Phe Val Ala Leu Thr Val Met Phe Gly Phe Thr Ala  
1 5 10 15  
Ala Leu Cys Cys Leu Gln Leu Leu Gly Ala Asp Thr Thr Ala Thr Thr  
20 25 30  
Thr Thr Gln Ser Gly Leu Ala Arg Leu Ala Ala Ala Ser Leu Val Pro  
35 40 45  
Ala Val Leu Xaa Ala Leu Thr Leu Thr Pro Leu Xaa Ala Phe Ala Arg  
50 55 60  
Val His Ala Arg Ala Gly Ala Glu Gly Ala Leu Val Ser Gly Leu Ala  
65 70 75 80  
Lys Ala Thr Leu Leu Ala Gly Thr Val Ala Leu Val Ala Ala Ala Val  
85 90 95  
Val Gln Leu Gly Ala Asp Gly His Leu Asp Arg Xaa Pro Thr Thr Ser  
100 105 110  
Arg Ala

(2) INFORMATION FOR SEQ ID NO:3531:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 782 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..782
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577198

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3531:

gccttcaacc atcgtttagag tttccttggt agtttttttc cctcttggtca cagcaccoccc 60  
caccacacac cacccaaggc cccaactgca gtgcccatcc ggcagacagg tcgatggcgg 120  
cggaagcagc ggcagcghng gaaggagaag atgcggacgc tagtcagcag cgacttcaag 180  
aagttcgatg tggaggagtc tgtggcgagg gaatcgctga ttatcctgaa cctgatggcg 240  
gactgogacg acagtgacat cccgggtcttc aacgtcaacg ccaatatcct cgacaaggtc 300  
atcgcgctact gcaggaagca cgccctyggcg ccgcgcscga NTtggcggtg atgcggaGcc 360  
aagtgtctgcg agtaacaagg cctcagcggg cgatctcaag tcctttgatg ctgagttcgt 420  
cgatgttgac ctgggtcacc tcttgagact cattaaggct gcagactacc tggagatcaa 480  
tgggctgctg gacctgacct gccaggccgt cgcggacatg atcaagggga agactccaga 540  
ggagatacgc gagacattcg acatcgagaa tgacttcaca cctgaggaag aggctaaagt 600  
gaggagggag aatcagtggt cctttgaatg aagaagctgc aggctagctc taacaaaaca 660  
atagcaatat catataacca ggccagagat gaagtgtctg ttcaggatgt tatgagtcga 720  
aggtttggtt ggtcgtgagc agactatatt gctgttccag tattttggct ggtttggttc 780  
cc

(2) INFORMATION FOR SEQ ID NO:3532:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..53
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577199

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3532:

Pro Ser Thr Ile Val Arg Val Ser Leu Val Val Phe Phe Pro Leu Val  
1 5 10 15  
Thr Ala Pro Pro Thr His Thr His Pro Arg Pro Gln Leu Gln Cys Pro  
20 25 30  
Ser Gly Arg Gln Val Asp Gly Gly Gly Ser Ser Gly Ser Xaa Gly Arg  
35 40 45  
Arg Arg Cys Gly Arg

50

(2) INFORMATION FOR SEQ ID NO:3533:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..66
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577200

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3533:

Met Arg Thr Leu Val Ser Ser Asp Phe Lys Lys Phe Asp Val Glu Glu  
1                      5                      10                      15  
Ser Val Ala Arg Glu Ser Leu Ile Ile Leu Asn Leu Met Ala Asp Cys  
                    20                      25                      30  
Asp Asp Ser Asp Ile Pro Val Phe Asn Val Asn Ala Asn Ile Leu Asp  
                    35                      40                      45  
Lys Val Ile Ala Tyr Cys Arg Lys His Ala Xaa Ala Pro Arg Xaa Xaa  
                    50                      55                      60  
Trp Arg  
65

(2) INFORMATION FOR SEQ ID NO:3534:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..48
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3534:

Met Arg Ser Gln Val Leu Arg Val Thr Arg Pro Gln Arg Thr Ile Ser  
1                      5                      10                      15  
Ser Pro Leu Met Leu Ser Ser Ser Met Leu Thr Trp Ser Pro Ser Trp  
                    20                      25                      30  
Ser Ser Leu Arg Leu Gln Thr Thr Trp Arg Ser Met Gly Cys Trp Thr  
                    35                      40                      45

(2) INFORMATION FOR SEQ ID NO:3535:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 870 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..870
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577206

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3535:

caatgtcgcg tgcggccact agatttttcc tgacgcggtg tctgctccca cttcccctcc                      60  
tctccccccag gtggcggcag cggcggcgagg gtagcatttg tgctacgagg gcttttgcaa                      120  
tggcggcttc ggggttcrge ggcggcgagg cgccaaaacc ctaccgccgc cgcgaatccc                      180  
gcacgacccc aaccatgacc gtgctgagcc gccctacccc gggcacggcc cagtgtctcg                      240  
ggcggaagaa gaccgccgtc gcggtcgcgt acacgaagcc ggggcgcggc ctgatcaagg                      300  
tgaacggcgt cccgattgar ctgatccgac cggagatgct ccgcctcaag gccttcgagc                      360

```
ccatcctgct ggcgggggcg gtcccggttc aaggacatcg acatgcggat ccgcgtccrc 420
ggcgggcgga agacgtcgca gatctacgcc atccgccAag vccgtcgscA aggggctcgt 480
cgctactac cagaagtacg tcgacgaggc cgcyagaag gagatcaagg acatctttac 540
ccgctacgat cgcacctcc tcgtcgctga cccccggcgc tgcgagccga agaagtccg 600
cggacgtggg gcccgcgcca gggtccagaa gtcgtaccgt tgagcggctg cctgctccat 660
ctcgattttt cagatcggtg tgggtgtttc tcgctttatt tcctatcaat ggatctgctt 720
atctggtttc atatctagct gctgctttac cataatgttt agactttaat gcctagcctg 780
aaacctgtt tgcaatgtga aattaatgtg agagattatg aagactattt tggctagctc 840
ctctattatg attttcatca ttccmgtatt
```

(2) INFORMATION FOR SEQ ID NO:3536:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..250

(D) OTHER INFORMATION: / Ceres Seq. ID 1577207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3536:

```
Met Ser Arg Ala Ala Thr Arg Phe Phe Leu Thr Arg Cys Leu Leu Pro
1          5          10          15
Leu Pro Leu Leu Ser Pro Arg Trp Arg Gln Arg Arg Arg Gly Ser Ile
          20          25          30
Cys Ala Thr Arg Ala Phe Ala Met Ala Ala Ser Gly Phe Xaa Gly Gly
          35          40          45
Glu Ala Pro Lys Pro Tyr Arg Arg Arg Glu Ser Arg Thr Thr Pro Thr
          50          55          60
Met Thr Val Leu Ser Arg Pro Thr Pro Gly Thr Ala Gln Cys Phe Gly
65          70          75          80
Arg Lys Lys Thr Ala Val Ala Val Ala Tyr Thr Lys Pro Gly Arg Gly
          85          90          95
Leu Ile Lys Val Asn Gly Val Pro Ile Xaa Leu Ile Arg Pro Glu Met
          100          105          110
Leu Arg Leu Lys Ala Phe Glu Pro Ile Leu Leu Ala Gly Ala Val Pro
          115          120          125
Val Gln Gly His Arg His Ala Asp Pro Arg Xaa Arg Arg Arg Glu Asp
          130          135          140
Val Ala Asp Leu Arg His Pro Pro Xaa Pro Ser Xaa Arg Gly Ser Ser
          145          150          155          160
Pro Thr Thr Arg Ser Thr Ser Thr Arg Pro Xaa Arg Arg Arg Ser Arg
          165          170          175
Thr Ser Leu Pro Ala Thr Ile Ala Pro Ser Ser Ser Leu Thr Pro Gly
          180          185          190
Ala Ala Ser Arg Arg Ser Ser Ala Asp Val Val Pro Ala Pro Gly Ser
          195          200          205
Arg Ser Arg Thr Val Glu Arg Leu Pro Ala Pro Ser Arg Phe Phe Arg
          210          215          220
Ser Leu Trp Val Phe Phe Ala Leu Phe Pro Ile Asn Gly Ser Ala Tyr
225          230          235          240
Leu Val Leu Tyr Leu Ala Ala Ala Leu Pro
          245          250
```

(2) INFORMATION FOR SEQ ID NO:3537:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..211

(D) OTHER INFORMATION: / Ceres Seq. ID 1577209

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3537:

Met Ala Ala Ser Gly Phe Xaa Gly Gly Glu Ala Pro Lys Pro Tyr Arg  
1 5 10 15  
Arg Arg Glu Ser Arg Thr Thr Pro Thr Met Thr Val Leu Ser Arg Pro  
20 25 30  
Thr Pro Gly Thr Ala Gln Cys Phe Gly Arg Lys Lys Thr Ala Val Ala  
35 40 45  
Val Ala Tyr Thr Lys Pro Gly Arg Gly Leu Ile Lys Val Asn Gly Val  
50 55 60  
Pro Ile Xaa Leu Ile Arg Pro Glu Met Leu Arg Leu Lys Ala Phe Glu  
65 70 75 80  
Pro Ile Leu Leu Ala Gly Ala Val Pro Val Gln Gly His Arg His Ala  
85 90 95  
Asp Pro Arg Xaa Arg Arg Arg Glu Asp Val Ala Asp Leu Arg His Pro  
100 105 110  
Pro Xaa Pro Ser Xaa Arg Gly Ser Pro Thr Thr Arg Ser Thr Ser  
115 120 125  
Thr Arg Pro Xaa Arg Arg Arg Ser Arg Thr Ser Leu Pro Ala Thr Ile  
130 135 140  
Ala Pro Ser Ser Ser Leu Thr Pro Gly Ala Ala Ser Arg Arg Ser Ser  
145 150 155 160  
Ala Asp Val Val Pro Ala Pro Gly Ser Arg Ser Arg Thr Val Glu Arg  
165 170 175  
Leu Pro Ala Pro Ser Arg Phe Phe Arg Ser Leu Trp Val Phe Phe Ala  
180 185 190  
Leu Phe Pro Ile Asn Gly Ser Ala Tyr Leu Val Leu Tyr Leu Ala Ala  
195 200 205  
Ala Leu Pro  
210

(2) INFORMATION FOR SEQ ID NO:3538:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 790 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..790

(D) OTHER INFORMATION: / Ceres Seq. ID 1577252

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3538:

atgctctacc ggagtagcgc aactccgcaa gcaaatacctc ctatctccaa gcctccaatc 60  
tgtgaacggt gaaccccaat cgaatgacgc cgacggsagc ctctctctcc cggctccccc 120  
attcgtctct atctccgatg tgcgcgcgct ccagctcccc ccgcgcggcg gccaccggcc 180  
tcgcccctgc tggaaagggct tggagtgcgg ctccgtacag acgcggatgg tctcttcttt 240  
cgttgggagc agaacacgcc gcagaaacgt tatatgtgct tccctgttcg gagttggagc 300  
tcccgaagca ctggtcattg gagtagtcgc cttgttggtg ttccggcccca agggcttagc 360  
agaggtagcc aggaatttgg ggaagacttt gcgtgctttc caaccaacca ttagagagat 420  
acaggatgta tcaaggaggat tcaggagcac tcttgaacga gaaatcgga ttgatgaggt 480  
ttcccagtcg acgaattata caccacgcac catgaataac aaccaacaac ctgctgccga 540  
ctcaaatatc aagcctgcac ctgcacctta caccagcgat gaacttgatga aagtAactga 600  
agaacaaatt gctgcatcag ctgctgcaga gagTtatcgt cagttggtgc ggtgtgtccg 660  
cttaaaacttt atttgtggtt gggttggtact tttgtggtg ttattttttt ggacctcgtg 720  
atagtcggtc gggtcaatgt tatcgcggct actggcaaac cttaagtgat acggtattct 780  
tcttttcggt

(2) INFORMATION FOR SEQ ID NO:3539:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 239 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..239
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1577253
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3539:

Cys Ser Thr Gly Val Ala Gln Leu Arg Lys Gln Ile Leu Leu Ser Pro  
1 5 10 15  
Ser Leu Gln Ser Val Asn Gly Glu Pro Gln Ser Asn Asp Ala Asp Xaa  
20 25 30  
Ser Leu Leu Leu Pro Ala Pro Pro Phe Val Ser Ile Ser Asp Val Arg  
35 40 45  
Arg Leu Gln Leu Pro Pro Arg Gly Gly His Arg Pro Arg Pro Cys Trp  
50 55 60  
Lys Gly Leu Glu Cys Gly Ser Val Gln Thr Arg Met Val Ser Ser Phe  
65 70 75 80  
Val Gly Ser Arg Thr Arg Arg Arg Asn Val Ile Cys Ala Ser Leu Phe  
85 90 95  
Gly Val Gly Ala Pro Glu Ala Leu Val Ile Gly Val Val Ala Leu Leu  
100 105 110  
Val Phe Gly Pro Lys Gly Leu Ala Glu Val Ala Arg Asn Leu Gly Lys  
115 120 125  
Thr Leu Arg Ala Phe Gln Pro Thr Ile Arg Glu Ile Gln Asp Val Ser  
130 135 140  
Arg Glu Phe Arg Ser Thr Leu Glu Arg Glu Ile Gly Ile Asp Glu Val  
145 150 155 160  
Ser Gln Ser Thr Asn Tyr Thr Pro Thr Thr Met Asn Asn Asn Gln Gln  
165 170 175  
Pro Ala Ala Asp Ser Asn Ile Lys Pro Ala Pro Ala Pro Tyr Thr Ser  
180 185 190  
Asp Glu Leu Val Lys Val Thr Glu Glu Gln Ile Ala Ala Ser Ala Ala  
195 200 205  
Ala Glu Ser Tyr Arg Gln Leu Val Arg Cys Val Arg Leu Asn Phe Ile  
210 215 220  
Cys Gly Trp Leu Val Leu Trp Trp Leu Phe Phe Trp Thr Ser  
225 230 235

(2) INFORMATION FOR SEQ ID NO:3540:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 164 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..164
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1577254
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3540:

Met Val Ser Ser Phe Val Gly Ser Arg Thr Arg Arg Arg Asn Val Ile  
1 5 10 15  
Cys Ala Ser Leu Phe Gly Val Gly Ala Pro Glu Ala Leu Val Ile Gly  
20 25 30  
Val Val Ala Leu Leu Val Phe Gly Pro Lys Gly Leu Ala Glu Val Ala  
35 40 45  
Arg Asn Leu Gly Lys Thr Leu Arg Ala Phe Gln Pro Thr Ile Arg Glu  
50 55 60  
Ile Gln Asp Val Ser Arg Glu Phe Arg Ser Thr Leu Glu Arg Glu Ile  
65 70 75 80

Gly Ile Asp Glu Val Ser Gln Ser Thr Asn Tyr Thr Pro Thr Thr Met  
85 90 95  
Asn Asn Asn Gln Gln Pro Ala Ala Asp Ser Asn Ile Lys Pro Ala Pro  
100 105 110  
Ala Pro Tyr Thr Ser Asp Glu Leu Val Lys Val Thr Glu Glu Gln Ile  
115 120 125  
Ala Ala Ser Ala Ala Ala Glu Ser Tyr Arg Gln Leu Val Arg Cys Val  
130 135 140  
Arg Leu Asn Phe Ile Cys Gly Trp Leu Val Leu Leu Trp Trp Leu Phe  
145 150 155 160  
Phe Trp Thr Ser

(2) INFORMATION FOR SEQ ID NO:3541:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 859 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..859

(D) OTHER INFORMATION: / Ceres Seq. ID 1577263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3541:

agtcttgtct gctagactgt cgacagattc cgctccaacg cgcacctgca gtcccgcacg 60  
ccctcgccca ccgtcgccct tcaaaaagct ggaggattct cgagarggag aagcgcgcct 120  
ggcagctccg ttccatccgc ccccacgaat gtccgacgar gccaggcgcg ggcccgcggg 180  
cgccgcgcag gcgantgtc cgggcctcct ccgaggaccg caagccgggtg ggcgctgggt 240  
ccccggcggc ggttgcgcac aagatccagc tcaagagcgc cgatatgaag gaggagatgc 300  
ggcaggacgc cttcgaaatt gccgcacatg cgttcgataa gcacagcatg gagaaggaca 360  
tcgctgagta cataaagaag gagttcgaca agaaccacgg cccaaCcctg gcactgcac 420  
gtcggccgca acttcggttc atacgtgacg cacgagacaa actactttgt atatttctac 480  
atcgactcta aagctgtcct gctattcaag tctgggtgat tgctcgcagc cgacgcaatc 540  
adccttgcac gcctacgttc cattgctccc atgtatgcac cgcacccttc ccccaggcc 600  
cagggtcgtc tgcagccaag ctggaagccg gtaattctaa tgagcctgca tgttgatgta 660  
tatcagcaac ggattattct tcgtatgcc attagtgtga gatcagattg catcttactt 720  
atgtctgata tatctagcta ggtaggtgt tgtgagtaca ttgtcttgtt gcaatatgat 780  
tgccggacaa ctgggtgaac tgcctctcgt ctgtttgtga ttatctcaat agaagcgtcc 840  
ttgctcatgc gtaatactc

(2) INFORMATION FOR SEQ ID NO:3542:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..112

(D) OTHER INFORMATION: / Ceres Seq. ID 1577264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3542:

Val Leu Ser Ala Arg Leu Ser Thr Asp Ser Ala Pro Thr Arg Thr Cys  
1 5 10 15  
Ser Pro Ala Arg Pro Arg Pro Pro Ser Pro Phe Lys Lys Leu Glu Asp  
20 25 30  
Ser Arg Xaa Gly Glu Ala Arg Leu Ala Ala Pro Phe His Pro Pro Pro  
35 40 45  
Arg Met Ser Asp Xaa Ala Arg Arg Gly Pro Ala Gly Ala Ala Gln Ala  
50 55 60  
Xaa Ala Pro Gly Leu Leu Arg Gly Pro Gln Ala Gly Gly Arg Trp Val  
65 70 75 80



Pro Gly Gly Gly Cys Ala Gln Asp Pro Ala Gln Glu Arg Arg Tyr Glu  
85 90 95  
Gly Gly Asp Ala Ala Gly Arg Leu Arg Asn Cys Pro His Arg Val Arg  
100 105 110

(2) INFORMATION FOR SEQ ID NO:3543:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 162 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..162

(D) OTHER INFORMATION: / Ceres Seq. ID 1577265

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3543:

Ser Cys Leu Leu Asp Cys Arg Gln Ile Pro Leu Gln Arg Ala Pro Ala  
1 5 10 15  
Val Pro His Ala Leu Ala His Arg Arg Leu Ser Lys Ser Trp Arg Ile  
20 25 30  
Leu Glu Xaa Glu Lys Arg Ala Trp Gln Leu Arg Ser Ile Arg Pro His  
35 40 45  
Glu Cys Pro Thr Xaa Pro Gly Ala Gly Pro Arg Ala Pro Arg Arg Arg  
50 55 60  
Xaa Leu Arg Ala Ser Ser Glu Asp Arg Lys Pro Val Gly Ala Gly Ser  
65 70 75 80  
Pro Ala Ala Val Ala His Lys Ile Gln Leu Lys Ser Ala Asp Met Lys  
85 90 95  
Glu Glu Met Arg Gln Asp Ala Phe Glu Ile Ala Arg Ile Ala Phe Asp  
100 105 110  
Lys His Ser Met Glu Lys Asp Ile Ala Glu Tyr Ile Lys Lys Glu Phe  
115 120 125  
Asp Lys Asn His Gly Pro Thr Leu Ala Leu His Arg Arg Pro Gln Leu  
130 135 140  
Arg Phe Ile Arg Asp Ala Arg Asp Lys Leu Leu Cys Ile Phe Leu His  
145 150 155 160  
Arg Leu

(2) INFORMATION FOR SEQ ID NO:3544:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 521 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..521

(D) OTHER INFORMATION: / Ceres Seq. ID 1577296

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3544:

taagattatt gatgttatcg agaagggaga gaaacagccc aacatcacta ttggcatttt 60  
ggtctccggt gtcacgtgtg tcgttacogt tctctgcaag ctctgttttg gtggcaagaa 120  
accagtggca cctgtgaaac ctgcagctga ggcgaagaag cccaaggccg cggagacgga 180  
cggtgctgga agcagtggtg acaaggatga gaaagaggat gaaaaggagg agacaggccc 240  
acgtcggagg acccgaaggr agNacataga cctgtttttg acgtgtttta gctcttctgg 300  
cgtctgctta ttttgagaac tcttaatat tgtgagtgt taataggagc ttatgtcacc 360  
tctgcggctt ccccgctgc tgatttggtt ttaatgggtta gaccaggacc cttcacgagc 420  
gtagaattta gttcttggtg gtcatttatg tgctgtgcct gacggtgttc aatcagatag 480  
aggatgatggt ttttttggtg gatcaaatca aggaatatatt c

(2) INFORMATION FOR SEQ ID NO:3545:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104

(D) OTHER INFORMATION: / Ceres Seq. ID 1577297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3545:

Lys Ile Ile Asp Val Ile Glu Lys Gly Glu Lys Gln Pro Asn Ile Thr  
1 5 10 15  
Ile Gly Ile Leu Val Ser Val Val Ile Val Phe Val Thr Val Leu Cys  
20 25 30  
Lys Leu Leu Phe Gly Gly Lys Lys Pro Val Ala Pro Val Lys Pro Ala  
35 40 45  
Ala Glu Ala Lys Lys Pro Lys Ala Ala Glu Thr Asp Gly Ala Gly Ser  
50 55 60  
Ser Gly Asp Lys Asp Glu Lys Glu Asp Glu Lys Glu Glu Thr Gly Pro  
65 70 75 80  
Arg Arg Arg Thr Arg Arg Xaa Xaa Ile Asp Leu Phe Leu Thr Cys Phe  
85 90 95  
Ser Ser Ser Gly Val Cys Leu Phe  
100

(2) INFORMATION FOR SEQ ID NO:3546:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 811 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..811

(D) OTHER INFORMATION: / Ceres Seq. ID 1577302

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3546:

aggaagaaag gaaccacca aagcttcaaa aaaagaaaaa gagctgcaca ctggtcactg 60  
gaaaacgaag gcaaacccta atcgctactc caccgcagcg cccactacac cgatcgggct 120  
ccgatggact tcgcggastg gaggccgtgg agggcctccg gtggccatgg cactcgtggc 180  
cgccgactac ccccgccgcc gcgtccctcg tcgtgccac ctccgtcctc tgctcgccgc 240  
tgcagcacc caccgcccgc gacctcctcc cgctgctacc ctacgcgccg ctccgctgcg 300  
cctccccggg ttgtggcgcc gcgctcaacc cgttctcgcg cgtgcaccac ggCtccgcgc 360  
gctggtcctg cgcttctgt Ggcgcgcgcg ccaaccgcgt ccccgcccta ctggcccccg 420  
acgcgctccc cgccgaactc ttccccaccc actccagcgt cgagtacttg ctgcccccg 480  
accccgctga gcccggggga ccggggccac ctgcgctcgt gttcgtgatc gatgcggcca 540  
cggcggccga ggagctcacc gtgctcaagg acgaggtgcg caggctcatg caggggctgc 600  
ctgaggggat caggggtggc ctcgtcaact tcgctgcgtc tgtgtgggtg cacgatcttg 660  
gatttgaggg ttgcgctcgg gtggttgtgc ttaatggcga gcgtgagctc gagtctgaca 720  
aggtttgtga atttgaata taatccttag gacaccgaat ttgtaatttg gttctgcgcc 780  
aatctatgtg acatgatcag cattctagtt c

(2) INFORMATION FOR SEQ ID NO:3547:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..162

(D) OTHER INFORMATION: / Ceres Seq. ID 1577303

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3547:

Gly Arg Lys Glu Pro Thr Lys Ala Ser Lys Lys Glu Lys Glu Leu His  
1 5 10 15  
Thr Gly His Trp Lys Thr Lys Ala Asn Pro Asn Arg Tyr Ser Thr Ala  
20 25 30  
Ala Pro Thr Thr Pro Ile Gly Leu Arg Trp Thr Ser Arg Xaa Gly Gly  
35 40 45  
Arg Gly Gly Pro Pro Val Ala Met Ala Leu Val Ala Ala Asp Tyr Pro  
50 55 60  
Arg Arg Arg Val Pro Arg Arg Ala His Leu Arg Pro Leu Leu Ala Ala  
65 70 75 80  
Ala Ala Pro His Gly Ala Gly Pro Pro Pro Ala Ala Thr Leu Arg Ala  
85 90 95  
Ala Pro Leu Arg Leu Pro Gly Leu Trp Arg Arg Ala Gln Pro Val Leu  
100 105 110  
Ala Arg Ala Pro Arg Leu Arg Ala Leu Val Leu Arg Leu Leu Trp Arg  
115 120 125  
Arg Arg Gln Pro Val Pro Pro Thr Gly Pro Arg Arg Ala Pro Arg  
130 135 140  
Arg Thr Leu Pro His Pro Leu Gln Arg Arg Val Leu Ala Ala Pro Gly  
145 150 155 160  
Pro Arg

(2) INFORMATION FOR SEQ ID NO:3548:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 246 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..246

(D) OTHER INFORMATION: / Ceres Seq. ID 1577304

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3548:

Glu Glu Arg Asn Pro Lys Leu Gln Lys Lys Lys Ser Cys Thr  
1 5 10 15  
Leu Val Thr Gly Lys Arg Arg Gln Thr Leu Ile Ala Thr Pro Pro Gln  
20 25 30  
Arg Pro Leu His Arg Ser Gly Ser Asp Gly Leu Arg Gly Xaa Glu Ala  
35 40 45  
Val Glu Gly Leu Arg Trp Pro Trp His Ser Trp Pro Pro Thr Thr Pro  
50 55 60  
Ala Ala Ala Ser Leu Val Val Pro Thr Ser Val Leu Cys Ser Pro Leu  
65 70 75 80  
Gln His Pro Thr Ala Pro Asp Leu Leu Pro Leu Leu Pro Tyr Ala Pro  
85 90 95  
Leu Arg Cys Ala Ser Pro Gly Cys Gly Ala Ala Leu Asn Pro Phe Ser  
100 105 110  
Arg Val His His Gly Ser Ala Arg Trp Ser Cys Ala Phe Cys Gly Ala  
115 120 125  
Ala Ala Asn Pro Phe Pro Arg Leu Leu Ala Pro Asp Ala Leu Pro Ala  
130 135 140  
Glu Leu Phe Pro Thr His Ser Ser Val Glu Tyr Leu Leu Pro Pro Asp  
145 150 155 160  
Pro Ala Glu Pro Gly Gly Pro Gly Pro Pro Ala Leu Val Phe Val Ile  
165 170 175  
Asp Ala Ala Thr Ala Ala Glu Glu Leu Thr Val Leu Lys Asp Glu Val  
180 185 190

Arg Arg Leu Met Gln Gly Leu Pro Glu Gly Ile Arg Val Ala Leu Val  
195 200 205  
Thr Phe Ala Ala Ser Val Trp Val His Asp Leu Gly Phe Glu Gly Cys  
210 215 220  
Ala Arg Val Val Val Leu Asn Gly Glu Arg Glu Leu Glu Ser Asp Lys  
225 230 235 240  
Val Cys Glu Phe Val Ile  
245

(2) INFORMATION FOR SEQ ID NO:3549:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 134 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..134

(D) OTHER INFORMATION: / Ceres Seq. ID 1577305

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3549:

Met Asp Phe Ala Xaa Trp Arg Pro Trp Arg Ala Ser Gly Gly His Gly  
1 5 10 15  
Thr Arg Gly Arg Arg Leu Pro Pro Pro Pro Arg Pro Ser Ser Cys Pro  
20 25 30  
Pro Pro Ser Ser Ala Arg Arg Cys Ser Thr Pro Arg Arg Arg Thr Ser  
35 40 45  
Ser Arg Cys Tyr Pro Thr Arg Arg Ser Ala Ala Pro Pro Arg Val Val  
50 55 60  
Ala Pro Arg Ser Thr Arg Ser Arg Ala Cys Thr Thr Ala Pro Arg Ala  
65 70 75 80  
Gly Pro Ala Pro Ser Val Ala Pro Pro Pro Thr Arg Ser Pro Ala Tyr  
85 90 95  
Trp Pro Pro Thr Arg Ser Pro Pro Asn Ser Ser Pro Pro Thr Pro Ala  
100 105 110  
Ser Ser Thr Cys Cys Pro Arg Thr Pro Leu Ser Pro Gly Asp Arg Gly  
115 120 125  
His Leu Arg Ser Cys Ser  
130

(2) INFORMATION FOR SEQ ID NO:3550:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 887 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..887

(D) OTHER INFORMATION: / Ceres Seq. ID 1577310

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3550:

acctgacggg ctgcgcatcgc acccgccacc cccaccgcac gcaccctctc gtcctctctg 60  
cgccgaccgg gctcttctcc cccaacacaa tctctcttcc ccgatccagt ctgcgggtcg 120  
cgccacgct gagggacagc gagaagagac agacacagat cgcgcgcgga gatgtcgtcg 180  
gactcgtcgt cgtgggcgcg cgccctggtg cagatctcgc cctacacctt ctccgcaatc 240  
ggatcgcgcc tctccatcgg cgtctccgtc ctgggcgcgg catgggggat cttcatcacg 300  
gggagcagcc tcatcggggc cgccatcaag ggcgccagga tcacttctaa gaacctcatc 360  
agtgtcatct tctgtgaggc tgtcgcaatt tatggcgtaa ttgtggcaat catcctccag 420  
acaaagcttg aaagtgtgcc aacatctcaa atgtatgata cggagtctct tcgagctggc 480  
tatgcaatct ttgcatctgg ccttatcggt ggctttgcta atcttgtttg cgggggatgc 540  
Ggtggggata attggaagca Gctgcgcact gtctgatgct cagaactcat cactcttcgt 600  
aaagattttg gtgattgaga tcttcggcag cgctctggga ctgttcggtg tcattgtggg 660

catcattatg tcatctcaag cgacatggcc agcaaaagct tgattttcac catttgtagc 720  
tctgtaaatt attcagatgg agtgtatcga aatgtgcatg tggcttaact gcattttcat 780  
gttcctttta tgtggcgtct tttttggcag aacacgaaat gcggcgcsqt accgccaccg 840  
attgtagagt tgctattctt actgccggag tactccatgt gtgttgg

(2) INFORMATION FOR SEQ ID NO:3551:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..132

(D) OTHER INFORMATION: / Ceres Seq. ID 1577311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3551:

Pro Asp Gly Leu Ala Ser His Pro Pro Pro Pro Pro His Ala Pro Ser  
1 5 10 15  
Arg Pro Leu Cys Ala Asp Pro Ala Leu Leu Pro Gln His Asn Pro Pro  
20 25 30  
Ser Pro Ile Gln Ser Arg Gly Arg Gly His Ala Glu Gly Gln Arg Glu  
35 40 45  
Glu Thr Asp Thr Asp Arg Ala Arg Arg Cys Arg Arg Thr Arg Arg Arg  
50 55 60  
Gly Arg Ala Pro Trp Cys Arg Ser Arg Pro Thr Pro Ser Pro Gln Ser  
65 70 75 80  
Val Ser Pro Ser Pro Ser Ala Ser Pro Ser Ser Ala Arg His Gly Val  
85 90 95  
Ser Ser Ser Arg Gly Ala Ala Ser Ser Gly Pro Pro Ser Arg Arg Pro  
100 105 110  
Gly Ser Leu Leu Arg Thr Ser Ser Val Ser Ser Ser Val Arg Leu Ser  
115 120 125  
Gln Phe Met Ala  
130

(2) INFORMATION FOR SEQ ID NO:3552:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..115

(D) OTHER INFORMATION: / Ceres Seq. ID 1577312

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3552:

Leu Thr Gly Ser His Arg Thr Arg His Pro His Arg Thr His Pro Leu  
1 5 10 15  
Val Leu Ser Ala Pro Thr Arg Leu Phe Ser Pro Asn Thr Ile Leu Leu  
20 25 30  
Pro Arg Ser Ser Leu Ala Val Ala Ala Thr Leu Arg Asp Ser Glu Lys  
35 40 45  
Arg Gln Thr Gln Ile Ala Arg Gly Asp Val Val Gly Leu Val Val Val  
50 55 60  
Gly Ala Arg Pro Gly Ala Asp Leu Ala Leu His Leu Leu Arg Asn Arg  
65 70 75 80  
Tyr Arg Arg Leu His Arg Arg Leu Arg Pro Arg Arg Gly Met Gly Tyr  
85 90 95  
Leu His His Gly Glu Gln Pro His Arg Gly Arg His Gln Gly Ala Gln  
100 105 110  
Asp His Phe

115

(2) INFORMATION FOR SEQ ID NO:3553:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..134

(D) OTHER INFORMATION: / Ceres Seq. ID 1577313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3553:

Met Ser Ser Asp Ser Ser Ser Trp Ala Arg Ala Leu Val Gln Ile Ser  
1 5 10 15  
Pro Tyr Thr Phe Ser Ala Ile Gly Ile Ala Val Ser Ile Gly Val Ser  
20 25 30  
Val Leu Gly Ala Ala Trp Gly Ile Phe Ile Thr Gly Ser Ser Leu Ile  
35 40 45  
Gly Ala Ala Ile Lys Ala Pro Arg Ile Thr Ser Lys Asn Leu Ile Ser  
50 55 60  
Val Ile Phe Cys Glu Ala Val Ala Ile Tyr Gly Val Ile Val Ala Ile  
65 70 75 80  
Ile Leu Gln Thr Lys Leu Glu Ser Val Pro Thr Ser Gln Met Tyr Asp  
85 90 95  
Pro Glu Ser Leu Arg Ala Gly Tyr Ala Ile Phe Ala Ser Gly Leu Ile  
100 105 110  
Val Gly Phe Ala Asn Leu Val Cys Gly Val Cys Gly Gly Asp Asn Trp  
115 120 125  
Lys Gln Leu Arg Thr Val  
130

(2) INFORMATION FOR SEQ ID NO:3554:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 876 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..876

(D) OTHER INFORMATION: / Ceres Seq. ID 1577318

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3554:

atccgaaacc agagcgaaga atcgccatca cagcaagcta cgcgcactga aatcctccaa 60  
tccacaggac acagctctac ttccgcagtt cgcactcgca cgcaccaagc cgctagcaac 120  
gaagcagaaa tgtcgtctggt gaggcgcasa gcgtgttcga cccattctcc gtggacctct 180  
tcgaccctgt cgacagcatg ttccgctcca tcgtgccgtc gtcgtcgtcg tcgggctccg 240  
agaccgccgc cttcgccagc gcccgcatcg actggaagga gacgcccag ggcacgtgt 300  
tcaaggccga cctccccggc gtgaagaaag aggaggtcaa ggtggaggtg gaggacggca 360  
acgtgctgct catcagcggg cagcgcaGca gggagaagga ggacaagggc gacaagtggc 420  
accgcgtgga gcgcagcagc ggccagttcg tgcggcgctt ccgcctgccg gagaacgcca 480  
agacggagga ggtgagggcc gcgctggaga acggcggtgct cacggtcacc gtgcccgaag 540  
ccgaggtcaa gaagcccag gtgaagagca tccagatctc cggctgaaga agacatggac 600  
gggaggtgaa tggntcgcgt cgcgttcgcg tcgcggcgct ggatcttggg ttccagcgac 660  
gcgactcgtg tgtgtgtgct gtgtgttgct tctgctttgg tatgtttggt gtgtacgtgt 720  
gctgttcagt gtttcctggt cctcgtctgt actttgcgct gttcggtgag cttcctggct 780  
cagtattgtg tgttgtgcga gtgaataaat aaawacaaac cagctgtagt atattcacct 840  
actactatcg tgtttcaaaa agaagaaaga acgctt

(2) INFORMATION FOR SEQ ID NO:3555:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..107  
(D) OTHER INFORMATION: / Ceres Seq. ID 1577319  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3555:

Ile Arg Asn Gln Ser Glu Glu Ser Pro Ser Gln Gln Ala Thr Arg Thr  
1 5 10 15  
Glu Ile Leu Gln Ser Thr Gly His Ser Ser Thr Ser Ala Val Arg Thr  
20 25 30  
Arg Thr His Gln Ala Ala Ser Asn Glu Ala Glu Met Ser Leu Val Arg  
35 40 45  
Arg Xaa Ala Cys Ser Thr His Ser Pro Trp Thr Ser Ser Thr Arg Ser  
50 55 60  
Thr Ala Cys Ser Ala Pro Ser Cys Arg Arg Arg Arg Arg Ala Pro  
65 70 75 80  
Arg Pro Pro Pro Ser Pro Ala Pro Ala Ser Thr Gly Arg Arg Arg Pro  
85 90 95  
Arg Arg Thr Cys Ser Arg Pro Thr Ser Pro Ala  
100 105

(2) INFORMATION FOR SEQ ID NO:3556:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 64 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..64  
(D) OTHER INFORMATION: / Ceres Seq. ID 1577320  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3556:

Met Ser Leu Val Arg Arg Xaa Ala Cys Ser Thr His Ser Pro Trp Thr  
1 5 10 15  
Ser Ser Thr Arg Ser Thr Ala Cys Ser Ala Pro Ser Cys Arg Arg Arg  
20 25 30  
Arg Arg Arg Ala Pro Arg Pro Pro Pro Ser Pro Ala Pro Ala Ser Thr  
35 40 45  
Gly Arg Arg Arg Pro Arg Arg Thr Cys Ser Arg Pro Thr Ser Pro Ala  
50 55 60

(2) INFORMATION FOR SEQ ID NO:3557:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 129 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..129  
(D) OTHER INFORMATION: / Ceres Seq. ID 1577321  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3557:

Met Phe Arg Ser Ile Val Pro Ser Ser Ser Ser Ser Gly Ser Glu Thr  
1 5 10 15  
Ala Ala Phe Ala Ser Ala Arg Ile Asp Trp Lys Glu Thr Pro Glu Ala  
20 25 30

(2) INFORMATION FOR SEQ ID NO:3558:

acggccaatc	aggagtcCaa	aggccCacat	gtatcMagag	cacgtccgtc	gccccctgga	60
ccacgcagcc	Cggcagccca	gagccggaga	gcccagtga	acagagccgg	tgaacgcagc	120
ccagtcagtg	acccccccga	tcccgaactcc	ggcgatctcc	ccaaccccat	ggcctccgcc	180
ggcgaggccc	ccagcacgct	cctccgcttc	ctctacttcg	tcggcgccgg	agtaatctgc	240
accaaggcca	tcaacacct	tcgcgactac	gagcacaaga	aggagtccac	cgccgcacctc	300
gccgccgcgc	aatcggCgtG	tggtctgtgc	cgcggcggcc	gagccccgctc	ctgcaaccgc	360
cgcgcgcgaag	ccCtgattgt	ggacagagggc	ctgtcttcgg	cggttagggc	tctcggaatg	420
ttgctctcca	taggggagat	agatattttc	ttttgtttct	gatgtttcag	ctacgtgtat	480
gtgctctttt	ggcttgaatc	aatcagtaat	aatactttct	ttcgtgtct		

(2) INFORMATION FOR SEQ ID NO:3559:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3559:

Arg 1	Pro	Ile	Arg	Ser 5	Pro	Lys	Ala	His	Met 10	Tyr	Xaa	Glu	His	Val 15	Arg
Arg	Pro	Leu 20	Asp	His	Ala	Ala	Arg	Gln 25	Pro	Arg	Ala	Gly	Glu 30	Pro	Ser
Glu	Thr 35	Glu	Pro	Val	Asn	Ala	Ala 40	Gln	Ser	Val	Thr	Pro 45	Pro	Ile	Pro
Thr	Pro 50	Ala	Ile	Ser	Pro	Thr 55	Pro	Trp	Pro	Pro	Pro 60	Ala	Arg	Pro	Pro
Ala 65	Arg	Ser	Ser	Ala	Ser 70	Ser	Thr	Ser	Ser	Ala 75	Pro	Glu			

(2) INFORMATION FOR SEO ID NO:3560:

(B) TYPE: amino acid



- (C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..68  
(D) OTHER INFORMATION: / Ceres Seq. ID 1577348  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3560:

Met Tyr Xaa Glu His Val Arg Arg Pro Leu Asp His Ala Ala Arg Gln  
1 5 10 15  
Pro Arg Ala Gly Glu Pro Ser Glu Thr Glu Pro Val Asn Ala Ala Gln  
20 25 30  
Ser Val Thr Pro Pro Ile Pro Thr Pro Ala Ile Ser Pro Thr Pro Trp  
35 40 45  
Pro Pro Pro Ala Arg Pro Pro Ala Arg Ser Ser Ala Ser Ser Thr Ser  
50 55 60  
Ser Ala Pro Glu  
65

(2) INFORMATION FOR SEQ ID NO:3561:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 97 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..97  
(D) OTHER INFORMATION: / Ceres Seq. ID 1577349  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3561:

Met Ala Ser Ala Gly Glu Ala Pro Ser Thr Leu Leu Arg Phe Leu Tyr  
1 5 10 15  
Phe Val Gly Ala Gly Val Ile Cys Thr Lys Ala Ile Asn Thr Tyr Arg  
20 25 30  
Asp Tyr Glu His Lys Lys Glu Ser Thr Ala Ala Leu Ala Ala Glu  
35 40 45  
Ser Ala Cys Gly Cys Cys Arg Gly Gly Arg Ala Arg Ser Cys Asn Arg  
50 55 60  
Arg Arg Glu Ala Leu Ile Val Asp Glu Gly Leu Ser Ser Ala Val Arg  
65 70 75 80  
Val Leu Gly Met Leu Leu Ser Ile Gly Glu Ile Asp Ile Phe Phe Cys  
85 90 95  
Phe

(2) INFORMATION FOR SEQ ID NO:3562:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 737 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..737  
(D) OTHER INFORMATION: / Ceres Seq. ID 1577353  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3562:

aaaaaattaa aatcctcccg gaaatcagag acgcgaatcc ctgcgccag gccccgaaac	60
ctccgagttc tctcgccaat tcgatccgcc tcaccgccgc cgcccgtcg ccggtcggcc	120
ttgactgctc cgtcgcacgt ggcggttcgc agcgcggaat ctaccttggtg ttgagagatc	180
cggggaaacc cttgttcccg gtcgttcggg ctcgaaatctt ctgcggactg gcaatgtaag	240
cgttctccat cggaggggcga cgatctacgg ggcggttggt ggcggggttk agggaaatgga	300

(2) INFORMATION FOR SEQ ID NO:3563:

(A) LENGTH: 57 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..57

(D) OTHER INFORMATION: / Ceres Seq. ID 1577354

Lys	Lys	Leu	Lys	Ser	Ser	Arg	Lys	Ser	Glu	Thr	Arg	Ile	Pro	Arg	Pro
1				5					10					15	
Arg	Pro	Arg	Asn	Leu	Arg	Val	Leu	Ser	Pro	Ile	Arg	Ser	Ala	Ser	Pro
			20					25					30		
Pro	Pro	Pro	Val	Arg	Arg	Ser	Ala	Leu	Thr	Ala	Pro	Ser	His	Val	Ala
		35					40					45			
Val	Arg	Ser	Ala	Glu	Ser	Thr	Leu	Cys							
	50					55									

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..78

(D) OTHER INFORMATION: / Ceres Seq. ID 1577355

Lys	Ile	Lys	Ile	Leu	Pro	Glu	Ile	Arg	Asp	Ala	Asn	Pro	Ser	Pro	Gln
1				5					10					15	
Ala	Pro	Lys	Pro	Pro	Ser	Ser	Leu	Ala	Asn	Ser	Ile	Arg	Leu	Thr	Ala
			20					25					30		
Ala	Ala	Arg	Pro	Pro	Val	Gly	Leu	Asp	Cys	Ser	Val	Ala	Arg	Gly	Gly
		35				40						45			
Ser	Gln	Arg	Gly	Ile	Tyr	Leu	Val	Leu	Arg	Asp	Pro	Gly	Lys	Pro	Leu
	50					55				60					
Phe	Pro	Val	Val	Pro	Ala	Arg	Ile	Phe	Cys	Gly	Leu	Ala	Met		
65					70				75						

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..42

(D) OTHER INFORMATION: / Ceres Seq. ID 1577356

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3565:

Met Glu His Val Phe Gly Gly Lys Phe Lys Leu Gly Lys Lys Ile Gly  
1 5 10 15  
Ser Gly Ser Phe Arg Arg Ala Leu Ser Arg Arg Gln His Thr Glu Arg  
20 25 30  
Arg Gly Gly Gly Tyr Gln Val Gly Met Arg  
35 40

(2) INFORMATION FOR SEQ ID NO:3566:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 667 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..667
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577374

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3566:

cgggccacct cgagctgctg aaccgogacc ccgacgacaa cccgctggtg acgttcaact 60  
acttctcgca ccccgaggac ctocgccgct gcgtggccgg cttgtcggtc atcgagcgcg 120  
tcatccactc ccaggccttc aagaacttca cgtacccoga cttctccatg gagacgctgc 180  
tcaacatgtc gacgggggttc cccgtcaacc tgetgccccg gcacgacaaac gactccacgt 240  
cgcttgagat gttctgcaag gacaccgtca tgaccatctg gcaactaccac ggtggctgcc 300  
aggtcggcag ggtcgtcgac gctgaatacc gagtgcctcg catcgaCGcg ctgcgcgtca 360  
ttgacggctc cactttcaac gcctcgccag gaaccaaccc gcaggcaacc gtcgatgatgc 420  
tcggcaggta tatgggagtc agaatacaca acgaaagggt ggcagctgaa ggattagagg 480  
gaacaaaacc gtgatgatcc tataatccaa gacagtaggc gaggcgtaTt taagaatctc 540  
tattgaacta tgtaatgctg gattcaatat tgttggtgtg attctgatat tgataggttg 600  
cacatatatt cggagttgta tcatgttggt tgttggttact atgtggacta ttatgagtga 660  
aatctgc

(2) INFORMATION FOR SEQ ID NO:3567:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..163
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3567:

Gly His Leu Glu Leu Arg Asn Arg Asp Pro Asp Asp Asn Pro Leu Val  
1 5 10 15  
Thr Phe Asn Tyr Phe Ser His Pro Glu Asp Leu Arg Arg Cys Val Ala  
20 25 30  
Gly Leu Ser Val Ile Glu Arg Val Ile His Ser Gln Ala Phe Lys Asn  
35 40 45  
Phe Thr Tyr Pro Asp Phe Ser Met Glu Thr Leu Leu Asn Met Ser Thr  
50 55 60  
Gly Phe Pro Val Asn Leu Leu Pro Arg His Asp Asn Asp Ser Thr Ser  
65 70 75 80  
Leu Glu Met Phe Cys Lys Asp Thr Val Met Thr Ile Trp His Tyr His  
85 90 95  
Gly Gly Cys Gln Val Gly Arg Val Val Asp Ala Glu Tyr Arg Val Leu  
100 105 110  
Gly Ile Asp Ala Leu Arg Val Ile Asp Gly Ser Thr Phe Asn Ala Ser  
115 120 125  
Pro Gly Thr Asn Pro Gln Ala Thr Val Met Met Leu Gly Arg Tyr Met  
130 135 140

Gly Val Arg Ile Thr Asn Glu Arg Leu Ala Ala Glu Gly Leu Glu Gly  
145                      150                      155                      160  
Thr Lys Pro

(2) INFORMATION FOR SEQ ID NO:3568:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..108
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577376

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3568:

Met Glu Thr Leu Leu Asn Met Ser Thr Gly Phe Pro Val Asn Leu Leu  
1                      5                      10                      15  
Pro Arg His Asp Asn Asp Ser Thr Ser Leu Glu Met Phe Cys Lys Asp  
                    20                      25                      30  
Thr Val Met Thr Ile Trp His Tyr His Gly Gly Cys Gln Val Gly Arg  
                    35                      40                      45  
Val Val Asp Ala Glu Tyr Arg Val Leu Gly Ile Asp Ala Leu Arg Val  
50                      55                      60  
Ile Asp Gly Ser Thr Phe Asn Ala Ser Pro Gly Thr Asn Pro Gln Ala  
65                      70                      75                      80  
Thr Val Met Met Leu Gly Arg Tyr Met Gly Val Arg Ile Thr Asn Glu  
                    85                      90                      95  
Arg Leu Ala Ala Glu Gly Leu Glu Gly Thr Lys Pro  
                    100                      105

(2) INFORMATION FOR SEQ ID NO:3569:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..102
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3569:

Met Ser Thr Gly Phe Pro Val Asn Leu Leu Pro Arg His Asp Asn Asp  
1                      5                      10                      15  
Ser Thr Ser Leu Glu Met Phe Cys Lys Asp Thr Val Met Thr Ile Trp  
                    20                      25                      30  
His Tyr His Gly Gly Cys Gln Val Gly Arg Val Val Asp Ala Glu Tyr  
                    35                      40                      45  
Arg Val Leu Gly Ile Asp Ala Leu Arg Val Ile Asp Gly Ser Thr Phe  
50                      55                      60  
Asn Ala Ser Pro Gly Thr Asn Pro Gln Ala Thr Val Met Met Leu Gly  
65                      70                      75                      80  
Arg Tyr Met Gly Val Arg Ile Thr Asn Glu Arg Leu Ala Ala Glu Gly  
                    85                      90                      95  
Leu Glu Gly Thr Lys Pro  
                    100

(2) INFORMATION FOR SEQ ID NO:3570:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 722 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3570:

(2) INFORMATION FOR SEQ ID NO:3571:

(A) LENGTH: 152 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..152

(D) OTHER INFORMATION: / Ceres Seq. ID 1577379

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3571:

[illegible]

(2) INFORMATION FOR SEQ ID NO:3572:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 130 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..130

(D) OTHER INFORMATION: / Ceres Seq. ID 1577380

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3572:

Leu Ser Ser Gly Ser Ser Arg Gly Ser Thr Ser Ala Ser Pro Thr Trp  
1 5 10 15  
Ser Arg Ser Arg Ala Arg Thr Pro Ser Ala Arg Pro Ala Ala Ser Pro  
20 25 30  
Ser Ser Ser Ala Ser Thr Thr Ser Leu Asp Pro Ala Ala Pro Thr Arg  
35 40 45  
Thr Trp Thr Pro Pro Thr Ala Ala Arg Ser Thr His Ser Ala Pro Arg  
50 55 60  
Ala Ala Thr Arg Arg Ser Arg Glu Ala Trp Thr Pro Pro His Ala Ser  
65 70 75 80  
Ser Thr Thr Ser Thr Ser Arg Thr Ser Xaa Arg Ser Ala Ala Ser Ser  
85 90 95  
Thr Pro Thr Arg Arg Ser Ser Leu Thr Thr Pro Gly Pro Val Gly Ser  
100 105 110  
Ser Ser Gly Ser Ala Arg Thr Arg Thr Pro Ser Ser Gly Pro Ser Ser  
115 120 125  
Arg Gly  
130

(2) INFORMATION FOR SEQ ID NO:3573:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 103 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..103

(D) OTHER INFORMATION: / Ceres Seq. ID 1577381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3573:

Ser His Pro Ala Leu Arg Gly Ala Gln Pro Gln Arg His Arg Pro Gly  
1 5 10 15  
Arg Ala Leu Gly Leu Ala Leu His Arg Arg Gly Pro Leu Leu His  
20 25 30  
Arg Leu Pro Pro Leu Gln Pro Val Trp Ile Arg Pro Pro Arg Pro Ala  
35 40 45  
His Gly His Arg Leu Pro Pro Leu Ala Arg Arg Thr Leu Pro Gln Gly  
50 55 60  
Arg Arg Arg Gly Gly His Gly Arg Pro Gly Arg His Pro Thr His Leu  
65 70 75 80  
Arg Gln Pro Val Leu Arg Gly Pro Arg Xaa Ala Pro Arg Leu Pro Gln  
85 90 95  
Leu Arg Pro Asp Ala Leu Leu  
100

(2) INFORMATION FOR SEQ ID NO:3574:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 761 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..761

(D) OTHER INFORMATION: / Ceres Seq. ID 1577382

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3574:

catttctcgt gcaggtgggt gaggttaatg ttaaggtgga aagtgcaggc acacataaca 60  
tgcacaataa tgatttctat gctaaagaga agttgctcaa atcaatgcgt gattgtgatc 120

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cttcgtcttt gcgccattgg attgtaagag ttgttttctt gttttatatt ttttttgta 180  
ttcctaccat tgaattgggc attcaatacc tgytcattat ctttatgctt atgcaatcca 240  
ataatgatgg aaaataactg acttggtgc tctcttgagt tgtggcaacC ggaagttcca 300  
ggccccattg cagcacYtac actgcgctaa tggaccttca ggactattct gagaatggaa 360  
ctgtaaccgt ggtatatcga gtgatactta aaggaactga tggagaggca tatagagatg 420  
ccacgggcac aacacagttG ccatgagggg cgcaggggaag atgctgttgc agccgcagag 480  
gaagctgcat tcagcaaagc ttgcgcatgg ttcggttttg gcctgtatct gtaccaccag 540  
gatgaatctc attacgacga ccacttccat tgaggctcaa tctgcaaaag agttgatcat 600  
aagttgtaac atgcgttga tatgccctta gaaaattcgt atctagaatc aatttttggt 660  
ctttgcgtag tatcatactc ataacacaaa gaagtgaacc tatgtagatg ctatttgaaa 720  
ccddkttatt aatattataa ttcttattaa tattattgta t

(2) INFORMATION FOR SEQ ID NO:3575:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..84
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577383

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3575:

Phe Leu Val Gln Val Val Glu Val Asn Val Lys Val Glu Ser Ala Gly  
1 5 10 15  
Thr His Asn Met His Asn Asn Asp Phe Tyr Ala Lys Glu Lys Leu Leu  
20 25 30  
Lys Ser Met Arg Asp Cys Asp Pro Ser Ser Leu Arg His Trp Ile Val  
35 40 45  
Arg Val Val Phe Leu Phe Tyr Ile Phe Phe Val Ile Pro Thr Ile Glu  
50 55 60  
Leu Gly Ile Gln Tyr Leu Xaa Ile Ile Phe Met Leu Met Gln Ser Asn  
65 70 75 80  
Asn Asp Gly Lys

(2) INFORMATION FOR SEQ ID NO:3576:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..65
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3576:

Met His Asn Asn Asp Phe Tyr Ala Lys Glu Lys Leu Leu Lys Ser Met  
1 5 10 15  
Arg Asp Cys Asp Pro Ser Ser Leu Arg His Trp Ile Val Arg Val Val  
20 25 30  
Phe Leu Phe Tyr Ile Phe Phe Val Ile Pro Thr Ile Glu Leu Gly Ile  
35 40 45  
Gln Tyr Leu Xaa Ile Ile Phe Met Leu Met Gln Ser Asn Asn Asp Gly  
50 55 60  
Lys  
65

(2) INFORMATION FOR SEQ ID NO:3577:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid

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- (C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..62  
(D) OTHER INFORMATION: / Ceres Seq. ID 1577385  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3577:

Met	Arg	Gly	Ala	Gly	Lys	Met	Leu	Leu	Gln	Pro	Gln	Arg	Lys	Leu	His
1				5					10					15	
Ser	Ala	Lys	Leu	Ala	His	Gly	Ser	Val	Leu	Ala	Cys	Ile	Cys	Thr	Thr
			20					25					30		
Arg	Met	Asn	Leu	Ile	Thr	Thr	Thr	Ser	Ile	Glu	Ala	Gln	Ser	Ala	
		35					40					45			
Lys	Glu	Leu	Ile	Ile	Ser	Cys	Asn	Met	Arg	Trp	Ile	Cys	Pro		
	50					55					60				

- (2) INFORMATION FOR SEQ ID NO:3578:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 780 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..780  
(D) OTHER INFORMATION: / Ceres Seq. ID 1577401

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3578:

gagctcgctg	cgccgtcttt	caatgctccc	cgccgccttc	cccgtataa	agcacctgcc	60
ttgccacctc	tctctcctca	cgaccacaca	ccaccgctcc	acacacaaga	agagagccga	120
gagctagcta	cctagcgcg	gatggcgatg	tccgcttcca	agatgatggc	ggtcgccgcc	180
gctngccctg	ctagccctgg	tcctggccgc	gtcgaccgcg	nagggcagga	acatcaagac	240
gacgacgacg	acgacggaga	agaaggacga	tgcggtggtg	bagccgcaga	ccttcccgcc	300
cttcgamcgc	ctcggcgcg	gNcgcgCcc	cggcggtccg	gtggcctccc	cggcacctcg	360
tcgggcgcca	gcagcattcc	agcgttcagc	atgcggggca	gcggcagcag	cctccccggc	420
gggtcgttct	tgcccggcag	cagcggcagc	atcggcagca	tgcccctctt	cagcggcggc	480
tccccggcct	tcagcggctt	cggcggcgatg	cccgggtccc	ncgccgccgg	ctccgtctcc	540
gtcgtccccg	tgcacggcag	caagccctga	aaatccgtcc	gtcgccggag	cccgggaagtc	600
tgtcgggcca	acttggtccc	tagtactcct	ttgcctgcat	tgtattggag	agttggtatc	660
gcgtttcggt	tggtgtttgc	tttgttatta	taggcgcgct	atctaccgag	acatgtgatg	720
tttggtgcgg	taaattaaaa	tcggttgat	tcatgctgct	gctgttgtct	ttaatttgct	780

- (2) INFORMATION FOR SEQ ID NO:3579:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 142 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..142  
(D) OTHER INFORMATION: / Ceres Seq. ID 1577402

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3579:

Met	Ala	Met	Ser	Ala	Ser	Lys	Met	Met	Ala	Val	Ala	Ala	Ala	Xaa	Pro
1				5					10					15	
Ala	Ser	Pro	Gly	Pro	Gly	Arg	Val	Asp	Arg	Xaa	Gly	Glu	Glu	His	Gln
			20					25					30		
Asp	Asp	Asp	Asp	Asp	Asp	Gly	Glu	Glu	Gly	Arg	Cys	Gly	Gly	Xaa	Ala
		35					40					45			
Ala	Asp	Leu	Pro	Ala	Leu	Arg	Xaa	Pro	Arg	Arg	Arg	Xaa	Arg	Pro	Pro



50 55 60  
Ala Ser Gly Gly Leu Pro Gly Thr Ser Ser Gly Gly Ser Ser Ile Pro  
65 70 75 80  
Ala Phe Ser Met Pro Gly Ser Gly Ser Ser Leu Pro Gly Gly Ser Phe  
85 90 95  
Leu Pro Gly Ser Ser Gly Ser Ile Gly Ser Met Pro Leu Phe Ser Gly  
100 105 110  
Gly Ser Pro Ala Phe Ser Gly Phe Gly Gly Met Pro Gly Ser Xaa Ala  
115 120 125  
Ala Gly Ser Val Ser Val Val Pro Val His Gly Ser Lys Pro  
130 135 140

(2) INFORMATION FOR SEQ ID NO:3580:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..140

(D) OTHER INFORMATION: / Ceres Seq. ID 1577403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3580:

Met Ser Ala Ser Lys Met Met Ala Val Ala Ala Ala Xaa Pro Ala Ser  
1 5 10 15  
Pro Gly Pro Gly Arg Val Asp Arg Xaa Gly Glu Glu His Gln Asp Asp  
20 25 30  
Asp Asp Asp Asp Gly Glu Glu Gly Arg Cys Gly Gly Xaa Ala Ala Asp  
35 40 45  
Leu Pro Ala Leu Arg Xaa Pro Arg Arg Arg Xaa Arg Pro Pro Ala Ser  
50 55 60  
Gly Gly Leu Pro Gly Thr Ser Ser Gly Gly Ser Ser Ile Pro Ala Phe  
65 70 75 80  
Ser Met Pro Gly Ser Gly Ser Ser Leu Pro Gly Gly Ser Phe Leu Pro  
85 90 95  
Gly Ser Ser Gly Ser Ile Gly Ser Met Pro Leu Phe Ser Gly Gly Ser  
100 105 110  
Pro Ala Phe Ser Gly Phe Gly Gly Met Pro Gly Ser Xaa Ala Ala Gly  
115 120 125  
Ser Val Ser Val Val Pro Val His Gly Ser Lys Pro  
130 135 140

(2) INFORMATION FOR SEQ ID NO:3581:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..135

(D) OTHER INFORMATION: / Ceres Seq. ID 1577404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3581:

Met Met Ala Val Ala Ala Ala Xaa Pro Ala Ser Pro Gly Pro Gly Arg  
1 5 10 15  
Val Asp Arg Xaa Gly Glu Glu His Gln Asp Asp Asp Asp Asp Asp Gly  
20 25 30  
Glu Glu Gly Arg Cys Gly Gly Xaa Ala Ala Asp Leu Pro Ala Leu Arg  
35 40 45  
Xaa Pro Arg Arg Arg Xaa Arg Pro Pro Ala Ser Gly Gly Leu Pro Gly  
50 55 60

Thr Ser Ser Gly Gly Ser Ser Ile Pro Ala Phe Ser Met Pro Gly Ser  
65 70 75 80  
Gly Ser Ser Leu Pro Gly Gly Ser Phe Leu Pro Gly Ser Ser Gly Ser  
85 90 95  
Ile Gly Ser Met Pro Leu Phe Ser Gly Gly Ser Pro Ala Phe Ser Gly  
100 105 110  
Phe Gly Gly Met Pro Gly Ser Xaa Ala Ala Gly Ser Val Ser Val Val  
115 120 125  
Pro Val His Gly Ser Lys Pro  
130 135

(2) INFORMATION FOR SEQ ID NO:3582:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 837 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..837
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3582:

accctctcca	cttcggtttc	cggatcccgt	ttccagctcc	gatccaaccc	agcatctgta	60
ccgcgcgcgc	gagcacgtcc	ggcgccggtg	cggcaggcga	aatccgagag	cactcctmcc	120
ccgctacgcc	gcaccgcca	tggccgcagc	tagccgcaga	tagagagagg	cgcaggcgag	180
ggcgtgcaga	tccagatccg	gtgggcggga	aggacttgat	cgccccacc	accatggccg	240
gcccgggtgc	ggcgctcttc	ctgctggaca	tgaagggccg	cgttctcgtc	tggcgcgact	300
accgcggcga	tgtctccgcg	ctccaggccg	agcgcttctt	caccaagctc	ctcgacaagg	360
agggcgattc	ggaagtgcac	tcgctgtgg	tctacgacga	cgctggcgtc	acttacatgt	420
tcattccagca	caacaatgtc	ttcctcctca	ccgcgcgtcg	ccagaactgt	aacgcggCcc	480
agcatcctcc	tcttctctcca	ccgtgtaata	gatgtgttta	agcactactt	cgaggagctg	540
gaggaggagt	cgctcagaga	taacttcgtc	gttggtgatg	agttgctcga	tgagatgatg	600
gattttgggt	accacaata	cacggaggcg	aagatattga	gtgagttcat	caagacagat	660
gcatacagga	tggaggtcac	acagcgtcca	cccatggccg	tgacaaatgc	tgtgtcatgg	720
aggagcgagg	ggatccggta	caagaagaat	gaagtcttct	tggatgtagt	ggagagtgtt	780
aacattctag	ttaacagcaa	tggccagatt	gtgagatcag	atgtggttgg	ggcactg	

(2) INFORMATION FOR SEQ ID NO:3583:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..172
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3583:

Pro Leu His Phe Arg Phe Arg Ile Pro Phe Pro Ala Pro Ile Gln Pro  
1 5 10 15  
Ser Ile Cys Thr Ala Pro Xaa Ser Thr Ser Gly Ala Gly Ala Ala Gly  
20 25 30  
Glu Ile Arg Glu His Ser Xaa Pro Ala Thr Pro His Arg Pro Trp Pro  
35 40 45  
Gln Leu Ala Ala Asp Arg Glu Arg Arg Arg Arg Gly Arg Ala Asp Pro  
50 55 60  
Asp Pro Val Gly Gly Lys Asp Leu Ile Ala Pro Thr Thr Met Ala Gly  
65 70 75 80  
Pro Val Ser Ala Leu Phe Leu Leu Asp Met Lys Gly Arg Val Leu Val  
85 90 95  
Trp Arg Asp Tyr Arg Gly Asp Val Ser Ala Leu Gln Ala Glu Arg Phe

(2) INFORMATION FOR SEO ID NO:3584:

(A) LENGTH: 176 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..176

(D) OTHER INFORMATION: / Ceres Seq. ID 1577407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3584:

(2) INFORMATION FOR SEQ ID NO:3585:

(A) LENGTH: 134 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..134

(D) OTHER INFORMATION: / Ceres Seq. ID 1577408

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3585:

Met	Ser	Ser	Ser	Ser	Pro	Pro	Leu	Ala	Arg	Thr	Val	Thr	Arg	Pro	Ser
1				5					10					15	
Ile	Leu	Leu	Phe	Leu	His	Arg	Val	Ile	Asp	Val	Phe	Lys	His	Tyr	Phe
			20					25					30		

Glu Glu Leu Glu Glu Glu Ser Leu Arg Asp Asn Phe Val Val Val Tyr  
35 40 45  
Glu Leu Leu Asp Glu Met Met Asp Phe Gly Tyr Pro Gln Tyr Thr Glu  
50 55 60  
Ala Lys Ile Leu Ser Glu Phe Ile Lys Thr Asp Ala Tyr Arg Met Glu  
65 70 75 80  
Val Thr Gln Arg Pro Pro Met Ala Val Thr Asn Ala Val Ser Trp Arg  
85 90 95  
Ser Glu Gly Ile Arg Tyr Lys Lys Asn Glu Val Phe Leu Asp Val Val  
100 105 110  
Glu Ser Val Asn Ile Leu Val Asn Ser Asn Gly Gln Ile Val Arg Ser  
115 120 125  
Asp Val Val Gly Ala Leu  
130

(2) INFORMATION FOR SEQ ID NO:3586:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 886 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..886
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577456

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3586:

aaaatttccc	ccccaatttc	cctccaccga	agcatcaccc	aatcagatcc	gatttcgtag	60
agatgaagcc	ggcagtagag	gcggaggctg	acgagcgagc	ggcggaggag	atggcaccta	120
agaaggcagc	ggctgccaag	aaagcngccg	aggaagttga	ggtggaggad	gtggtggacg	180
gggacgaggc	ggtcgatggg	gagggcgacg	gtgacgagga	cgacgatggg	gaaggcggtg	240
acgaggagga	tgatgatgab	gaggtggatg	gggaggagaa	ggangcggca	ggggttggtg	300
agatctccga	cGgaagacga	cgacgacggt	gacggggakg	cggacgacga	cgacgacgat	360
gacggggatg	acgacgacga	cgacgacgag	gactcagacg	acgaggaaga	ggtcgacggt	420
gaagacgatc	aggaggagga	gctgggaacc	gagtatctgg	ttcagcctct	tgggcgggct	480
gaagacgaag	agcactcgag	cgactttgaa	cgggaagaaa	acggtgaggg	tgccgacgat	540
gaggagatcg	atgaagagga	cgatgacggt	gaggactctg	tgaaggcgca	gacctctacg	600
aagaggaaga	ggtcaggcga	cgaagaagaa	gaagacgacg	acgatgggga	tgatgatggt	660
gacgatgatg	acgatgggag	gccaccatca	aagcgatagt	atggttagct	ctagttttgt	720
agctgtgtcc	ttgggtgttt	ggtaggtagg	tagtgctgct	gatgttggtt	tagaagaact	780
catcatcacc	tgggatatgt	gtgtgatttg	gcttggccga	tggatgaatg	atgaaggtct	840
tgtacttggt	gctgottott	tcatgttgat	gaactcgcac	tgattc		

(2) INFORMATION FOR SEQ ID NO:3587:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..167
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577457

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3587:

Met Gly Arg Ala Thr Val Thr Arg Thr Met Gly Lys Ala Val Thr	
1 5 10 15	
Arg Arg Met Met Met Xaa Arg Trp Met Gly Arg Arg Arg Xaa Arg Gln	
20 25 30	
Gly Leu Trp Arg Ser Pro Thr Glu Asp Asp Asp Asp Gly Asp Gly Xaa	
35 40 45	
Ala Asp Asp Asp Asp Asp Asp Asp Gly Asp Asp Asp Asp Asp Asp	
50 55 60	

Glu Asp Ser Asp Asp Glu Glu Glu Val Asp Gly Glu Asp Asp Gln Glu  
65 70 75 80  
Glu Glu Leu Gly Thr Glu Tyr Leu Val Gln Pro Leu Gly Arg Ala Glu  
85 90 95  
Asp Glu Glu His Ser Ser Asp Phe Glu Pro Glu Glu Asn Gly Glu Gly  
100 105 110  
Ala Asp Asp Glu Glu Ile Asp Glu Glu Asp Asp Asp Gly Glu Asp Ser  
115 120 125  
Val Lys Ala Gln Thr Ser Thr Lys Arg Lys Arg Ser Gly Asp Glu Glu  
130 135 140  
Glu Glu Asp Asp Asp Asp Gly Asp Asp Asp Asp Asp Asp  
145 150 155 160  
Gly Arg Pro Pro Ser Lys Arg  
165

(2) INFORMATION FOR SEQ ID NO:3588:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..157
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577458

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3588:

Met Gly Lys Ala Val Thr Arg Arg Met Met Met Xaa Arg Trp Met Gly  
1 5 10 15  
Arg Arg Arg Xaa Arg Gln Gly Leu Trp Arg Ser Pro Thr Glu Asp Asp  
20 25 30  
Asp Asp Gly Asp Gly Xaa Ala Asp Asp Asp Asp Asp Asp Gly Asp  
35 40 45  
Asp Asp Asp Asp Asp Asp Glu Asp Ser Asp Asp Glu Glu Glu Val Asp  
50 55 60  
Gly Glu Asp Asp Gln Glu Glu Leu Gly Thr Glu Tyr Leu Val Gln  
65 70 75 80  
Pro Leu Gly Arg Ala Glu Asp Glu Glu His Ser Ser Asp Phe Glu Pro  
85 90 95  
Glu Glu Asn Gly Glu Gly Ala Asp Asp Glu Glu Ile Asp Glu Glu Asp  
100 105 110  
Asp Asp Gly Glu Asp Ser Val Lys Ala Gln Thr Ser Thr Lys Arg Lys  
115 120 125  
Arg Ser Gly Asp Glu Glu Glu Asp Asp Asp Asp Gly Asp Asp Asp  
130 135 140  
Gly Asp Asp Asp Asp Asp Gly Arg Pro Pro Ser Lys Arg  
145 150 155

(2) INFORMATION FOR SEQ ID NO:3589:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..149
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577459

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3589:

Met Met Met Xaa Arg Trp Met Gly Arg Arg Arg Xaa Arg Gln Gly Leu  
1 5 10 15  
Trp Arg Ser Pro Thr Glu Asp Asp Asp Asp Gly Asp Gly Xaa Ala Asp

20 25 30  
Asp Asp Asp Asp Asp Gly Asp Asp Asp Asp Asp Asp Asp Glu Asp  
35 40 45  
Ser Asp Asp Glu Glu Glu Val Asp Gly Glu Asp Asp Gln Glu Glu Glu  
50 55 60  
Leu Gly Thr Glu Tyr Leu Val Gln Pro Leu Gly Arg Ala Glu Asp Glu  
65 70 75 80  
Glu His Ser Ser Asp Phe Glu Pro Glu Glu Asn Gly Glu Gly Ala Asp  
85 90 95  
Asp Glu Glu Ile Asp Glu Glu Asp Asp Asp Gly Glu Asp Ser Val Lys  
100 105 110  
Ala Gln Thr Ser Thr Lys Arg Lys Arg Ser Gly Asp Glu Glu Glu Glu  
115 120 125  
Asp Asp Asp Asp Gly Asp Asp Asp Gly Asp Asp Asp Asp Asp Gly Arg  
130 135 140  
Pro Pro Ser Lys Arg  
145

(2) INFORMATION FOR SEQ ID NO:3590:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..620
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577480

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3590:

accggacagc	tccccacaaa	acogtcagtt	ctctttttccc	ctgtaaatcg	caaattcgtc	60
ttccctgccc	atctatcgct	tggacacctc	tgcaagggag	cacatggctc	tcgagaaggc	120
caaggagatc	atcgcgctcct	ccccggtcga	cctagctctc	cgaaaggcca	aggagaccgt	180
cgcctcccac	cccgctgctcg	tcttcagcaa	aacttactgc	cctttctgca	cccgagtga	240
acaattgcta	gcaaagttgg	gggcaagtta	caaggctatt	gagttKggat	gtggaaagt	300
atggcgctga	gctgcagtca	gctctcgctg	aatggactgg	ccagagaact	gttcccaatg	360
tcttcgtgaa	aggggagcgg	attgggtggct	gtgacgcaac	catggcaatg	cacgacgggtg	420
aagctGggtg	cctctgctca	ccgaggctgg	agcaattgtc	actgccaggg	ctactgcaac	480
tactaccact	ccgtctttKg	tagacatgtt	ttacagcgct	gttccgctcg	cttcgtggct	540
atatgcaaat	gcaagtgttg	tacggagtag	taaactcata	cgtggcaaaa	gatgaataaa	600
gacttaaaca	tttcttcgcc					

(2) INFORMATION FOR SEQ ID NO:3591:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..93
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577481

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3591:

Thr Gly Gln Leu Pro Thr Lys Pro Ser Val Leu Phe Ser Pro Val Asn  
1 5 10 15  
Arg Lys Phe Val Phe Pro Ala His Leu Ser Leu Gly His Leu Cys Lys  
20 25 30  
Gly Ala His Gly Ser Arg Glu Gly Gln Gly Asp His Arg Val Leu Pro  
35 40 45  
Gly Arg Pro Ser Ser Pro Lys Gly Gln Gly Asp Arg Arg Leu Pro Pro  
50 55 60  
Arg Arg Arg Leu Gln Gln Asn Leu Leu Pro Phe Leu His Pro Ser Glu

(2) INFORMATION FOR SEQ ID NO:3592:

(A) LENGTH: 50 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..50

(D) OTHER INFORMATION: / Ceres Seq. ID 1577482

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3592:

(2) INFORMATION FOR SEQ ID NO:3593:

(A) LENGTH: 65 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..65

(D) OTHER INFORMATION: / Ceres Seq. ID 1577483

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3593:

(2) INFORMATION FOR SEQ ID NO:3594:

(A) LENGTH: 923 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: sing

(D) TOPOLOGY: linear

MOLECULE TYPE: DNA (α

(ix) FEATURE:

(A) NAM

(B) LOCATION: 1

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:3594:

tatcar gaggcactac agtggaggat gcgggagcca aa

ccttggtggt	ggtggagtcg	agaagacagg	tgaggagatt	gcgactgcac	tgaacaacat	120
tgacattagc	tctgagtatg	ttctgaagct	ccgtcatgag	attgaggagc	tctgcgtgga	180
ggtttttcat	actccagctg	atcgagagaa	gatcaagtcc	tgtttatcag	agctaggaga	240

ggtcagtgc tcatttaaga agatccttca ttctgcactg gagcatttgg tggcatctgt 300  
ggtaccacgc attcgtccag tccttgacac tgttgctact gtcagttatg agttggatga 360  
tactgaatat ggggaaaatg aggtgaacga tccatgggtg cagaagctta tacttacagt 420  
waacagtaat gttgcttggc tccagccagt tatgacatta aacaactacg attcctttgt 480  
gcacttgatc attgacttca ttgtcaagag gctcgaggtg attatgatgc agaagagggtt 540  
cagccagctc ggcggtctcc agctcgataa ggaggtccgc tctctgatca accatttctc 600  
agagatgtCc cagagaccag tcagagacaa gttctctagg ctttcgcaga tgtcgaccat 660  
tttgaacttc gagcgggtat cggagatatt ggatttcttg ggtgacaatg ctggccatct 720  
gacgtggctg ttgacacctg cagaggtgcg gagagtgtta ggacttagga ttgacttcag 780  
gcctgaagct attgctgctt tgaggctctg aatcgtgcat ttatttgtac ttgttaattc 840  
attatatgtg atatatagca acgagatgcc ttagaaattt ttgttgtaat gacgaaagac 900  
ctgcattgta gaagaaatct gcg

(2) INFORMATION FOR SEQ ID NO:3595:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..269
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3595:

Glu Tyr Xaa Glu Ala Leu Gln Trp Arg Met Arg Glu Pro Asn Leu Gly  
1 5 10 15  
Ala Lys Leu Phe Leu Gly Gly Val Gly Val Gln Lys Thr Gly Glu Glu  
20 25 30  
Ile Ala Thr Ala Leu Asn Asn Ile Asp Ile Ser Ser Glu Tyr Val Leu  
35 40 45  
Lys Leu Arg His Glu Ile Glu Glu Leu Cys Val Glu Val Phe His Thr  
50 55 60  
Pro Ala Asp Arg Glu Lys Ile Lys Ser Cys Leu Ser Glu Leu Gly Glu  
65 70 75 80  
Val Ser Ala Ser Phe Lys Lys Ile Leu His Ser Ala Leu Glu His Leu  
85 90 95  
Val Ala Ser Val Val Pro Arg Ile Arg Pro Val Leu Asp Thr Val Ala  
100 105 110  
Thr Val Ser Tyr Glu Leu Asp Asp Thr Glu Tyr Gly Glu Asn Glu Val  
115 120 125  
Asn Asp Pro Trp Val Gln Lys Leu Ile Leu Thr Xaa Asn Ser Asn Val  
130 135 140  
Ala Trp Leu Gln Pro Val Met Thr Leu Asn Asn Tyr Asp Ser Phe Val  
145 150 155 160  
His Leu Ile Ile Asp Phe Ile Val Lys Arg Leu Glu Val Ile Met Met  
165 170 175  
Gln Lys Arg Phe Ser Gln Leu Gly Gly Leu Gln Leu Asp Lys Glu Val  
180 185 190  
Arg Ser Leu Ile Asn His Phe Ser Glu Met Ser Gln Arg Pro Val Arg  
195 200 205  
Asp Lys Phe Ser Arg Leu Ser Gln Met Ser Thr Ile Leu Asn Phe Glu  
210 215 220  
Arg Val Ser Glu Ile Leu Asp Phe Trp Gly Asp Asn Ala Gly His Leu  
225 230 235 240  
Thr Trp Leu Leu Thr Pro Ala Glu Val Arg Arg Val Leu Gly Leu Arg  
245 250 255  
Ile Asp Phe Arg Pro Glu Ala Ile Ala Ala Leu Arg Leu  
260 265

(2) INFORMATION FOR SEQ ID NO:3596:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 amino acids

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- (B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..260  
(D) OTHER INFORMATION: / Ceres Seq. ID 1577490

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3596:

Met Arg Glu Pro Asn Leu Gly Ala Lys Leu Phe Leu Gly Gly Val Gly  
1 5 10 15  
Val Gln Lys Thr Gly Glu Glu Ile Ala Thr Ala Leu Asn Asn Ile Asp  
20 25 30  
Ile Ser Ser Glu Tyr Val Leu Lys Leu Arg His Glu Ile Glu Glu Leu  
35 40 45  
Cys Val Glu Val Phe His Thr Pro Ala Asp Arg Glu Lys Ile Lys Ser  
50 55 60  
Cys Leu Ser Glu Leu Gly Glu Val Ser Ala Ser Phe Lys Lys Ile Leu  
65 70 75 80  
His Ser Ala Leu Glu His Leu Val Ala Ser Val Val Pro Arg Ile Arg  
85 90 95  
Pro Val Leu Asp Thr Val Ala Thr Val Ser Tyr Glu Leu Asp Asp Thr  
100 105 110  
Glu Tyr Gly Glu Asn Glu Val Asn Asp Pro Trp Val Gln Lys Leu Ile  
115 120 125  
Leu Thr Xaa Asn Ser Asn Val Ala Trp Leu Gln Pro Val Met Thr Leu  
130 135 140  
Asn Asn Tyr Asp Ser Phe Val His Leu Ile Ile Asp Phe Ile Val Lys  
145 150 155 160  
Arg Leu Glu Val Ile Met Met Gln Lys Arg Phe Ser Gln Leu Gly Gly  
165 170 175  
Leu Gln Leu Asp Lys Glu Val Arg Ser Leu Ile Asn His Phe Ser Glu  
180 185 190  
Met Ser Gln Arg Pro Val Arg Asp Lys Phe Ser Arg Leu Ser Gln Met  
195 200 205  
Ser Thr Ile Leu Asn Phe Glu Arg Val Ser Glu Ile Leu Asp Phe Trp  
210 215 220  
Gly Asp Asn Ala Gly His Leu Thr Trp Leu Leu Thr Pro Ala Glu Val  
225 230 235 240  
Arg Arg Val Leu Gly Leu Arg Ile Asp Phe Arg Pro Glu Ala Ile Ala  
245 250 255  
Ala Leu Arg Leu  
260

(2) INFORMATION FOR SEQ ID NO:3597:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 760 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..760  
(D) OTHER INFORMATION: / Ceres Seq. ID 1577513

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3597:

accaaagcct	ccrccccctt	ccctgacacc	ctcgccgcg	cgcaagcag	cacgaaccag	60
cgaagagatg	ggcgtctaca	ccttcgtgtg	cgcacrcrc	ggcggsgcga	ngtggaccgc	120
caagcagcac	tccggcgaga	tggaggcctc	cgccgccacc	ccctacgagc	tgcagcgccg	180
cctcgtcgcc	gCgcctccg	cGgccgactc	cgcgtccggc	gtccagtcgt	ccttctCcca	240
tggtcacccc	caGctccgcc	gtcttccagg	tgatcgtcgg	tggtggcgcg	atgatggtta	300
gtgGAngcgg	cgCgcggcgg	tGcggccgAy	ngccgCdckg	gktgNgcgct	gcggccgaag	360

ctcccaaGgg aggagaagaa ggaagaggag aaggaagaga gcgacgacga catggggattc 420  
tccctgttgc actagagtta agctgcgtgt gcatgggttc gggtcGggtc gtgtcgcgcg 480  
aaacgtgaag agctcaagcg gcctttttgt tccagtccca catgtgagag ctttgatacg 540  
ttgtctggaa tgaaaaaatt tccccttgac accttgtctg caccgagggg ggagtaggcg 600  
tgggggaaaa actgtagaac ctgtgggatg caaaatctat ctagtctagt tttgggatcg 660  
gttacgaatt tgtcttcaac aaatagtttg gatgagacga gtggaaaaca tgggtggtgt 720  
tgatttcaga aacgaatggc gatatgacat gtgttgtggc

(2) INFORMATION FOR SEQ ID NO:3598:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..90

(D) OTHER INFORMATION: / Ceres Seq. ID 1577514

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3598:

Thr Lys Ala Ser Xaa Pro Phe Pro Asp Thr Leu Ala Ala Ala His Ala  
1 5 10 15  
Arg Thr Asn Gln Arg Arg Asp Gly Arg Leu His Leu Arg Val Pro Xaa  
20 25 30  
Xaa Arg Arg Xaa Xaa Val Asp Arg Gln Ala Ala Leu Arg Arg Asp Gly  
35 40 45  
Gly Leu Arg Arg His Pro Leu Arg Ala Ala Ala Pro Pro Arg Arg Arg  
50 55 60  
Arg Leu Arg Gly Arg Leu Arg Val Arg Arg Pro Val Val Leu Leu Pro  
65 70 75 80  
Trp Ser Pro Pro Ala Pro Pro Ser Ser Arg  
85 90

(2) INFORMATION FOR SEQ ID NO:3599:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..99

(D) OTHER INFORMATION: / Ceres Seq. ID 1577515

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3599:

Pro Lys Pro Xaa Pro Pro Ser Leu Thr Pro Ser Pro Pro Arg Thr His  
1 5 10 15  
Ala Arg Thr Ser Glu Glu Met Gly Val Tyr Thr Phe Val Cys Arg Xaa  
20 25 30  
Xaa Gly Xaa Ala Xaa Trp Thr Ala Lys Gln His Ser Gly Glu Met Glu  
35 40 45  
Ala Ser Ala Ala Thr Pro Tyr Glu Leu Gln Arg Arg Leu Val Ala Ala  
50 55 60  
Ala Ser Ala Ala Asp Ser Ala Ser Gly Val Gln Ser Ser Phe Ser His  
65 70 75 80  
Gly His Pro Gln Leu Arg Arg Leu Pro Gly Asp Arg Arg Trp Trp Arg  
85 90 95  
Asp Asp Gly

(2) INFORMATION FOR SEQ ID NO:3600:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..82
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1577516
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3600:

Met	Val	Thr	Pro	Ser	Ser	Ala	Val	Phe	Gln	Val	Ile	Val	Gly	Gly	Gly
1			5						10					15	
Ala	Met	Met	Val	Ser	Gly	Xaa	Gly	Ala	Arg	Arg	Cys	Gly	Arg	Xaa	Pro
			20					25					30		
Xaa	Arg	Xaa	Xaa	Ala	Ala	Ala	Glu	Ala	Pro	Lys	Gly	Gly	Glu	Glu	Gly
			35				40					45			
Arg	Gly	Glu	Gly	Arg	Glu	Arg	Arg	Arg	His	Gly	Ile	Leu	Pro	Val	Arg
			50			55				60					
Leu	Glu	Leu	Ser	Cys	Val	Cys	Met	Val	Ala	Val	Arg	Val	Val	Ser	Arg
65				70						75					80
Glu	Thr														

- (2) INFORMATION FOR SEQ ID NO:3601:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1006 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..1006
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1577517
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3601:

ctagggttta	catcccttat	aaaatctcgt	cttccacccc	tgcctccctc	agtcgcactt	60
cctccggcgg	cggcaactcg	acggccaacc	gcgccaccct	gccgcggcag	ccatggtgca	120
tgtaacttc	taccgcaact	atgggaagac	tttcaagaag	ccaaggcggc	cgtatgagaa	180
ggagcgcta	gatgctgagc	tgaagctggt	tggtgagtat	ggcctgcggt	gcaagcgcca	240
gctgtggcgc	gtgcagtatg	ccctgagccg	tatcaggaat	gcagccaggg	agctgctcac	300
cctggatgag	aagaaccac	gcggtatctt	tgagggcgag	gcgctccctc	gccgcatgaa	360
cagatatggt	cttcttggtg	agggacagaa	caagcttgat	tacgtgcttg	ctctcactgt	420
tgagaacttc	ctccagcgcc	gcctccagac	catcgtcttc	aagaatggca	tggccaagtc	480
catccaccat	gctcgtgtcc	tgatcaggca	gcgcCacatc	aggggtggga	ggcagctcgt	540
caacatcccc	tcgttcatgg	tcagggtcga	atcagagaag	cacatcgact	tctccctcac	600
cagccctctg	ggtggtggtc	ctgccggaag	ggtgaagcgg	aagaaccaga	agaaggcctc	660
agggggcggc	gacgctgagg	aggacgagga	gtaaaggggg	ggggggcacg	taggattctg	720
ggacggcaat	tggtttaaat	gtgaggtgga	cactttagtt	gttgtgcctg	agtgtgtttg	780
tggtgtaatg	aatacaaatt	ctactgtggt	agacaatttt	gcacccccac	tactgacact	840
cgtgtttaaa	tttaaacatt	ggcatcgtgt	ctggacacga	tgaattgtat	tctggtttgg	900
gtggctattt	gctagtttgg	tctttaggcc	aatgtttaag	actgaaacaa	attggtagcc	960
aactttacta	tcttatgctc	tgctggtctg	tttggtgatt	tttttt		

- (2) INFORMATION FOR SEQ ID NO:3602:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 193 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..193
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1577518
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3602:

Met Val His Val Asn Phe Tyr Arg Asn Tyr Gly Lys Thr Phe Lys Lys  
1 5 10 15  
Pro Arg Arg Pro Tyr Glu Lys Glu Arg Leu Asp Ala Glu Leu Lys Leu  
20 25 30  
Val Gly Glu Tyr Gly Leu Arg Cys Lys Arg Glu Leu Trp Arg Val Gln  
35 40 45  
Tyr Ala Leu Ser Arg Ile Arg Asn Ala Ala Arg Glu Leu Leu Thr Leu  
50 55 60  
Asp Glu Lys Asn Pro Arg Arg Ile Phe Glu Gly Glu Ala Leu Leu Arg  
65 70 75 80  
Arg Met Asn Arg Tyr Gly Leu Leu Gly Glu Gly Gln Asn Lys Leu Asp  
85 90 95  
Tyr Val Leu Ala Leu Thr Val Glu Asn Phe Leu Gln Arg Arg Leu Gln  
100 105 110  
Thr Ile Val Phe Lys Asn Gly Met Ala Lys Ser Ile His His Ala Arg  
115 120 125  
Val Leu Ile Arg Gln Arg His Ile Arg Val Gly Arg Gln Leu Val Asn  
130 135 140  
Ile Pro Ser Phe Met Val Arg Val Glu Ser Glu Lys His Ile Asp Phe  
145 150 155 160  
Ser Leu Thr Ser Pro Leu Gly Gly Gly Pro Ala Gly Arg Val Lys Arg  
165 170 175  
Lys Asn Gln Lys Lys Ala Ser Gly Gly Gly Asp Ala Glu Glu Asp Glu  
180 185 190  
Glu

(2) INFORMATION FOR SEQ ID NO:3603:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 112 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..112

(D) OTHER INFORMATION: / Ceres Seq. ID 1577519

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3603:

Met Asn Arg Tyr Gly Leu Leu Gly Glu Gly Gln Asn Lys Leu Asp Tyr  
1 5 10 15  
Val Leu Ala Leu Thr Val Glu Asn Phe Leu Gln Arg Arg Leu Gln Thr  
20 25 30  
Ile Val Phe Lys Asn Gly Met Ala Lys Ser Ile His His Ala Arg Val  
35 40 45  
Leu Ile Arg Gln Arg His Ile Arg Val Gly Arg Gln Leu Val Asn Ile  
50 55 60  
Pro Ser Phe Met Val Arg Val Glu Ser Glu Lys His Ile Asp Phe Ser  
65 70 75 80  
Leu Thr Ser Pro Leu Gly Gly Gly Pro Ala Gly Arg Val Lys Arg Lys  
85 90 95  
Asn Gln Lys Lys Ala Ser Gly Gly Gly Asp Ala Glu Glu Asp Glu Glu  
100 105 110

(2) INFORMATION FOR SEQ ID NO:3604:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 851 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(D) OTHER INFORMATION: / Ceres Seq. ID 1577526

aagagctccc	cacctcgccc	cccccatcc	agctccgacc	ctagggtttc	catccggctc	60
ttccggaagc	ttccgaaat	ggccaccgac	gagctcgccc	acgccgtcgc	ccccgccccg	120
gccgggggag	accactcccc	ggcctttctcg	ttcagcatct	ggccgccgac	gcagcgcaag	180
cgnhgacgsg	ntggtgcggc	gcctcgtgga	gacgctcgcg	ggagacacca	tcctctgcaa	240
gcgctacggt	gcggtgcggc	ccgccgacgc	cgagcccgcg	gcgcgcgcca	tcgaggccga	300
ggccttcgac	gccgcggcct	ccacgggagg	cgccgcgcgc	gcctccgtgg	aggaggggat	360
cgaggcgctg	cagttcCtac	tccaaaggagg	tgagccgcg	cctcctyvgc	ttcgtcaagt	420
ycGctccgcg	ggacgccaag	gcgggtgaca	cgccgtcgga	ggaggcccg	gccctcggeg	480
gcgccgaggc	cgaggccgcc	cagcccgcgg	cgtgagcgcc	gdacgccat	tcgttccgtt	540
ttgtattttc	tgcagcctgt	gtttggcctt	ggtctgagtt	tgtatgactt	gaacgttagc	600
tgtttgacaa	tctatgcaat	tcttgttctt	ccatgaatag	ccccgttcta	gtgcgtgttc	660
ctgtttttct	gggaatccct	gcccgatcct	gaggttgta	aaccatcgca	gcattgacct	720
ctgtctgtgt	gcagcttcga	gtgatggctg	aattgttccg	gagaccgaat	tgacaagcaa	780
ttaaagattcc	tcccatcttt	caagccacat	ttatatgtat	aataataatc	tgaccgttga	840
tttgaatttc	t					

(D) OTHER INFORMATION: / Ceres Seq. ID 1577527

[illegible]

(D) OTHER INFORMATION: / Ceres Seq. ID 1577528

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3606:

Arg Ala Pro His Leu Ala Pro Pro His Pro Ala Pro Thr Leu Gly Phe  
1 5 10 15  
Pro Ser Gly Ser Ser Gly Ser Phe Arg Lys Trp Pro Pro Thr Ser Ser  
20 25 30  
Pro Thr Pro Ser Pro Pro Pro Arg Pro Gly Glu Thr Thr Pro Arg Pro  
35 40 45  
Ser Arg Ser Ala Ser Gly Arg Arg Arg Ser Ala Arg Xaa Asp Xaa Xaa  
50 55 60  
Val Arg Arg Leu Val Glu Thr Leu Ala Gly Asp Thr Ile Leu Cys Lys  
65 70 75 80  
Arg Tyr Gly Ala Val Pro Ala Ala Asp Ala Glu Pro Ala Ala Arg Ala  
85 90 95  
Ile Glu Ala Glu Ala Phe Asp Ala Ala Ala Ser Thr Gly Gly Ala Ala  
100 105 110  
Ala Ala Ser Val Glu Glu Gly Ile Glu Ala Leu Gln Phe Leu Leu Gln  
115 120 125  
Gly Gly Glu Pro Pro Pro Pro Xaa Leu Arg Gln Xaa Pro Leu Arg Gly  
130 135 140  
Arg Gln Gly Arg  
145

(2) INFORMATION FOR SEQ ID NO:3607:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577529

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3607:

Met Ala Thr Asp Glu Leu Ala His Ala Val Ala Pro Ala Pro Ala Gly  
1 5 10 15  
Gly Asp His Ser Pro Ala Phe Ser Phe Ser Ile Trp Pro Pro Thr Gln  
20 25 30  
Arg Thr Arg Xaa Xaa Xaa Gly Ala Ala Pro Arg Gly Asp Ala Arg Gly  
35 40 45  
Arg His His Pro Leu Gln Ala Leu Arg Cys Gly Ala Gly Arg Arg Arg  
50 55 60  
Arg Ala Arg Gly Ala Arg His Arg Gly Arg Gly Leu Arg Arg Arg Gly  
65 70 75 80  
Leu His Gly Arg Arg Arg Arg Arg Leu Arg Gly Gly Gly Asp Arg Gly  
85 90 95  
Ala Ala Val Pro Thr Pro Arg Arg  
100

(2) INFORMATION FOR SEQ ID NO:3608:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 842 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..842
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577539

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3608:

agtggtgtgt cctagcgccg cgcgcgcccc aactcgctt gcgtgactga aagctcgctg 60  
gcttcgctcc acgcgagaag cgagagcatg gacacccagg tgaagcttgc tgttgtgtg 120

aaggtgatgg gcaggaccgg ctccaggggt caggtgaccc aggtcagagt taagttcttg 180  
gatgaccaga accggctcat catgaggaat gtcaaggcac ttgtcaccac ttgacgagaa 240  
gaacccccgt cgtatctttg aggggtgaggc gcttcttcgc cgcatagaacc gctatgggct 300  
gcttgctgag ggtcagaaca agcttgatta tgttcttgcc ctcaccgctg agaacttcct 360  
cgcaaggcgg cttcaaacac ttgtcttcaa ggctggcatg gccaaagtcca ttcaccatgc 420  
tcgtgtcttg atcaagcagc gtcacatcag gggtggcagg caaattgtca acgtcccatc 480  
attcatggtg aggggtggagt ctgagaagca cattgacttt tcaactgtcaa gccattcgg 540  
tgaggagcccc gcaGgaaggg tgaagagaaa gaatcagaag aaggcaagcg gtggcggcga 600  
tgctggcgat gaggatgagg agtgaggatg gacaagtagc gttacccaat ataataatat 660  
tatctagttt tcttgaactt gttogaatga tgagtgttta gctgtgtgat ctgacgcaga 720  
gttcctgtg ctgactctgt gtcatggatg gtccatttta tcttgtggta ttatcagcct 780  
ttacataact gctatgtttg gatatgttca attctgttgc aattttatgt ggttgttttt 840  
tg

(2) INFORMATION FOR SEQ ID NO:3609:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..138
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577540

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3609:

Met Ser Arg His Leu Leu Thr Leu Asp Glu Lys Asn Pro Arg Arg Ile  
1 5 10 15  
Phe Glu Gly Glu Ala Leu Leu Arg Arg Met Asn Arg Tyr Gly Leu Leu  
20 25 30  
Ala Glu Gly Gln Asn Lys Leu Asp Tyr Val Leu Ala Leu Thr Ala Glu  
35 40 45  
Asn Phe Leu Ala Arg Arg Leu Gln Thr Leu Val Phe Lys Ala Gly Met  
50 55 60  
Ala Lys Ser Ile His His Ala Arg Val Leu Ile Lys Gln Arg His Ile  
65 70 75 80  
Arg Val Gly Arg Gln Ile Val Asn Val Pro Ser Phe Met Val Arg Val  
85 90 95  
Glu Ser Glu Lys His Ile Asp Phe Ser Leu Ser Ser Pro Phe Gly Gly  
100 105 110  
Gly Pro Ala Gly Arg Val Lys Arg Lys Asn Gln Lys Lys Ala Ser Gly  
115 120 125  
Gly Gly Asp Ala Gly Asp Glu Asp Glu Glu  
130 135

(2) INFORMATION FOR SEQ ID NO:3610:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..113
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3610:

Met Asn Arg Tyr Gly Leu Leu Ala Glu Gly Gln Asn Lys Leu Asp Tyr  
1 5 10 15  
Val Leu Ala Leu Thr Ala Glu Asn Phe Leu Ala Arg Arg Leu Gln Thr  
20 25 30  
Leu Val Phe Lys Ala Gly Met Ala Lys Ser Ile His His Ala Arg Val  
35 40 45

Leu Ile Lys Gln Arg His Ile Arg Val Gly Arg Gln Ile Val Asn Val  
50 55 60  
Pro Ser Phe Met Val Arg Val Glu Ser Glu Lys His Ile Asp Phe Ser  
65 70 75 80  
Leu Ser Ser Pro Phe Gly Gly Gly Pro Ala Gly Arg Val Lys Arg Lys  
85 90 95  
Asn Gln Lys Lys Ala Ser Gly Gly Gly Asp Ala Gly Asp Glu Asp Glu  
100 105 110  
Glu

(2) INFORMATION FOR SEQ ID NO:3611:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..75

(D) OTHER INFORMATION: / Ceres Seq. ID 1577542

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3611:

Met Ala Lys Ser Ile His His Ala Arg Val Leu Ile Lys Gln Arg His  
1 5 10 15  
Ile Arg Val Gly Arg Gln Ile Val Asn Val Pro Ser Phe Met Val Arg  
20 25 30  
Val Glu Ser Glu Lys His Ile Asp Phe Ser Leu Ser Ser Pro Phe Gly  
35 40 45  
Gly Gly Pro Ala Gly Arg Val Lys Arg Lys Asn Gln Lys Lys Ala Ser  
50 55 60  
Gly Gly Gly Asp Ala Gly Asp Glu Asp Glu Glu  
65 70 75

(2) INFORMATION FOR SEQ ID NO:3612:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 569 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..569

(D) OTHER INFORMATION: / Ceres Seq. ID 1577548

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3612:

aaaacagaca ggaagcccg cgaacatcac aaggctgcga acctcctaga agctcgagga 60  
gatgctctcc aagctgtcgg cgtggttcgt gaacccgcgg aggaatygb tcgcgcgtct 120  
ccaccggaac gccgtgcgct ccgcctccg caaatacggg ctccaggtatg acgacctcta 180  
cgaccggtac cagcacctag acatcaagga ggcgCtgggc cggctgccgc gggaggtggt 240  
ggacgcccgt aaccagcgcc tcaagcgggc catggacctc tccatgaagc accagtacct 300  
acccgacgac gtccaggcta tacagacgcc attcaggagc tacctttttg acatgcttgc 360  
tcttgatgaaa aaggagagcg cagagcgtga agcattggga gcgcttccac tctaccagag 420  
aaccatccca taaagtgcct ctttgcatga tccaatcaat agtgcacgcg atgatcagca 480  
gaggctgata ctgtaatgtg tattgtgttt ttccgaggaa atctctacta cttattaaga 540  
cgataagggt agcctgccgt tctgacgtc

(2) INFORMATION FOR SEQ ID NO:3613:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide



(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..123

(D) OTHER INFORMATION: / Ceres Seq. ID 1577549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3613:

Met Leu Ser Lys Leu Ser Ala Trp Phe Val Asn Pro Arg Arg Asn Xaa  
1 5 10 15  
Xaa Ala Arg Leu His Arg Asn Ala Val Ala Ser Arg Leu Arg Lys Tyr  
20 25 30  
Gly Leu Arg Tyr Asp Asp Leu Tyr Asp Pro Tyr His Asp Leu Asp Ile  
35 40 45  
Lys Glu Ala Leu Ala Arg Leu Pro Arg Glu Val Val Asp Ala Arg Asn  
50 55 60  
Gln Arg Leu Lys Arg Ala Met Asp Leu Ser Met Lys His Gln Tyr Leu  
65 70 75 80  
Pro Asp Asp Val Gln Ala Ile Gln Thr Pro Phe Arg Ser Tyr Leu Phe  
85 90 95  
Asp Met Leu Ala Leu Val Lys Lys Glu Ser Ala Glu Arg Glu Ala Leu  
100 105 110  
Gly Ala Leu Pro Leu Tyr Gln Arg Thr Ile Pro  
115 120

(2) INFORMATION FOR SEQ ID NO:3614:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 704 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..704

(D) OTHER INFORMATION: / Ceres Seq. ID 1577550

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3614:

gtgctttctt agaggtgggt tggcttctcc tccccctccg gttcgggttc gggttcgtga 60  
ggttctccgg ggttcgggtt cgtgggtgav cggatcgaga tggcggcgtc ggatgttgag 120  
taccgctgct tcgctcggcag ctacagcvgt ggcggcgggc gctacgggtg cggcggcgcc 180  
accacttgct cgccttcgcc ccttctgtct cccttcgtcc gtagcagacc aggaacgcc 240  
aaggcgctaG cgtctccaag atggtgctgc aaaacgacat tgacttactc aatccaccgg 300  
cagagcttga gaagctaaag cacaagaaga agcggctagt ccagtcccc aactccttct 360  
tcatggatgt caagtgccag ggctgtttca gcataaccac tgtgttcagc cactcccaga 420  
ctgtggttgt gtgccaggc tgccaaactg ttctgtgcc acctaccggt gggaaggcca 480  
ggctcaccga ggggtgctcc ttccgtcgca agggcgatta ggtCctgctt ctcttaacgt 540  
gagaagagat aaatttggtg ttttgcaact ttctcaggat atgtactgta ctcggtgagg 600  
attttgttaa ttattatggc tgttagcgtg gcttgacaat gcttgtgtgt maacctgcac 660  
tttgtttgag cgtagtgaca tctaatatgg tgctgtttgg cttt

(2) INFORMATION FOR SEQ ID NO:3615:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 82 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..82

(D) OTHER INFORMATION: / Ceres Seq. ID 1577551

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3615:

Cys Phe Leu Arg Gly Gly Leu Ala Ser Pro Pro Pro Pro Val Arg Val  
1 5 10 15  
Arg Val Arg Glu Val Leu Arg Gly Ser Val Ser Trp Val Xaa Gly Ser  
20 25 30

20250904 14:33:50

Arg Trp Arg Arg Arg Met Leu Ser Thr Ala Ala Ser Ser Ala Ala Thr  
35 40 45  
Xaa Val Ala Ala Ala Ala Thr Val Ala Ala Ala Pro Pro Leu Ala Arg  
50 55 60  
Leu Arg Pro Phe Cys Leu Pro Ser Ser Val Ala Asp Gln Glu Arg Pro  
65 70 75 80  
Arg Arg

(2) INFORMATION FOR SEQ ID NO:3616:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..72

(D) OTHER INFORMATION: / Ceres Seq. ID 1577552

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3616:

Met Ala Ala Ser Asp Val Glu Tyr Arg Cys Phe Val Gly Ser Tyr Ser  
1 5 10 15  
Xaa Gly Gly Gly Gly Tyr Gly Gly Gly Gly Ala Thr Thr Cys Ser Pro  
20 25 30  
Ser Pro Leu Leu Ser Pro Phe Val Arg Ser Arg Pro Gly Thr Pro Lys  
35 40 45  
Ala Leu Ala Ser Pro Arg Trp Cys Cys Lys Thr Thr Leu Thr Tyr Ser  
50 55 60  
Ile His Arg Gln Ser Leu Arg Ser  
65 70

(2) INFORMATION FOR SEQ ID NO:3617:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 86 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..86

(D) OTHER INFORMATION: / Ceres Seq. ID 1577553

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3617:

Met Val Leu Gln Asn Asp Ile Asp Leu Leu Asn Pro Pro Ala Glu Leu  
1 5 10 15  
Glu Lys Leu Lys His Lys Lys Lys Arg Leu Val Gln Ser Pro Asn Ser  
20 25 30  
Phe Phe Met Asp Val Lys Cys Gln Gly Cys Phe Ser Ile Thr Thr Val  
35 40 45  
Phe Ser His Ser Gln Thr Val Val Val Cys Pro Gly Cys Gln Thr Val  
50 55 60  
Leu Cys Gln Pro Thr Gly Gly Lys Ala Arg Leu Thr Glu Gly Cys Ser  
65 70 75 80  
Phe Arg Arg Lys Gly Asp  
85

(2) INFORMATION FOR SEQ ID NO:3618:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 941 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..941

(D) OTHER INFORMATION: / Ceres Seq. ID 1577582

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3618:

aggccagggc	acttgcaaag	gatttatcct	cccaaagagc	aacgagagat	agggattttg	60
cttttgcattg	gttcatttgt	ttgcggcgctc	aaagagctcg	ttaaataatgg	acgtntctgga	120
tcactcggac	gatgaggagg	agcagcagga	cgggtgcggc	accagcagcg	gcagatcagg	180
ctccaggctc	ggcgcgcggg	csggcggcag	aagcggaggt	caggcggcag	cgccagaacc	240
tgctgctcat	ggactgcgtc	ggcggcaacg	gcggcgacgg	ggacggcgcg	ttggaggaca	300
ccgcgccgct	gccagactac	gagctcttgt	cccagtcggc	ccgcctccac	gacgacgcca	360
agaatccgcc	tccggcgctg	ctggttgcag	avgaggagga	gcagcagaag	gcgccggcca	420
agcaggggaa	gCggtccccc	ccacagcctc	cgcccggtgc	actgccacag	cggcagcaga	480
agccggcgctg	gaggctgata	gagtagctga	ggtaaggaa	cagktcgggc	ggcgcagggc	540
cgggggtcgg	tgggtgcggc	gcctggtctg	acggcgactc	caagagctcc	gaggacggcg	600
aggacggggg	cggcgaaggg	aagaaagata	agaagaagaa	gcggtcgtcc	tggctgccgg	660
accccgaccg	cgggtggccg	gtgcagggat	tctactagcg	cgttcatcgt	cttcgcagtc	720
tagtaaaacc	gtgttagtca	tgatgcgcct	ctgactcatg	cgttggtttg	gttgctccgg	780
gccctgtttg	gaagtgaagt	ttttttcata	gtttttgaga	aatactatag	tatccgttaa	840
tattagagta	ttctggacta	ttaatagatt	attagaaaaat	agagtttcta	atatcatggt	900
ttttttaagt	atttgatata	tagttctgga	cctaagtttt	t		

(2) INFORMATION FOR SEQ ID NO:3619:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 167 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..167

(D) OTHER INFORMATION: / Ceres Seq. ID 1577583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3619:

Met	Val	His	Trp	Phe	Ala	Ala	Ser	Lys	Ser	Ser	Leu	Asn	Met	Asp	Xaa
1				5					10					15	
Leu	Asp	His	Ser	Asp	Asp	Glu	Glu	Glu	Gln	Gln	Asp	Arg	Cys	Gly	Thr
			20					25					30		
Ser	Ser	Gly	Arg	Ser	Gly	Ser	Arg	Leu	Gly	Ala	Arg	Xaa	Gly	Gly	Arg
		35					40				45				
Ser	Gly	Gly	Gln	Ala	Ala	Ala	Pro	Glu	Pro	Ala	Ala	His	Gly	Leu	Arg
	50					55				60					
Arg	Arg	Gln	Arg	Arg	Arg	Arg	Gly	Arg	Arg	Val	Gly	Gly	His	Arg	Ala
65				70				75					80		
Ala	Ala	Arg	Leu	Arg	Ala	Leu	Val	Pro	Val	Arg	Pro	Pro	Pro	Arg	Arg
			85					90					95		
Arg	Gln	Glu	Ser	Ala	Ser	Gly	Ala	Ala	Gly	Cys	Arg	Xaa	Gly	Gly	Ala
		100						105					110		
Ala	Glu	Gly	Ala	Gly	Gln	Ala	Gly	Glu	Gly	Val	Pro	Ala	Thr	Ala	Ser
	115					120					125				
Ala	Arg	Ala	Thr	Ala	Thr	Ala	Ala	Ala	Glu	Ala	Gly	Val	Glu	Ala	Asp
	130					135					140				
Arg	Val	Arg	Glu	Val	Lys	Glu	Gln	Xaa	Gly	Arg	Arg	Arg	Ala	Gly	Gly
145					150					155				160	
Arg	Trp	Val	Arg	Arg	Leu	Val									
					165										

(2) INFORMATION FOR SEQ ID NO:3620:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..154

(D) OTHER INFORMATION: / Ceres Seq. ID 1577584

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3620:

Met Asp Xaa Leu Asp His Ser Asp Asp Glu Glu Glu Gln Gln Asp Arg  
1 5 10 15  
Cys Gly Thr Ser Ser Gly Arg Ser Gly Ser Arg Leu Gly Ala Arg Xaa  
20 25 30  
Gly Gly Arg Ser Gly Gly Gln Ala Ala Pro Glu Pro Ala Ala His  
35 40 45  
Gly Leu Arg Arg Arg Gln Arg Arg Arg Arg Gly Arg Arg Val Gly Gly  
50 55 60  
His Arg Ala Ala Ala Arg Leu Arg Ala Leu Val Pro Val Arg Pro Pro  
65 70 75 80  
Pro Arg Arg Arg Gln Glu Ser Ala Ser Gly Ala Ala Gly Cys Arg Xaa  
85 90 95  
Gly Gly Ala Ala Glu Gly Ala Gly Gln Ala Gly Glu Gly Val Pro Ala  
100 105 110  
Thr Ala Ser Ala Arg Ala Thr Ala Ala Ala Glu Ala Gly Val  
115 120 125  
Glu Ala Asp Arg Val Arg Glu Val Lys Glu Gln Xaa Gly Arg Arg Arg  
130 135 140  
Ala Gly Gly Arg Trp Val Arg Arg Leu Val  
145 150

(2) INFORMATION FOR SEQ ID NO:3621:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 188 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..188

(D) OTHER INFORMATION: / Ceres Seq. ID 1577585

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3621:

Met Arg Arg Ser Ser Arg Thr Gly Ala Ala Pro Ala Ala Asp Gln  
1 5 10 15  
Ala Pro Gly Ser Ala Arg Gly Xaa Ala Ala Glu Ala Glu Val Arg Arg  
20 25 30  
Gln Arg Gln Asn Leu Leu Leu Met Asp Cys Val Gly Gly Asn Gly Gly  
35 40 45  
Asp Gly Asp Gly Ala Leu Glu Asp Thr Ala Pro Leu Pro Asp Tyr Glu  
50 55 60  
Leu Leu Ser Gln Ser Ala Arg Leu His Asp Asp Ala Lys Asn Pro Pro  
65 70 75 80  
Pro Ala Leu Leu Val Ala Xaa Glu Glu Glu Gln Gln Lys Ala Pro Ala  
85 90 95  
Lys Gln Gly Lys Ala Ser Pro Pro Gln Pro Pro Pro Val Pro Leu Pro  
100 105 110  
Gln Arg Gln Gln Lys Pro Ala Trp Arg Leu Ile Glu Tyr Val Arg Ser  
115 120 125  
Arg Asn Xaa Ser Gly Gly Ala Gly Pro Gly Val Gly Gly Cys Gly Ala  
130 135 140  
Trp Ser Asp Gly Asp Ser Lys Ser Ser Glu Asp Gly Glu Asp Gly Gly  
145 150 155 160  
Gly Glu Gly Lys Lys Asp Lys Lys Lys Lys Arg Ser Ser Trp Leu Pro  
165 170 175  
Asp Pro Asp Arg Arg Trp Pro Val Gln Gly Phe Tyr

180 185  
(2) INFORMATION FOR SEQ ID NO:3622:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 854 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..854  
(D) OTHER INFORMATION: / Ceres Seq. ID 1577601  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3622:  
acttgctcca tatcccatcc atcacagcta gctagcgtac agacgaataa tctcttcttc 60  
acctcactag ctaacaccag ctagcagctc gatcgctctg tcctgcaata atggccgctc 120  
gctcctcctc ccagcagctg gtcgcggcgg cggctcctggc agcggcgcts ctgctgctgg 180  
cggcgggggc cgggacggcg tcggcggcgg tgagctgcgg cgaggtgacg tcgtcggtgg 240  
cgccgtgcct cgggtacggc atgggcagcg cggcgctgcc ctccgcggcg tgcgtgcagcg 300  
gggtgcgctc gctcaacagc cgcgcgtcgt cggcggcgga ccgncaggcc acctgcaact 360  
gcctcaagag catgacgggc cggctcggcg gcggcgctcag Catggccaac gccgccaaca 420  
tcccgggcaa atgcggcgct tccgtcggcg tgcccatcag cccaccgctc gactgcacca 480  
agatcaactg atcgatggaa ccatagtggg ggtagctcgc tcgttggatg gcagcgtagc 540  
tggccatcag cagcatgcag tcgtcgtcgt agcagagatg tcctagctac gtgtgtgtca 600  
tgcacagac tggcacataa taaagaagta gatcatgcac ccactagtga tcacttcgtc 660  
tagtgtccct ccgttcgtcg ttgtcgtcgt cgtcgtcgtg gtgtacctcg tacgtgacat 720  
gccgtagcac gtacgctagc agagcagcac ctcaatgtcc ttgggtttgc tttgctggct 780  
ctctgttttc gtctcgtgtt gcttttaatc tggcacaggt ttctaaatta taataatgaa 840  
tacttttttg tcct

(2) INFORMATION FOR SEQ ID NO:3623:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 126 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..126  
(D) OTHER INFORMATION: / Ceres Seq. ID 1577602  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3623:  
Met Ala Ala Arg Ser Ser Ser Gln Gln Leu Val Ala Ala Ala Val Leu  
1 5 10 15  
Ala Ala Ala Xaa Leu Leu Leu Ala Ala Gly Ala Gly Thr Ala Ser Ala  
20 25 30  
Ala Val Ser Cys Gly Glu Val Thr Ser Ser Val Ala Pro Cys Leu Gly  
35 40 45  
Tyr Ala Met Gly Ser Ala Ala Ser Pro Ser Ala Ala Cys Cys Ser Gly  
50 55 60  
Val Arg Ser Leu Asn Ser Arg Ala Ser Ser Ala Ala Asp Xaa Gln Ala  
65 70 75 80  
Thr Cys Asn Cys Leu Lys Ser Met Thr Gly Arg Leu Gly Gly Gly Val  
85 90 95  
Ser Met Ala Asn Ala Ala Asn Ile Pro Gly Lys Cys Gly Val Ser Val  
100 105 110  
Gly Val Pro Ile Ser Pro Thr Val Asp Cys Thr Lys Ile Asn  
115 120 125

(2) INFORMATION FOR SEQ ID NO:3624:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 76 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..76  
(D) OTHER INFORMATION: / Ceres Seq. ID 1577603

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3624:

Met Gly Ser Ala Ala Ser Pro Ser Ala Ala Cys Cys Ser Gly Val Arg  
1 5 10 15  
Ser Leu Asn Ser Arg Ala Ser Ser Ala Ala Asp Xaa Gln Ala Thr Cys  
20 25 30  
Asn Cys Leu Lys Ser Met Thr Gly Arg Leu Gly Gly Gly Val Ser Met  
35 40 45  
Ala Asn Ala Ala Asn Ile Pro Gly Lys Cys Gly Val Ser Val Gly Val  
50 55 60  
Pro Ile Ser Pro Thr Val Asp Cys Thr Lys Ile Asn  
65 70 75

(2) INFORMATION FOR SEQ ID NO:3625:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 572 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..572  
(D) OTHER INFORMATION: / Ceres Seq. ID 1577610

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3625:

aagaaaagcc tccattcccg agtctccagc caaccgcatc cagtcaccc catccccctc 60  
gacccccgaca accccgagtc ccgaccgat ggcgcccaag gccgagaaga agccagcgga 120  
gaagaagccg gcggccgagg agaaggcgga gaagacgacc gcagGtaaga ggctttggct 180  
ttgtgaacta ctccgacagt gatgctgcc aggaagctat ttctgcaatg gatggcaagg 240  
aaattgatgg gcggcaggta cgtgtcaaca tggctaata gagacctgct gggaaccgtg 300  
gtggtggcgg ctatggtggc ggcggctatg gaggtggtg ctacggaggt ggtggcggct 360  
acggaggtgg tggctatggt ggtggcagcc aaagctatga tgcttgaagg gggcaggatc 420  
ctattaagtc attatcaacc aagatatattg aaataatgaa ctttaggact tggatgacg 480  
ttttatgta agcattgtca ggttttgcta ttcgtgttat gctgaattgt tggaactcct 540  
agatgcagaa tattacgtat tggttttggt cc

(2) INFORMATION FOR SEQ ID NO:3626:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 134 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..134  
(D) OTHER INFORMATION: / Ceres Seq. ID 1577611

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3626:

Glu Lys Pro Pro Phe Pro Ser Leu Gln Pro Thr Ala Ser Ser Pro Pro  
1 5 10 15  
His Pro Pro Arg Pro Arg Gln Pro Arg Val Pro Thr Arg Trp Arg Pro  
20 25 30  
Arg Pro Arg Arg Ser Gln Arg Arg Arg Ser Arg Arg Pro Arg Arg Arg  
35 40 45  
Arg Arg Arg Arg Pro Gln Val Arg Gly Phe Gly Phe Val Asn Tyr Ser  
50 55 60  
Asp Ser Asp Ala Ala Lys Glu Ala Ile Ser Ala Met Asp Gly Lys Glu  
65 70 75 80

Ile Asp Gly Arg Gln Val Arg Val Asn Met Ala Asn Glu Arg Pro Ala  
85 90 95  
Gly Asn Arg Gly Gly Gly Tyr Gly Gly Gly Tyr Gly Gly Gly  
100 105 110  
Gly Tyr Gly Gly Gly Gly Tyr Gly Gly Gly Tyr Gly Gly Gly  
115 120 125  
Ser Gln Ser Tyr Asp Ala  
130

(2) INFORMATION FOR SEQ ID NO:3627:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 84 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..84

(D) OTHER INFORMATION: / Ceres Seq. ID 1577612

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3627:

Met Leu Pro Arg Lys Leu Phe Leu Gln Trp Met Ala Arg Lys Leu Met  
1 5 10 15  
Gly Gly Arg Tyr Val Ser Thr Trp Leu Met Arg Asp Leu Leu Gly Thr  
20 25 30  
Val Val Val Ala Ala Met Val Ala Ala Ala Met Glu Val Val Ala Thr  
35 40 45  
Glu Val Val Ala Ala Thr Glu Val Val Ala Met Val Val Ala Ala Lys  
50 55 60  
Ala Met Met Leu Glu Gly Arg Ile Leu Leu Ser His Tyr Gln Pro  
65 70 75 80  
Arg Tyr Leu Lys

(2) INFORMATION FOR SEQ ID NO:3628:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..74

(D) OTHER INFORMATION: / Ceres Seq. ID 1577613

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3628:

Met Ala Arg Lys Leu Met Gly Gly Arg Tyr Val Ser Thr Trp Leu Met  
1 5 10 15  
Arg Asp Leu Leu Gly Thr Val Val Val Ala Ala Met Val Ala Ala Ala  
20 25 30  
Met Glu Val Val Ala Thr Glu Val Val Ala Ala Thr Glu Val Val Ala  
35 40 45  
Met Val Val Ala Ala Lys Ala Met Met Leu Glu Gly Gly Arg Ile Leu  
50 55 60  
Leu Ser His Tyr Gln Pro Arg Tyr Leu Lys  
65 70

(2) INFORMATION FOR SEQ ID NO:3629:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 731 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..731

(D) OTHER INFORMATION: / Ceres Seq. ID 1577614

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3629:

aaaaacccta	gcagccaccc	ggttctccct	cgctccaggt	ggcggcgcg	ccccctcggt	60
ttgtttcttac	tccctccggt	tccctcacta	gtcgttactg	acttctcgct	tgccctgctcc	120
agatctccct	tgcagccgg	ccagggaccc	cttcacagcg	cgggagatgg	ctgatcagga	180
ggccccagtt	gcagttgagg	caccaacccc	agttcttgga	gagccaatgg	acttgatgac	240
tgcgctgcag	ctggtgatga	agaagtcaag	tgctcatgat	ggacttgatga	agggctcttcg	300
cgaggctgcc	aaggccattg	agaagcatgc	tgctcagctt	tgcgttcttg	ctgaggactg	360
tgaccagcca	gattatgtca	agctggtgaa	ggcgctctgt	gctgaacaca	atgttcaoct	420
tgctactggt	cctgctgcta	agactcttgg	cgagtgggct	gggctttgca	agattgactc	480
cgagggcaag	gcaaggaagg	ttgtaggctg	ctcctgtgtc	gttgtcaagg	actacggtga	540
agaatctgag	ggccttaaca	tagtgcagga	gtatgtcaag	tgcactaga	tgtAacacgt	600
ttcagtaata	ctctacattt	ggatctgggc	ttaatattat	gcttgcgtct	tgggcttgc	660
aggagattag	gacaatttac	tacaagagcc	catgaggata	tgagcaattt	ggaattctaa	720
atgttttggt	t					

(2) INFORMATION FOR SEQ ID NO:3630:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 140 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..140

(D) OTHER INFORMATION: / Ceres Seq. ID 1577615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3630:

Met	Ala	Asp	Gln	Glu	Ala	Pro	Val	Ala	Val	Glu	Ala	Pro	Thr	Pro	Val
1			5						10					15	
Leu	Gly	Glu	Pro	Met	Asp	Leu	Met	Thr	Ala	Leu	Gln	Leu	Val	Met	Lys
			20					25					30		
Lys	Ser	Ser	Ala	His	Asp	Gly	Leu	Val	Lys	Gly	Leu	Arg	Glu	Ala	Ala
			35				40						45		
Lys	Ala	Ile	Glu	Lys	His	Ala	Ala	Gln	Leu	Cys	Val	Leu	Ala	Glu	Asp
			50				55				60				
Cys	Asp	Gln	Pro	Asp	Tyr	Val	Lys	Leu	Val	Lys	Ala	Leu	Cys	Ala	Glu
65					70					75				80	
His	Asn	Val	His	Leu	Val	Thr	Val	Pro	Ala	Ala	Lys	Thr	Leu	Gly	Glu
			85						90					95	
Trp	Ala	Gly	Leu	Cys	Lys	Ile	Asp	Ser	Glu	Gly	Lys	Ala	Arg	Lys	Val
			100					105					110		
Val	Gly	Cys	Ser	Cys	Val	Val	Val	Lys	Asp	Tyr	Gly	Glu	Glu	Ser	Glu
			115				120					125			
Gly	Leu	Asn	Ile	Val	Gln	Glu	Tyr	Val	Lys	Ser	His				
			130				135				140				

(2) INFORMATION FOR SEQ ID NO:3631:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..120

(D) OTHER INFORMATION: / Ceres Seq. ID 1577616

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3631:

Met Asp Leu Met Thr Ala Leu Gln Leu Val Met Lys Lys Ser Ser Ala



1 5 10 15  
His Asp Gly Leu Val Lys Gly Leu Arg Glu Ala Ala Lys Ala Ile Glu  
20 25 30  
Lys His Ala Ala Gln Leu Cys Val Leu Ala Glu Asp Cys Asp Gln Pro  
35 40 45  
Asp Tyr Val Lys Leu Val Lys Ala Leu Cys Ala Glu His Asn Val His  
50 55 60  
Leu Val Thr Val Pro Ala Ala Lys Thr Leu Gly Glu Trp Ala Gly Leu  
65 70 75 80  
Cys Lys Ile Asp Ser Glu Gly Lys Ala Arg Lys Val Val Gly Cys Ser  
85 90 95  
Cys Val Val Val Lys Asp Tyr Gly Glu Ser Glu Gly Leu Asn Ile  
100 105 110  
Val Gln Glu Tyr Val Lys Ser His  
115 120

(2) INFORMATION FOR SEQ ID NO:3632:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..117

(D) OTHER INFORMATION: / Ceres Seq. ID 1577617

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3632:

Met Thr Ala Leu Gln Leu Val Met Lys Lys Ser Ser Ala His Asp Gly  
1 5 10 15  
Leu Val Lys Gly Leu Arg Glu Ala Ala Lys Ala Ile Glu Lys His Ala  
20 25 30  
Ala Gln Leu Cys Val Leu Ala Glu Asp Cys Asp Gln Pro Asp Tyr Val  
35 40 45  
Lys Leu Val Lys Ala Leu Cys Ala Glu His Asn Val His Leu Val Thr  
50 55 60  
Val Pro Ala Ala Lys Thr Leu Gly Glu Trp Ala Gly Leu Cys Lys Ile  
65 70 75 80  
Asp Ser Glu Gly Lys Ala Arg Lys Val Val Gly Cys Ser Cys Val Val  
85 90 95  
Val Lys Asp Tyr Gly Glu Glu Ser Glu Gly Leu Asn Ile Val Gln Glu  
100 105 110  
Tyr Val Lys Ser His  
115

(2) INFORMATION FOR SEQ ID NO:3633:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 790 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..790

(D) OTHER INFORMATION: / Ceres Seq. ID 1577622

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3633:

aaaggccaaa atcatcgctg crogccagt rgacggttc gactccggcc gccgcccctg 60  
ctcctcctgc ccacccgcac cggccattgc cctgcctgc totgccacc gcaccttcca 120  
ccgccccgc gtgctcctcc gcagtctggc cggtgcacc acctgcwccc caccaccgcc 180  
gccccacca cttatccacc gttgcmggtc gtgcmccam ctgctcccc actgacaccg 240  
gtcgaggtat aatctcacc tgggtgaagc ttcaccgcac tgctccgac acaccgaacc 300  
aaacccatcc gagcgcatat acccagcaaa aaagtggaca cattttttac agcctaggtt 360

tNtccgCtgc gccccctggt ttcgaaatcc tttccctagc gatcataact gacgccccga 420  
atcgCcgcgcg ggcgggggag gagattcatc acgttttctg ctagggtttt gtatttggac 480  
tagacagagc ggaaatctgg tgggtggtgat tctgtaacca gaagatcaga aactacggag 540  
gagtgggggt ttgtgattgg ttaccgatag gggttttgat tcatcggcac ccaaattgct 600  
gttgattttt tcctgcagtt tctctcaatg ttttatggt catggtagta ctggattatg 660  
gatacatttt tttcaagtga ttcataatct gcatcactcc tttttaaaaa agatcatcaa 720  
tgaggagtga tgatatgatg atttttttat ttatctgtta acatcagtaa catcataata 780  
gttttttttc

(2) INFORMATION FOR SEQ ID NO:3634:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..83
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577623

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3634:

Lys Gly Gln Asn His Arg Cys Xaa Ala Ser Xaa Arg Val Arg Leu Arg  
1 5 10 15  
Pro Pro Pro Leu Leu Leu Leu Pro Thr Arg Thr Gly His Cys Pro Arg  
20 25 30  
Leu Leu Cys His Pro His Leu Pro Pro Pro Pro Arg Ala Pro Pro Gln  
35 40 45  
Ser Gly Arg Cys Thr His Leu Xaa Pro Thr Thr Ala Ala Pro Pro Thr  
50 55 60  
Tyr Pro Pro Leu Xaa Val Val Xaa Pro Xaa Ala Pro Pro Leu Thr Pro  
65 70 75 80  
Val Glu Val

(2) INFORMATION FOR SEQ ID NO:3635:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..77
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577624

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3635:

Lys Ala Lys Ile Ile Ala Xaa Pro Pro Xaa Asp Ala Phe Asp Ser Gly  
1 5 10 15  
Arg Arg Pro Cys Ser Ser Cys Pro Pro Ala Pro Ala Ile Ala Leu Ala  
20 25 30  
Cys Ser Ala Thr Arg Thr Phe His Arg Pro Arg Val Leu Leu Arg Ser  
35 40 45  
Leu Ala Val Ala Pro Thr Cys Xaa Pro Pro Pro Pro Pro His Pro Leu  
50 55 60  
Ile His Arg Cys Xaa Ser Ser Xaa Xaa Leu Leu Pro His  
65 70 75

(2) INFORMATION FOR SEQ ID NO:3636:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1577625

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3636:

Arg	Pro	Lys	Ser	Ser	Leu	Xaa	Arg	Gln	Xaa	Thr	Arg	Ser	Thr	Pro	Ala
1				5					10					15	
Ala	Ala	Pro	Ala	Pro	Pro	Ala	His	Pro	His	Arg	Pro	Leu	Pro	Ser	Pro
			20					25					30		
Ala	Leu	Pro	Pro	Ala	Pro	Ser	Thr	Ala	Pro	Ala	Cys	Ser	Ser	Ala	Val
		35					40					45			
Trp	Pro	Leu	His	Pro	Pro	Xaa	Pro	His	His	Arg	Arg	Pro	Thr	His	Leu
	50					55					60				
Ser	Thr	Val	Xaa	Gly	Arg	Arg	Xaa	Xaa	Cys	Ser	Pro	Thr	Asp	Thr	Gly
65					70					75					80
Arg	Gly	Ile	Ile	Ser	Pro	Trp	Val	Lys	Leu	His	Pro	Thr	Ala	Pro	Ile
				85					90					95	
Thr	Pro	Asn	Gln	Thr	His	Pro	Ser	Ala	Tyr	Thr	Gln	Gln	Lys	Ser	Gly
		100						105					110		
His	Ile	Phe	Tyr	Ser	Leu	Gly	Xaa	Ser	Ala	Ala	Pro	Pro	Val	Phe	Glu
		115					120					125			
Ile	Leu	Ser	Leu	Ala	Ile	Ile	Thr	Asp	Ala	Pro	Asn	Arg	Arg	Ala	Ala
	130						135					140			
Gly	Glu	Glu	Ile	His	His	Val	Phe	Cys							
145						150									

(2) INFORMATION FOR SEQ ID NO:3637:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 798 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..798

(D) OTHER INFORMATION: / Ceres Seq. ID 1577634

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3637:

aacctcgctg	tgtctcggt	tggcttggt	tcctctccc	cgacgaccac	cccgcgcttc	60
tcctctcccc	ccgtcccacc	ttccgagagg	ctcgagccct	gatccacgc	tgagggcggc	120
ggtgttagga	gttagcgat	ggcgaggtgg	cggccggcgg	cgctgctggt	agtggcgctg	180
acagcgggtc	tgtcggcrgc	gcr gcgggcg	gatgcgctct	cagtgcggt	gaccgacacc	240
gagtgcaccc	accgcctcg	cgcacccggt	tccgcgtgcc	tttccccacc	tactctcgcg	300
Gctctcgcca	gccagctctag	ggtttcggtc	cggcggtgct	tatccgcccc	cgccggccat	360
gtcgaagcaa	ggaggggaagg	ccaagccgct	gaaggcgccc	aaggccgaca	agaaggagta	420
cgacgagact	gatcttgcat	atctgcagaa	gaagaaagat	gaggaaaaag	cactgaagga	480
gcttaaggcc	aaggcacaga	agggcgcgat	tgggggctcg	ggtctgaaga	aaagtggaaa	540
gaaatgagac	tggtcaccog	tctccaatac	ctagaggatg	ataaggcagc	tgtctatctg	600
tggtgcgctt	cactaagtgt	gattgtaaca	gtggtacctc	ttgtgttctg	tgttccgcga	660
tggtgcagtt	ggttgcttga	tcgaaagatg	tttcaacctc	ccatctgcta	gctatgatac	720
agatggtccc	ctgataataa	tgatgacata	ttctgtgatg	gatgccacag	cattttttgt	780
ttttgttttt	gcattcag					

(2) INFORMATION FOR SEQ ID NO:3638:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..97

(D) OTHER INFORMATION: / Ceres Seq. ID 1577635

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3638:

Met Ala Arg Trp Arg Pro Ala Ala Leu Val Val Ala Leu Thr Ala  
1 5 10 15  
Val Leu Ser Xaa Ala Xaa Arg Ala Asp Ala Leu Ser Val Thr Val Thr  
20 25 30  
Asp Thr Glu Cys Ile His Pro Pro Arg Ala Pro Gly Ser Ala Cys Leu  
35 40 45  
Ser Pro Pro Thr Leu Ala Ala Leu Ala Ser Gln Ser Arg Val Ser Val  
50 55 60  
Pro Ala Cys Leu Ser Ala Pro Ala Gly His Val Glu Ala Arg Arg Glu  
65 70 75 80  
Gly Gln Ala Ala Glu Gly Ala Gln Gly Arg Gln Glu Gly Val Arg Arg  
85 90 95  
Asp

(2) INFORMATION FOR SEQ ID NO:3639:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 62 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..62

(D) OTHER INFORMATION: / Ceres Seq. ID 1577636

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3639:

Met Ser Lys Gln Gly Gly Lys Ala Lys Pro Leu Lys Ala Pro Lys Ala  
1 5 10 15  
Asp Lys Lys Glu Tyr Asp Glu Thr Asp Leu Ala Tyr Leu Gln Lys Lys  
20 25 30  
Lys Asp Glu Glu Lys Ala Leu Lys Glu Leu Lys Ala Lys Ala Gln Lys  
35 40 45  
Gly Ala Ile Gly Gly Ser Gly Leu Lys Lys Ser Gly Lys Lys  
50 55 60

(2) INFORMATION FOR SEQ ID NO:3640:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..55

(D) OTHER INFORMATION: / Ceres Seq. ID 1577637

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3640:

Met Arg Leu Val Thr Arg Leu Gln Tyr Leu Glu Asp Asp Lys Ala Ala  
1 5 10 15  
Val Tyr Leu Cys Cys Ala Ser Leu Ser Val Ile Val Thr Val Val Pro  
20 25 30  
Leu Val Phe Cys Val Pro Arg Cys Cys Ser Trp Leu Leu Asp Arg Lys  
35 40 45  
Met Phe Gln Pro Pro Ile Cys  
50 55

(2) INFORMATION FOR SEQ ID NO:3641:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 810 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

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- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..810  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1577653

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3641:

gtogagttcg accctggatt tggcgatgrg ccccggcgcc ctcctcccc gcagcgcgctc	60
ccgtacgcct ccttcgctcc aggaagggga aggagcgcga sgggaacgag gagcaggaat	120
ctggcgctct ccgcttcctc ctccaacggt gcagcagtg catccctgac aacagattcG	180
ggagaagaag ggcccagtga taatggaaat tccactggac caaatccgga ggccactgat	240
gcgaacgcgg gccaatgac cagtcaaggt gcaagaactc atgggcagta tccgtgtcat	300
cggcctccaa gtacctattg atgtgttggg ggtcgatggg gtctattatg gcttctctgg	360
atgccaccgc tacgaggtc accagcgct tggctctcca accatccgct gcaaagttcg	420
ccgtgggaca aaggaaacac tgaggcacca tatgcgatga gttatatattt attcagttac	480
aaagtgatct gtgtatctag agctaaaaca gaagcttcca tggctctttc gtogtctcgt	540
ctgcaattct ccatacctgt aaatgttgct caaacagagt ggtgaatagt acttctgtac	600
ccagcagcat cagaaaatgt taattttgcc tacaacactc ttttcgatca gtggatggat	660
gagtaaccacc cgtcagtag atcattccat ttctacgaga tttttgtaaa aaaagaaaaa	720
tgcagcagca gtcggcacgc tgtgtcattt agatcatcta gaaaaccaga aaaacagagt	780
catgtaactt gtttggtcgc tgcaaaaaat	

(2) INFORMATION FOR SEQ ID NO:3642:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 85 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..85  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1577654

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3642:

Val	Glu	Phe	Asp	Pro	Gly	Phe	Gly	Asp	Xaa	Pro	Arg	Arg	Pro	Pro	Pro
1				5				10					15		
Pro	Gln	Arg	Val	Pro	Tyr	Ala	Ser	Phe	Ala	Pro	Gly	Arg	Gly	Arg	Ser
			20				25					30			
Ala	Xaa	Gly	Thr	Arg	Ser	Arg	Asn	Leu	Ala	Leu	Ser	Ala	Ser	Ser	Ser
			35				40				45				
Asn	Gly	Ala	Ala	Val	Pro	Ser	Leu	Thr	Thr	Asp	Ser	Gly	Glu	Glu	Gly
			50				55				60				
Pro	Ser	Asp	Asn	Gly	Asn	Ser	Thr	Gly	Pro	Asn	Pro	Glu	Ala	Thr	Asp
			65				70				75			80	
Ala	Asn	Ala	Gly	Gln											
				85											

(2) INFORMATION FOR SEQ ID NO:3643:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 85 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..85  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1577655

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3643:

Met	Glu	Ile	Pro	Leu	Asp	Gln	Ile	Arg	Arg	Pro	Leu	Met	Arg	Thr	Arg
1				5				10					15		
Ala	Asn	Asp	Pro	Val	Lys	Val	Gln	Glu	Leu	Met	Gly	Ser	Ile	Arg	Val
			20				25				30				

Ile Gly Leu Gln Val Pro Ile Asp Val Leu Glu Val Asp Gly Val Tyr  
35 40 45  
Tyr Gly Phe Ser Gly Cys His Arg Tyr Glu Ala His Gln Arg Leu Gly  
50 55 60  
Leu Pro Thr Ile Arg Cys Lys Val Arg Arg Gly Thr Lys Glu Thr Leu  
65 70 75 80  
Arg His His Met Arg  
85

(2) INFORMATION FOR SEQ ID NO:3644:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..74
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577656

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3644:

Met Pro Pro Leu Arg Gly Ser Pro Ala Pro Trp Ser Pro Asn His Pro  
1 5 10 15  
Leu Gln Ser Ser Pro Trp Asp Lys Gly Asn Thr Glu Ala Pro Tyr Ala  
20 25 30  
Met Ser Tyr Ile Leu Phe Ser Tyr Lys Val Ile Cys Val Ser Arg Ala  
35 40 45  
Lys Thr Glu Ala Ser Met Val Phe Ser Ser Ser Arg Leu Gln Phe Ser  
50 55 60  
Ile Pro Val Asn Val Val Gln Thr Glu Trp  
65 70

(2) INFORMATION FOR SEQ ID NO:3645:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 770 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..770
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577661

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3645:

atgttatgta ataatgtatg aagttatgaa gtccgaccca taccaccgcg cctagactgt	60
gcctgcaccc ctcacgcgtc ggctcgatcg ctgatcagtt ctgcrgccgg cgacgtgtgc	120
tagctcacga cgacgacatg ggctcggcgg tgaagatcgg gacgtggggc ggcgacggcG	180
ggagccccgt cgacatcacg gtggcgccgc ggcggctgga gagcatcacc atccgctgga	240
accagaggtg ggctgacaaa gcatacaaga agagccactt gggcaatgag tggaaaaaac	300
cttttgctgg atcatctcac gccaaaggga tcgttctgga gaagattggt attgaggcca	360
agcagccaaa ttccggccatc cgtaagtgtg cccgtgttca gctggtgaag aatggaaaga	420
agattgctgc ctttgtgccc aatgatggtt gcctaaacta catcgaggag aatgatgagg	480
tgttgattgc tggatttggt cgtaagggtc atgctgtggg agacattcct ggtgtcagggt	540
tcaaggttgt taagggtgtc ggtgtgtcgc tgcttgact cttcaaggag aagaaggaga	600
agCcaaggtc ttagatcact ttccgtagtc aagaatggtg taaactgccc aaggctctat	660
tgttaaagtt ctgctagcaa cagagctggt aattctgagc tgtacctttt tgtaaacatt	720
gttacagtct tacagagttc tgtttccatt ttgaagatat taatattgcg	

(2) INFORMATION FOR SEQ ID NO:3646:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..158  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1577662  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3646:

Met Gly Ser Ala Val Lys Ile Gly Thr Trp Gly Gly Asp Gly Gly Ser  
1                  5                  10                  15  
Pro Cys Asp Ile Thr Val Ala Pro Arg Arg Leu Glu Ser Ile Thr Ile  
                  20                  25                  30  
Arg Trp Asn Gln Arg Trp Ala Asp Lys Ala Tyr Lys Lys Ser His Leu  
                  35                  40                  45  
Gly Asn Glu Trp Lys Lys Pro Phe Ala Gly Ser Ser His Ala Lys Gly  
50                  55                  60  
Ile Val Leu Glu Lys Ile Gly Ile Glu Ala Lys Gln Pro Asn Ser Ala  
65                  70                  75                  80  
Ile Arg Lys Cys Ala Arg Val Gln Leu Val Lys Asn Gly Lys Lys Ile  
                  85                  90                  95  
Ala Ala Phe Val Pro Asn Asp Gly Cys Leu Asn Tyr Ile Glu Glu Asn  
                  100                 105                 110  
Asp Glu Val Leu Ile Ala Gly Phe Gly Arg Lys Gly His Ala Val Gly  
                 115                 120                 125  
Asp Ile Pro Gly Val Arg Phe Lys Val Val Lys Val Ser Gly Val Ser  
130                 135                 140  
Leu Leu Ala Leu Phe Lys Glu Lys Lys Glu Lys Pro Arg Ser  
145                 150                 155

- (2) INFORMATION FOR SEQ ID NO:3647:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 969 base pairs  
        (B) TYPE: nucleic acid  
        (C) STRANDEDNESS: single  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: DNA (genomic)  
    (ix) FEATURE:

- (A) NAME/KEY: -  
    (B) LOCATION: 1..969  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1577663

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3647:

acataaccgc ccatamccac ncccctcgcc gctgcrctcc acctccgccc cccgccctcc 60  
ccgcgtcccc cctctcctac gcagatcgtc caggtaagat gtcgtccgag gcggtgaagg 120  
tggcggtgcc ggagtcggta ctccgcaagc ggaagcgcn aggagcagtg gcccgccgag 180  
aagaaggaga agtccctggc cgagaggaag aagtccatcg agaaccggaa gtcctcttc 240  
acccgcgcca agcagtagc cgaggagtac gatgccagg agaaggaact ggtacagctt 300  
aagcgtgagg cccgtttgaa ggggtggttc tatgtcagtc ctgagGcaaa gctgctattt 360  
gtgatccgca tccgtggtat caatgccatg catcctaaga ccaggaagat attgcagctt 420  
ctgcgtttga ggcagatatt caatggcgtg ttcctgaaag tcaacaaggc taccattaac 480  
atgCttcgca gggttgagcc ttatgttgca tatgggtacc Cgaacttgaa gagtgtcagg 540  
gagttgatct acaagagggg ctacggaaaa ctgaacaagc agaggatccc tctgtctaac 600  
aaccaagtca tcgaggaggg cttgggcaag cacaacatca tttgcattga ggatcttggt 660  
catgagatca tgactgtcgg cccacacttc aaggaggcga acaacttcct ttggccattt 720  
aagctgaagg caccgctggg aggtctgaag aagaagagga accactatgt ggagggtggt 780  
gatgccggtg accgtgagaa ttacatcaac gagctcatca aaaggatgaa ttaggttcac 840  
gatcaagctc tattgtgttc taagaaactt tctgtgctct cccaatttta cattattag 900  
aagcggatga atatgcatgc agttttgttg tttggaacta gatgtgtatg gaagaaacat 960  
gatcttttc

- (2) INFORMATION FOR SEQ ID NO:3648:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 99 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear

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- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..99
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1577664
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3648:

Ile Thr Arg His Xaa His Xaa Pro Arg Arg Leu Xaa Pro Pro Pro Pro  
1 5 10 15  
Pro Ala Leu Pro Ala Ser Pro Leu Ser Tyr Ala Asp Arg Pro Gly Lys  
20 25 30  
Met Ser Ser Glu Ala Val Lys Val Ala Val Pro Glu Ser Val Leu Arg  
35 40 45  
Lys Arg Lys Arg Xaa Gly Ala Val Gly Arg Arg Glu Glu Gly Glu Val  
50 55 60  
Pro Gly Arg Glu Glu Glu Val His Arg Glu Pro Glu Ala His Leu His  
65 70 75 80  
Pro Arg Gln Ala Val Arg Arg Gly Val Arg Cys Pro Gly Glu Gly Thr  
85 90 95  
Gly Thr Ala

- (2) INFORMATION FOR SEQ ID NO:3649:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 148 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..148
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1577665
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3649:

Met His Pro Lys Thr Arg Lys Ile Leu Gln Leu Leu Arg Leu Arg Gln  
1 5 10 15  
Ile Phe Asn Gly Val Phe Leu Lys Val Asn Lys Ala Thr Ile Asn Met  
20 25 30  
Leu Arg Arg Val Glu Pro Tyr Val Ala Tyr Gly Tyr Pro Asn Leu Lys  
35 40 45  
Ser Val Arg Glu Leu Ile Tyr Lys Arg Gly Tyr Gly Lys Leu Asn Lys  
50 55 60  
Gln Arg Ile Pro Leu Ser Asn Asn Gln Val Ile Glu Glu Gly Leu Gly  
65 70 75 80  
Lys His Asn Ile Ile Cys Ile Glu Asp Leu Val His Glu Ile Met Thr  
85 90 95  
Val Gly Pro His Phe Lys Glu Ala Asn Asn Phe Leu Trp Pro Phe Lys  
100 105 110  
Leu Lys Ala Pro Leu Gly Gly Leu Lys Lys Lys Arg Asn His Tyr Val  
115 120 125  
Glu Gly Gly Asp Ala Gly Asn Arg Glu Asn Tyr Ile Asn Glu Leu Ile  
130 135 140  
Lys Arg Met Asn  
145

- (2) INFORMATION FOR SEQ ID NO:3650:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 117 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide



(B) LOCATION: 1..117

(D) OTHER INFORMATION: / Ceres Seq. ID 1577666

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3650:

Met Leu Arg Arg Val Glu Pro Tyr Val Ala Tyr Gly Tyr Pro Asn Leu  
1 5 10 15  
Lys Ser Val Arg Glu Leu Ile Tyr Lys Arg Gly Tyr Gly Lys Leu Asn  
20 25 30  
Lys Gln Arg Ile Pro Leu Ser Asn Asn Gln Val Ile Glu Glu Gly Leu  
35 40 45  
Gly Lys His Asn Ile Ile Cys Ile Glu Asp Leu Val His Glu Ile Met  
50 55 60  
Thr Val Gly Pro His Phe Lys Glu Ala Asn Asn Phe Leu Trp Pro Phe  
65 70 75 80  
Lys Leu Lys Ala Pro Leu Gly Gly Leu Lys Lys Lys Arg Asn His Tyr  
85 90 95  
Val Glu Gly Gly Asp Ala Gly Asn Arg Glu Asn Tyr Ile Asn Glu Leu  
100 105 110  
Ile Lys Arg Met Asn  
115

(2) INFORMATION FOR SEQ ID NO:3651:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..433

(D) OTHER INFORMATION: / Ceres Seq. ID 1577678

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3651:

atcattggtc tgctagcaga aacctcagag atatgttaca gagaaataaa ggacatcaag 60  
tgcatacact gccctcacia gccagaaggt tccatgtttg tcatggtgaa attaaatttg 120  
tatcttttgg aggggattca tgacgatatt gatttttgct gcaagCtggc aaaagaagag 180  
tctgtgattt tgtgtccagg gagtgttttg ggaatggaaa actggatccg catcactttc 240  
gchattgatt catcttctct tcttgatggg cttgagagga tcaaattctt ctgccaaagg 300  
cataagaaga agaatttgct taatggccat taactgtatc tacgttcaaa gttacccagt 360  
tccattgttt ttcattgtat catcaacaaa tgtggaactt tgaaatccct ctgaattaat 420  
aaagttttcc ttg

(2) INFORMATION FOR SEQ ID NO:3652:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..110

(D) OTHER INFORMATION: / Ceres Seq. ID 1577679

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3652:

Ile Ile Gly Leu Leu Ala Glu Thr Ser Glu Ile Cys Tyr Arg Glu Ile  
1 5 10 15  
Lys Asp Ile Lys Cys Ile Thr Cys Pro His Lys Pro Glu Gly Ser Met  
20 25 30  
Phe Val Met Val Lys Leu Asn Leu Tyr Leu Leu Glu Gly Ile His Asp  
35 40 45  
Asp Ile Asp Phe Cys Cys Lys Leu Ala Lys Glu Glu Ser Val Ile Leu  
50 55 60  
Cys Pro Gly Ser Val Leu Gly Met Glu Asn Trp Ile Arg Ile Thr Phe  
65 70 75 80

Xaa Ile Asp Ser Ser Ser Leu Leu Asp Gly Leu Glu Arg Ile Lys Ser  
85 90 95  
Phe Cys Gln Arg His Lys Lys Lys Asn Leu Leu Asn Gly His  
100 105 110

(2) INFORMATION FOR SEQ ID NO:3653:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..79
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577680

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3653:

Met Phe Val Met Val Lys Leu Asn Leu Tyr Leu Leu Glu Gly Ile His  
1 5 10 15  
Asp Asp Ile Asp Phe Cys Cys Lys Leu Ala Lys Glu Glu Ser Val Ile  
20 25 30  
Leu Cys Pro Gly Ser Val Leu Gly Met Glu Asn Trp Ile Arg Ile Thr  
35 40 45  
Phe Xaa Ile Asp Ser Ser Ser Leu Leu Asp Gly Leu Glu Arg Ile Lys  
50 55 60  
Ser Phe Cys Gln Arg His Lys Lys Lys Asn Leu Leu Asn Gly His  
65 70 75

(2) INFORMATION FOR SEQ ID NO:3654:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..76
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577681

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3654:

Met Val Lys Leu Asn Leu Tyr Leu Leu Glu Gly Ile His Asp Asp Ile  
1 5 10 15  
Asp Phe Cys Cys Lys Leu Ala Lys Glu Glu Ser Val Ile Leu Cys Pro  
20 25 30  
Gly Ser Val Leu Gly Met Glu Asn Trp Ile Arg Ile Thr Phe Xaa Ile  
35 40 45  
Asp Ser Ser Ser Leu Leu Asp Gly Leu Glu Arg Ile Lys Ser Phe Cys  
50 55 60  
Gln Arg His Lys Lys Lys Asn Leu Leu Asn Gly His  
65 70 75

(2) INFORMATION FOR SEQ ID NO:3655:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1045 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1045
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577688

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3655:

atcaagtcgg ctatcttctc cggccatcgg tcgcaccccc acgtgggggc ggcggcggtc

```
ccgcagcagc agcagctggg gagcacgcgt tcgttccact cgacacccat tctgcagcgg 120
aagcacaaga cccagtggca caacagattc aactattata cgagacgtag gaggaaccga 180
gaaactaaaa ggtcaatgct acggaacatg tcagaatatg cagagtctct ctttcagagt 240
tggcgtgatg aagatgagaa aaatgctgca tctgctgggc cttcatgggt tagaggacat 300
cgttgggtca gaaattcaag caacaatggt ttccgtacac acgattttta ttacgggaat 360
ttcaaaagca aaggaggatt tgagttttgc acaagtgatg aggatgaacc agagaatctg 420
tttcgtaatg tttttcgaga ccagcacaca tattattggt ctttttcatac tgataatttt 480
cagagGaact ccaaactgtc tcgctcacia aaatccagaa actggagttt tgaaacagac 540
gaggaggatg aagtatcagc tccatcagag gtatctttgg cacgacaagc tcttgggttg 600
agcactttctg gtccgcttaa acttgaagat gttaaaagcg cataccgagc atgtgcactt 660
agatggcatc cagatcgcca caatggatca tctaagtcta cagcggagga gaaattcaag 720
cattgcagtg cagcatataca gaccttatgt gatagtttgg ccgctgcata gataattttg 780
aatgaagatg gactctggat gagccccctc caaactttct agctgcaaat tctgaagagc 840
tgccacatgc ttgtggtagc tccgaccatc ccaatcccaa gaggcgggag tgcattttct 900
tggttattga ggcgattgag tcaattcaaa attgaccgga taatatatgt actgtaccgt 960
gtaaaatttt ttgtcacagc tcattgttgt attattttta tagatatgaa gatattgttc 1020
acaccactca ataaattttt ttggc
```

(2) INFORMATION FOR SEQ ID NO:3656:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..256
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3656:

```
Ile Lys Ser Ala Ile Phe Ser Gly His Arg Ser His Pro His Val Gly
1           5           10           15
Ala Ala Ala Val Pro Gln Gln Gln Gln Leu Gly Ser Thr Ala Ser Phe
20           25           30
His Ser Thr Pro Ile Leu Gln Arg Lys His Lys Thr Gln Trp His Asn
35           40           45
Arg Phe Asn Tyr Tyr Thr Arg Arg Arg Arg Asn Arg Glu Thr Lys Arg
50           55           60
Ser Met Leu Arg Asn Met Ser Glu Tyr Ala Glu Ser Leu Phe Gln Ser
65           70           75           80
Trp Arg Asp Glu Asp Glu Lys Asn Ala Ala Ser Ala Gly Pro Ser Trp
85           90           95
Phe Arg Gly His Arg Trp Val Arg Asn Ser Ser Asn Asn Gly Phe Arg
100          105          110
Thr His Asp Phe Tyr Tyr Gly Asn Phe Lys Ser Lys Gly Gly Phe Glu
115          120          125
Phe Cys Thr Ser Asp Glu Asp Glu Pro Glu Asn Leu Phe Arg Asn Val
130          135          140
Phe Arg Asp Gln His Thr Tyr Tyr Trp Ser Phe Ser Ser Asp Asn Phe
145          150          155          160
Gln Arg Asn Ser Lys Arg Ala Arg Ser Gln Lys Ser Arg Asn Trp Ser
165          170          175
Phe Glu Thr Asp Glu Glu Asp Glu Val Ser Ala Pro Ser Glu Val Ser
180          185          190
Leu Ala Arg Gln Ala Leu Gly Leu Ser Thr Ser Gly Pro Leu Lys Leu
195          200          205
Glu Asp Val Lys Ser Ala Tyr Arg Ala Cys Ala Leu Arg Trp His Pro
210          215          220
Asp Arg His Asn Gly Ser Ser Lys Ser Thr Ala Glu Glu Lys Phe Lys
225          230          235          240
His Cys Ser Ala Ala Tyr Lys Thr Leu Cys Asp Ser Leu Ala Ala Ala
245          250          255
```

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(2) INFORMATION FOR SEQ ID NO:3657:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..199

(D) OTHER INFORMATION: / Ceres Seq. ID 1577690

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3657:

Ser Ser Arg Leu Ser Ser Pro Ala Ile Gly Arg Thr Pro Thr Trp Gly  
1 5 10 15  
Arg Arg Arg Ser Arg Ser Ser Ser Ser Trp Gly Ala Pro Leu Arg Ser  
20 25 30  
Thr Arg His Pro Phe Cys Ser Gly Ser Thr Arg Pro Ser Gly Thr Thr  
35 40 45  
Asp Ser Thr Ile Ile Arg Asp Val Gly Gly Thr Glu Lys Leu Lys Gly  
50 55 60  
Gln Cys Tyr Gly Thr Cys Gln Asn Met Gln Ser Leu Ser Phe Arg Val  
65 70 75 80  
Gly Val Met Lys Met Arg Lys Met Leu His Leu Leu Gly Leu His Gly  
85 90 95  
Leu Glu Asp Ile Val Gly Ser Glu Ile Gln Ala Thr Met Val Ser Val  
100 105 110  
His Thr Ile Phe Ile Thr Gly Ile Ser Lys Ala Lys Glu Asp Leu Ser  
115 120 125  
Phe Ala Gln Val Met Arg Met Asn Gln Arg Ile Cys Phe Val Met Phe  
130 135 140  
Phe Glu Thr Ser Thr His Ile Ile Gly Leu Phe His Leu Ile Ile Phe  
145 150 155 160  
Arg Gly Thr Pro Asn Val Leu Ala His Lys Asn Pro Glu Thr Gly Val  
165 170 175  
Leu Lys Gln Thr Arg Arg Met Lys Tyr Gln Leu His Gln Arg Tyr Leu  
180 185 190  
Trp His Asp Lys Leu Leu Gly  
195

(2) INFORMATION FOR SEQ ID NO:3658:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..191

(D) OTHER INFORMATION: / Ceres Seq. ID 1577691

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3658:

Met Leu Arg Asn Met Ser Glu Tyr Ala Glu Ser Leu Phe Gln Ser Trp  
1 5 10 15  
Arg Asp Glu Asp Glu Lys Asn Ala Ala Ser Ala Gly Pro Ser Trp Phe  
20 25 30  
Arg Gly His Arg Trp Val Arg Asn Ser Ser Asn Asn Gly Phe Arg Thr  
35 40 45  
His Asp Phe Tyr Tyr Gly Asn Phe Lys Ser Lys Gly Gly Phe Glu Phe  
50 55 60  
Cys Thr Ser Asp Glu Asp Glu Pro Glu Asn Leu Phe Arg Asn Val Phe

65		70		75		80									
Arg	Asp	Gln	His	Thr	Tyr	Tyr	Trp	Ser	Phe	Ser	Ser	Asp	Asn	Phe	Gln
		85							90					95	
Arg	Asn	Ser	Lys	Arg	Ala	Arg	Ser	Gln	Lys	Ser	Arg	Asn	Trp	Ser	Phe
		100						105					110		
Glu	Thr	Asp	Glu	Glu	Asp	Glu	Val	Ser	Ala	Pro	Ser	Glu	Val	Ser	Leu
		115					120					125			
Ala	Arg	Gln	Ala	Leu	Gly	Leu	Ser	Thr	Ser	Gly	Pro	Leu	Lys	Leu	Glu
		130				135					140				
Asp	Val	Lys	Ser	Ala	Tyr	Arg	Ala	Cys	Ala	Leu	Arg	Trp	His	Pro	Asp
		145				150					155				160
Arg	His	Asn	Gly	Ser	Ser	Lys	Ser	Thr	Ala	Glu	Glu	Lys	Phe	Lys	His
		165						170						175	
Cys	Ser	Ala	Ala	Tyr	Lys	Thr	Leu	Cys	Asp	Ser	Leu	Ala	Ala	Ala	
		180						185					190		

(2) INFORMATION FOR SEQ ID NO:3659:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 875 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..875
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577698

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3659:

atcgggtgcc	cattggccac	tggcccctag	ccctcgccct	cccttttcta	ttgctccgaa	60
gcccagagttg	cgagctgtct	cctccactct	tctccttcac	tgtcgcagcc	gccccttgta	120
gaagcttcga	ggctgtgct	gctgcgcca	tggcgcgga	aggcaagacg	ccgtccctcg	180
ccgaggagta	ttcacttcca	ccacaggaag	ttccagtggg	aaaggcagct	gaggagaagc	240
cctctagtgg	tactgagtct	gaagctgctc	cctcaaccCa	atgatgaaac	tcctccatct	300
gtagaagaca	agaatggaac	ttctgaagta	caagatgctg	ctgaaaatcc	agaggcagaa	360
gaaactaaca	ctgctgcaga	ggaaacacct	gctgtagagg	aagcaagtga	gactaccgag	420
gaggaagagg	ctgagaaacc	tgagatcaag	atcgaaacag	ctccagcaga	ttttcgtttc	480
ccaacaacaa	accaaacaag	gcattgtttc	acacgcctatg	ttgaatatca	caggtgtgtg	540
gctgcaaaaag	gtgaggatgc	acctgagtgt	gataagttcg	ccaagtacta	tcgatccctg	600
tgcccaggtg	aatgggttga	tcgctggaac	gagcaacgcg	aaaacggcac	cttccctgga	660
cctctgtaat	cctacaatgc	aaaagaagta	tgaactcacg	atgttggtgcc	ggctttctctt	720
ccttggtaac	tggcgccaag	ttaccttttt	tggagctctc	tacagaataa	gaaatccctt	780
ttggcttgaa	gaatgccctg	ttgctcttcc	taacgggtcat	gttggtgcgct	gctgagaaac	840
tagcgtcaca	gttaacaatt	ttctttatac	agttc			

(2) INFORMATION FOR SEQ ID NO:3660:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..93
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577699

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3660:

Arg	Val	Pro	Ile	Gly	His	Trp	Pro	Leu	Ala	Leu	Pro	Phe	Leu		
1			5				10					15			
Leu	Leu	Arg	Ser	Pro	Ser	Cys	Glu	Leu	Ser	Pro	Pro	Leu	Phe	Ser	Phe
		20					25					30			
Thr	Val	Ala	Ala	Ala	Pro	Cys	Arg	Ser	Phe	Glu	Ala	Ala	Ala	Ala	Ala
		35				40					45				
Pro	Met	Ala	Ala	Glu	Gly	Lys	Thr	Pro	Ser	Leu	Ala	Glu	Glu	Tyr	Ser

(2) INFORMATION FOR SEQ ID NO:3661:

(A) LENGTH: 105 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptid

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..105

(D) OTHER INFORMATION: / Ceres Seq. ID 1577700

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3661:

(2) INFORMATION FOR SEQ ID NO:3662:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..92

(D) OTHER INFORMATION: / Ceres Seq. ID 1577701

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3662:

(2) INFORMATION FOR SEQ ID NO:3663:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1009 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1009

(D) OTHER INFORMATION: / Ceres Seq. ID 1577714

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3663:

gtcgtctctcc	gaactctgat	tgaggaggag	tgaagcttct	tttctttcttc	ctccagtcac	60
cccattgcaa	aagtagaagc	aggggaaggaa	ttggaagcat	gaacaagcag	cagcaggcgt	120
acgggtacgg	aaatgggcag	caggccgacg	tcccaggcta	ctgctgtttc	catccccggg	180
aggtcggcgt	cggcgtctgc	gctcaactgcc	tcaaggatcg	cctcctcctc	ctcctcgccg	240
ctgccaacaa	caataagatc	gacgacgacg	cccgcgcgaa	aagcaggagc	aggagcagga	300
gcatctccct	ccccaaagtc	ttcgcgctcg	gctctctcct	cctccagcgc	ctcgactccc	360
gccaccaccg	gggacgaggg	cgggacaaca	actgctactc	cgacgacgac	gacgccaccg	420
cctccgtcgc	aagcctcgat	gattccttca	tctccatcaa	attcgaggac	aacggcaagg	480
cgacgtggga	cagccagagc	cagcacaagg	cggcagCtcc	cgcgagggtc	cgtcgacgac	540
gaccatggta	gcggtggagc	acgtcaagcg	tktcggcgtc	acccggtggc	gcaaacaggt	600
ggtggggccgc	atgtctcagc	tggcgcgctg	gaggaggtcg	tccgctgctg	cgggtgggct	660
ggacggcaag	aaggcggcgg	cggcgggcgg	tgagcggctc	aaggccagag	ggagaggctg	720
gatccggagc	ctactcggga	ggcgcgcgca	cggggaccgg	gcgtggtagg	tcgccgtcgt	780
cggtaaggag	gcccggtcgg	tcggggggcg	ggcagcccat	gcatgcatgc	atggtgtccg	840
atggatggat	ggatctgcga	gcttcccccc	ttgctttgga	tggagacgta	gtaattgctt	900
gcttgtgctt	tgtaccaagt	gagatgagtg	agtgcctcct	tttacctact	ataggctact	960
atacgtacag	ttaatagcag	ctagctgttg	gtgtggattg	ctatgcgtg		

(2) INFORMATION FOR SEQ ID NO:3664:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..150

(D) OTHER INFORMATION: / Ceres Seq. ID 1577715

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3664:

Met	Asn	Lys	Gln	Gln	Gln	Ala	Tyr	Gly	Tyr	Gly	Asn	Gly	Gln	Gln	Ala
1			5					10					15		
Asp	Val	Pro	Gly	Tyr	Cys	Cys	Phe	His	Pro	Arg	Glu	Val	Gly	Val	Gly
			20					25					30		
Val	Cys	Ala	His	Cys	Leu	Lys	Asp	Arg	Leu	Leu	Leu	Leu	Leu	Ala	Ala
			35					40					45		
Ala	Asn	Asn	Asn	Lys	Ile	Asp	Asp	Asp	Ala	Arg	Arg	Lys	Ser	Arg	Ser
			50					55				60			
Arg	Ser	Arg	Ser	Ile	Ser	Leu	Pro	Lys	Val	Phe	Ala	Leu	Gly	Ser	Ser
								70							
Phe	Leu	Gln	Arg	Leu	Asp	Ser	Arg	His	His	Arg	Gly	Arg	Gly	Arg	Asp
			85					90					95		
Asn	Asn	Cys	Tyr	Ser	Asp	Asp	Asp	Asp	Ala	Thr	Ala	Ser	Val	Ala	Ser
			100					105					110		
Leu	Asp	Asp	Ser	Phe	Ile	Ser	Ile	Lys	Phe	Glu	Asp	Asn	Gly	Lys	Ala
			115					120					125		
Thr	Trp	Asp	Ser	Gln	Ser	Gln	His	Lys	Ala	Ala	Ala	Pro	Ala	Arg	Ser
			130					135					140		
Arg	Arg	Arg	Arg	Pro	Trp										
145															

(2) INFORMATION FOR SEQ ID NO:3665:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 186 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

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- (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..186  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1577716

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3665:

Met Gly Ser Arg Pro Thr Ser Gln Ala Thr Ala Val Ser Ile Pro Gly  
1                    5                    10                    15  
Arg Ser Ala Ser Ala Ser Ala Leu Thr Ala Ser Arg Ile Ala Ser Ser  
                    20                    25                    30  
Ser Ser Ser Pro Leu Pro Thr Thr Thr Thr Thr Thr Thr Thr Thr Ala  
                    35                    40                    45  
Ala Lys Ala Gly Ala Gly Ala Gly Ala Ser Pro Ser Pro Arg Ser Ser  
                    50                    55                    60  
Arg Ser Ala Pro Pro Ser Ser Ser Ala Ser Thr Pro Ala Thr Thr Gly  
65                    70                    75                    80  
Asp Glu Gly Gly Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Pro Pro  
                    85                    90                    95  
Pro Pro Ser Gln Ala Ser Met Ile Pro Ser Ser Pro Ser Asn Ser Arg  
                    100                    105                    110  
Thr Thr Ala Arg Arg Arg Gly Thr Ala Arg Ala Ser Thr Arg Arg Gln  
                    115                    120                    125  
Leu Pro Arg Gly Leu Val Asp Asp Asp His Gly Ser Gly Gly Ala Arg  
                    130                    135                    140  
Gln Ala Xaa Arg Arg His Pro Val Ala Gln Thr Gly Gly Gly Pro His  
145                    150                    155                    160  
Ala Ala Ala Gly Ala Leu Glu Glu Val Val Arg Cys Cys Gly Trp Ala  
                    165                    170                    175  
Gly Arg Gln Glu Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly  
                    180                    185

(2) INFORMATION FOR SEQ ID NO:3666:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 588 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..588  
(D) OTHER INFORMATION: / Ceres Seq. ID 1577717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3666:

aactaggcaa ctactccgtc tcacgcctct cctgtcccct ctgcgcgCtc tgcggccggcc	60
tctgcctccg cctcctccat cgcacccagc tttcctcccc accccaccac cactcctacc	120
ccgccacgtc gtgtagtcgc ggcgggcgat atgcaggccg ccgccgcctt caaccaggca	180
gccttcaccg cccgctcgct gcacgcgccc ccgaggcccc tccacctagc tgttgcgag	240
gatgcttttg cggggataag aggcgcgcct tttacacggc cccggtgctg cgggagcctc	300
tctgtcggcg tcggcagcta caacagcgag cacactccag tatttccaag acaacaatca	360
tgggatccct acaagcttct tggtgttgat caagatgcat ctgaagaaga ggtccggagt	420
gcacggaatt ttctttctaaa acaatacgcc ggatatgaag aaagtgaaga ggccattgaa	480
ggtgcttatg acaagataat aatgaatagc tacacagacc gtaagaaatc caaattcaat	540
ctgaaaagca agctaaaaga gcaagttgaa ggatccccat catggcctt	

(2) INFORMATION FOR SEQ ID NO:3667:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

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(B) LOCATION: 1..128

(D) OTHER INFORMATION: / Ceres Seq. ID 1577718

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3667:

Leu	Gly	Asn	Tyr	Ser	Val	Ser	Arg	Leu	Ser	Cys	Pro	Leu	Ser	Pro	Leu	
1				5				10						15		
Ser	Pro	Arg	Leu	Cys	Leu	Arg	Leu	Leu	His	Arg	Thr	Gln	Leu	Ser	Ser	
			20					25					30			
Pro	Pro	His	His	His	Ser	Tyr	Pro	Ala	Thr	Ser	Cys	Ser	Arg	Gly	Gly	
			35					40					45			
Gly	Tyr	Ala	Gly	Arg	Arg	Arg	Leu	Gln	Pro	Gly	Ser	Leu	His	Arg	Pro	
	50					55					60					
Leu	Ala	Ala	Ser	Pro	Pro	Glu	Ala	Pro	Pro	Pro	Ser	Cys	Cys	Gly	Gly	
65					70					75					80	
Cys	Phe	Cys	Gly	Asp	Lys	Arg	Arg	Ala	Phe	Tyr	Thr	Ala	Pro	Val	Leu	
				85					90					95		
Arg	Glu	Pro	Leu	Cys	Arg	Arg	Arg	Gln	Leu	Gln	Gln	Arg	Ala	His	Ser	
			100					105					110			
Ser	Ile	Ser	Lys	Thr	Thr	Ile	Met	Gly	Ser	Leu	Gln	Ala	Ser	Trp	Cys	
			115				120					125				

(2) INFORMATION FOR SEQ ID NO:3668:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 146 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..146

(D) OTHER INFORMATION: / Ceres Seq. ID 1577719

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3668:

Met	Gln	Ala	Ala	Ala	Ala	Phe	Asn	Gln	Ala	Ala	Phe	Thr	Ala	Arg	Ser	
1				5				10						15		
Leu	His	Arg	Pro	Pro	Arg	Pro	Leu	His	Leu	Ala	Val	Ala	Glu	Asp	Ala	
			20					25					30			
Phe	Ala	Gly	Ile	Arg	Gly	Ala	Pro	Phe	Thr	Arg	Pro	Arg	Cys	Cys	Gly	
		35				40						45				
Ser	Leu	Ser	Val	Gly	Val	Gly	Ser	Tyr	Asn	Ser	Glu	His	Thr	Pro	Val	
	50					55					60					
Phe	Pro	Arg	Gln	Gln	Ser	Trp	Asp	Pro	Tyr	Lys	Leu	Leu	Gly	Val	Asp	
65					70				75						80	
Gln	Asp	Ala	Ser	Glu	Glu	Glu	Val	Arg	Ser	Ala	Arg	Asn	Phe	Leu	Leu	
				85					90					95		
Lys	Gln	Tyr	Ala	Gly	Tyr	Glu	Glu	Ser	Glu	Glu	Ala	Ile	Glu	Gly	Ala	
			100					105					110			
Tyr	Asp	Lys	Ile	Ile	Met	Asn	Ser	Tyr	Thr	Asp	Arg	Lys	Lys	Ser	Lys	
		115					120					125				
Phe	Asn	Leu	Lys	Ser	Lys	Leu	Lys	Glu	Gln	Val	Glu	Gly	Ser	Pro	Ser	
		130				135						140				
Trp	Leu															
145																

(2) INFORMATION FOR SEQ ID NO:3669:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 790 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..790

(D) OTHER INFORMATION: / Ceres Seq. ID 1577737

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3669:

tatttttcta	agcatggaag	ggtggttgg	tgccatgttg	ttcttgaacc	ccatacacgt	60
gtttcccgtg	gatttgcctt	tgtcagcatg	gacactgttg	aagaagcgga	sswtgcataa	120
agtatcttaa	tggttctgta	atggaaggtc	gaaacatcac	agttgaaaag	tcacgccgtg	180
gtcgcccaag	gacaccaact	cctggaagct	atcttggcca	tcggtacgag	cgtagggagc	240
gtgggaggtt	ccatagaggc	tatggtggtg	ggcgtgatga	gtattacggc	aatggcggcg	300
gcgggtatgg	ctaccgcagG	tctccgcctc	ccatgtactc	ttcctacagg	gagagtcggg	360
attattatcc	ctcctacaag	gacagccggg	actaccctcc	ctacagggac	ggcagggact	420
actctcctcc	ccacagggac	cctcgggact	actacgaaag	caggggtggc	cggggctact	480
cgccgcctcc	ttatggtggt	ggtaggtcaa	ggagggaccg	antcggtttc	accgtatcgg	540
atgccagaaa	ggggctacgg	tggaggccgc	cgggtgggtg	gcggcggata	tgacaggtaa	600
tgtagaggtt	ttctctccgc	cgggtggctgc	tgctgcgatg	gctgcgtatg	gctctcgcag	660
ctctggtgat	atggttagac	tgctgcctgt	agctgtgtac	ttggtgtact	gtcttcccgc	720
gtatgtggat	ttggtgaaaa	cttctgtatg	agcacctttt	atttgtagcc	tgcaatgatt	780
ccttcttaag						

(2) INFORMATION FOR SEQ ID NO:3670:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..150

(D) OTHER INFORMATION: / Ceres Seq. ID 1577738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3670:

Met	Glu	Gly	Arg	Asn	Ile	Thr	Val	Glu	Lys	Ser	Arg	Arg	Gly	Arg	Pro
1				5					10					15	
Arg	Thr	Pro	Thr	Pro	Gly	Ser	Tyr	Leu	Gly	His	Arg	Tyr	Glu	Arg	Arg
			20					25					30		
Glu	Arg	Gly	Arg	Phe	His	Arg	Gly	Tyr	Gly	Gly	Gly	Arg	Asp	Glu	Tyr
		35					40					45			
Tyr	Gly	Asn	Gly	Gly	Gly	Gly	Tyr	Gly	Tyr	Arg	Arg	Ser	Pro	Pro	Pro
	50				55					60					
Met	Tyr	Ser	Ser	Tyr	Arg	Glu	Ser	Arg	Asp	Tyr	Tyr	Pro	Ser	Tyr	Lys
65				70					75					80	
Asp	Ser	Arg	Asp	Tyr	Pro	Pro	Tyr	Arg	Asp	Gly	Arg	Asp	Tyr	Ser	Pro
			85					90					95		
Pro	His	Arg	Asp	Pro	Arg	Asp	Tyr	Tyr	Glu	Ser	Arg	Gly	Gly	Arg	Gly
		100					105					110			
Tyr	Ser	Pro	Pro	Pro	Tyr	Gly	Gly	Arg	Ser	Arg	Arg	Arg	Asp	Arg	Xaa
	115				120						125				
Gly	Phe	Thr	Val	Ser	Asp	Ala	Arg	Lys	Gly	Leu	Arg	Trp	Arg	Pro	Pro
	130				135						140				
Gly	Gly	Trp	Arg	Arg	Ile										
145				150											

(2) INFORMATION FOR SEQ ID NO:3671:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 112 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..112

(D) OTHER INFORMATION: / Ceres Seq. ID 1577739

005890004-104200

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3671:

Met	Val	Val	Gly	Val	Met	Ser	Ile	Thr	Ala	Met	Ala	Ala	Ala	Gly	Met
1				5					10					15	
Ala	Thr	Ala	Gly	Leu	Arg	Leu	Pro	Cys	Thr	Leu	Pro	Thr	Gly	Arg	Val
			20					25					30		
Gly	Ile	Ile	Ile	Pro	Pro	Thr	Arg	Thr	Ala	Gly	Thr	Thr	Leu	Pro	Thr
		35				40					45				
Gly	Thr	Ala	Gly	Thr	Thr	Leu	Leu	Pro	Thr	Gly	Thr	Leu	Gly	Thr	Thr
	50					55				60					
Thr	Lys	Ala	Gly	Val	Ala	Gly	Ala	Thr	Arg	Arg	Leu	Leu	Met	Val	Val
65				70					75					80	
Val	Gly	Gln	Gly	Gly	Thr	Xaa	Ser	Val	Ser	Pro	Tyr	Arg	Met	Pro	Glu
			85					90					95		
Arg	Gly	Tyr	Gly	Gly	Gly	Arg	Arg	Val	Gly	Gly	Gly	Gly	Tyr	Asp	Arg
			100					105					110		

(2) INFORMATION FOR SEQ ID NO:3672:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..107

(D) OTHER INFORMATION: / Ceres Seq. ID 1577740

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3672:

Met	Ser	Ile	Thr	Ala	Met	Ala	Ala	Ala	Gly	Met	Ala	Thr	Ala	Gly	Leu
1				5					10					15	
Arg	Leu	Pro	Cys	Thr	Leu	Pro	Thr	Gly	Arg	Val	Gly	Ile	Ile	Ile	Pro
			20					25					30		
Pro	Thr	Arg	Thr	Ala	Gly	Thr	Thr	Leu	Pro	Thr	Gly	Thr	Ala	Gly	Thr
		35				40					45				
Thr	Leu	Leu	Pro	Thr	Gly	Thr	Leu	Gly	Thr	Thr	Thr	Lys	Ala	Gly	Val
	50				55					60					
Ala	Gly	Ala	Thr	Arg	Arg	Leu	Leu	Met	Val	Val	Val	Gly	Gln	Gly	Gly
65				70					75					80	
Thr	Xaa	Ser	Val	Ser	Pro	Tyr	Arg	Met	Pro	Glu	Arg	Gly	Tyr	Gly	Gly
		85				90						95			
Gly	Arg	Arg	Val	Gly	Gly	Gly	Gly	Tyr	Asp	Arg					
			100					105							

(2) INFORMATION FOR SEQ ID NO:3673:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 926 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..926

(D) OTHER INFORMATION: / Ceres Seq. ID 1577749

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3673:

aaaagatctc	agccgccgctc	gtctccgctcg	ctccgccgca	cctcccccca	tcaccgcctc	60
actaaaaccc	taatccctag	ccgccatggc	ggctgttgcg	gcggccacct	cgcacctcct	120
acgccaccac	cgcaaccccc	accttctcct	cctccgcgca	gantnctcat	cctcccgctgc	180
tttacccccag	cagccggagc	tgtcccccgga	cccgaccgcc	ggcaccccccg	acctcgccgg	240
cgcggcccca	ctccctccaa	accccagcac	ggggagcccc	ttctacaccc	agaactggcg	300
caaccagcc	gcmgccaacc	cgsmtcctc	gcttctgcmc	amcgtcgtcg	cmggmagcmc	360

(2) INFORMATION FOR SEQ ID NO:3674:

(A) LENGTH: 202 amino acids

(C) STRANDEDNESS:

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(D) OTHER INFORMATION: / Ceres Seq. ID 1577750

Lys	Arg	Ser	Gln	Pro	Pro	Ser	Ser	Pro	Ser	Leu	Arg	Arg	Thr	Ser	Pro
1			5					10						15	
His	His	Arg	Leu	Thr	Lys	Thr	Leu	Ile	Pro	Ser	Arg	His	Gly	Gly	Cys
			20					25					30		
Cys	Gly	Gly	His	Leu	Ala	Pro	Pro	Thr	Pro	Pro	Pro	Gln	Pro	Pro	Pro
		35				40						45			
Ser	Pro	Pro	Pro	Arg	Arg	Xaa	Leu	Ile	Leu	Pro	Cys	Phe	Thr	Pro	Ala
	50					55					60				
Ala	Gly	Ala	Val	Pro	Arg	Pro	Asp	Arg	Arg	His	Pro	Arg	Pro	Arg	Arg
65				70						75					80
Arg	Gly	Pro	Thr	Pro	Ser	Lys	Pro	Gln	His	Gly	Glu	Pro	Leu	Leu	His
				85				90						95	
Pro	Glu	Leu	Ala	Gln	Pro	Ser	Arg	Xaa	Gln	Pro	Xaa	Leu	Leu	Ala	Ser
			100					105					110		
Xaa	Xaa	Arg	Arg	Arg	Xaa	Xaa	Xaa	Leu	Arg	Gly	Ala	Ala	Leu	His	Gly
		115				120						125			
Arg	Leu	Leu	Arg	Cys	Thr	Arg	Arg	His	Gly	Ala	Gln	Gly	Asp	Val	Arg
	130					135					140				
Gln	Val	Tyr	Gly	Gly	Ala	Ala	Val	Gly	Arg	His	Glu	Ala	Pro	Val	Arg
145					150					155					160
Pro	Leu	Gly	Ala	Leu	Pro	Arg	Arg	Arg	His	Gly	Glu	Ala	Gln	Pro	Pro
				165					170					175	
Arg	Arg	Arg	Pro	Leu	Gln	Ser	Leu	Pro	Pro	Arg	Gln	Pro	His	Asp	Gln
			180					185					190		
Gly	Pro	Ala	Ala	Arg	Asp	Ala	Arg	Ser	Arg						
		195					200								

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..211

(D) OTHER INFORMATION: / Ceres Seq. ID 1577751

Met Ala Ala Val Ala Ala Ala Thr Ser His Leu Leu Arg His His Arg

1 5 10 15  
Asn Pro His Leu Leu Leu Arg Ala Xaa Xaa Ser Ser Ser Arg Ala  
20 25 30  
Leu Pro Gln Gln Pro Glu Leu Ser Pro Asp Pro Thr Ala Gly Thr Pro  
35 40 45  
Asp Leu Ala Gly Ala Ala Pro Leu Pro Pro Asn Pro Ser Thr Gly Ser  
50 55 60  
Pro Phe Tyr Thr Gln Asn Trp Arg Asn Pro Ala Xaa Ala Asn Pro Xaa  
65 70 75 80  
Ser Ser Leu Leu Xaa Xaa Val Val Xaa Xaa Ser Xaa Phe Gly Ala Gln  
85 90 95  
His Phe Met Ala Ala Phe Tyr Asp Ala Pro Asp Val Thr Gly Leu Lys  
100 105 110  
Glu Thr Phe Ala Lys Tyr Met Ala Glu Gln Arg Trp Glu Asp Met Lys  
115 120 125  
His Leu Phe Asp His Trp Val Arg Ser Leu Asp Ala Ala Thr Gly Lys  
130 135 140  
Pro Asn His Pro Asp Val Asp Leu Phe Asn His Tyr Leu Arg Ala Asn  
145 150 155 160  
Leu Met Thr Arg Ala Leu Pro His Glu Met Leu Asp Leu Ala Asp His  
165 170 175  
Met Leu Glu Phe Glu Leu Gln Pro Asn Thr Ala Ser Tyr Asn Leu Val  
180 185 190  
Leu Lys Ser Met Val Ala Ser Gln Glu Thr Glu Gly Ala Glu Lys Leu  
195 200 205  
Ile Glu Arg  
210

(2) INFORMATION FOR SEQ ID NO:3676:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..113

(D) OTHER INFORMATION: / Ceres Seq. ID 1577752

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3676:

Met Ala Ala Phe Tyr Asp Ala Pro Asp Val Thr Gly Leu Lys Glu Thr  
1 5 10 15  
Phe Ala Lys Tyr Met Ala Glu Gln Arg Trp Glu Asp Met Lys His Leu  
20 25 30  
Phe Asp His Trp Val Arg Ser Leu Asp Ala Ala Thr Gly Lys Pro Asn  
35 40 45  
His Pro Asp Val Asp Leu Phe Asn His Tyr Leu Arg Ala Asn Leu Met  
50 55 60  
Thr Arg Ala Leu Pro His Glu Met Leu Asp Leu Ala Asp His Met Leu  
65 70 75 80  
Glu Phe Glu Leu Gln Pro Asn Thr Ala Ser Tyr Asn Leu Val Leu Lys  
85 90 95  
Ser Met Val Ala Ser Gln Glu Thr Glu Gly Ala Glu Lys Leu Ile Glu  
100 105 110  
Arg

(2) INFORMATION FOR SEQ ID NO:3677:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1017 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3677:

(2) INFORMATION FOR SEQ ID NO:3678:

(A) LENGTH: 150 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..150

(D) OTHER INFORMATION: / Ceres Seq. ID 1577772

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3678:

(2) INFORMATION FOR SEQ ID NO:3679:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3679:

(2) INFORMATION FOR SEQ ID NO:3680:

(ii) MOLECULE TYPE: DNA (genomic)

(A) NAME/KEY: -

(B) LOCATION: 1..792

(D) OTHER INFORMATION: / Ceres Seq. ID 1577774

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3680:

(X1)	SEQUENCE	DESCRIPTION	SEQ ID NO	60		
aagatttgcc	ttggccttgc	gtgccctgcg	ggagccaagc	caaggacggc	tagcgctcgc	60
cacgcgcgat	gtccgggctt	ctccgggcgc	cgcgaccgct	gctaccgtct	ccctgcgcct	120
cttctctcgt	tggtcgggog	aaggcagcgt	cgcatgtctg	ctccagccta	aagcagtcgc	180
gcccagggcg	aagtgcctgc	gccccttcca	ccgtcgccgc	gcgtcaggcc	gcgccgctct	240
tggctgcggc	gctcgctcct	gtagcggcac	ccccctggct	gcctgctgct	atctcaccag	300
catttgacaca	gccagatttca	gaaggcgcag	Cgctgttccg	gaaggcttgt	attggttgc	360
atgacatggg	aggaacaatt	ctacagccag	gagccactct	ttctctgaag	gacctcgaga	420
gaaacggagt	tgccacggag	gaggaaactgt	ataacatcac	atactatggg	aaaggaagaa	480
tgcccgggtt	tggagagaaa	tgcaccccaa	gaggacagtg	cacCttcggc	ccccggctat	540
cggaagacga	catcaagatc	ctagctttgt	ttgtcaagtc	gcaagccaag	aacgggtggc	600
cgaagattga	gggggatgga	gattgatcaa	actgaaaaaa	cgatgagaag	acggtgcttg	660
ttagtcagat	gaaaaatggt	acgggaagat	agtgtttgta	tagtttagga	atctggtctt	720
tctgaacttg	taacctttta	gtctctggtt	ctgaactgaa	cttgtaacct	tctggtccgt	780
gtttcagttt	tc					

(2) INFORMATION FOR SEQ ID NO:3681:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..120

(D) OTHER INFORMATION: / Ceres Seq. ID 1577775

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3681:

Arg	Phe	Ala	Leu	Ala	Cys	Arg	Ala	Leu	Arg	Glu	Pro	Ser	Gln	Gly	Arg
1				5				10						15	
Leu	Ala	Leu	Ala	Thr	Arg	Asp	Val	Arg	Ala	Ser	Ser	Gly	Arg	Ala	Thr
			20				25						30		
Ala	Ala	Thr	Val	Ser	Leu	Arg	Leu	Phe	Leu	Arg	Cys	Ser	Gly	Glu	Gly
		35				40					45				
Ser	Val	Gly	Met	Leu	Leu	Gln	Pro	Lys	Ala	Val	Ala	Pro	Arg	Pro	Lys

(2) INFORMATION FOR SEQ ID NO:3682:

(A) LENGTH: 185 amino acids

(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3682:

(2) INFORMATION FOR SEQ ID NO:3683:

(A) LENGTH: 923 base pairs

(C) STRANDEDNESS: single

(ii) MOLECULE TYPE: DNA (genomic)

(A) NAME/KEY: -

(D) OTHER INFORMATION: / Ceres Seq. ID 1577787

atacgccttt	tctgcwgcg	ctgcattctc	cactcgcgtc	aagaaacgaa	accagctgc	60
accgaacatt	tctgccagca	gacccaacga	cgaagcttt	tttttcctt	tcttttcac	120
gccgcgctc	ggggttcaag	gttcagcgcg	tccccgaatg	acgggcacgt	acgargcctc	180
cgaccgtcct	cctcctccca	actccgcggg	ccaccggacc	gacaaagtcc	ggcgaagcg	240



(2) INFORMATION FOR SEQ ID NO:3684:

(A) LENGTH: 263 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..263

(D) OTHER INFORMATION: / Ceres Seq. ID 1577788

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3684:

(2) INFORMATION FOR SEQ ID NO:3685:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 231 amino acids

[illegible]

- (B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..231  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1577789  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3685:

Tyr Ala Phe Ser Xaa Ala Ala Ala Ser Thr Arg Val Lys Lys Arg  
1                   5                   10                   15  
Asn Pro Ala Ala Pro Ala Thr Ser Ala Ser Arg Pro Asn Asp Arg Ser  
                  20                   25                   30  
Phe Phe Phe Pro Phe Phe Ser Ser Pro Pro Leu Gly Val Gln Gly Ser  
                  35                   40                   45  
Ala Arg Pro Arg Met Thr Gly Thr Tyr Xaa Ala Ser Asp Arg Pro Pro  
                  50                   55                   60  
Pro Pro Asn Ser Ala Gly His Arg Thr Asp Lys Val Arg Arg Lys Arg  
65                   70                   75                   80  
Leu Thr Ala Gln Lys Arg Lys Glu Ile Lys Glu Ala Phe Asp Leu Phe  
                  85                   90                   95  
Asp Ile Asp Gly Ser Gly Thr Ile Asp Ala Arg Glu Leu Asn Val Ala  
                  100                   105                   110  
Met Arg Ala Leu Gly Phe Glu Met Thr Pro Glu Gln Ile Gly Gln Met  
                  115                   120                   125  
Ile Ala Glu Val Asp Lys Asp Gly Ser Gly Thr Ile Asp Phe Asp Glu  
                  130                   135                   140  
Phe Val His Met Met Thr Asp Lys Met Gly Glu Arg Asp Ala Arg Asp  
145                   150                   155                   160  
Glu Leu His Lys Ala Phe Arg Ile Ile Asp Gln Asp Ala Asn Gly Lys  
                  165                   170                   175  
Ile Ser Asp Met Asp Ile Gln Arg Leu Ala Ile Glu Thr Gly Glu His  
                  180                   185                   190  
Phe Thr Leu Asp Glu Val Arg Glu Met Ile Glu Ala Ala Asp Glu Asp  
                  195                   200                   205  
Gly Asp Gly Glu Ile Asp Leu Glu Glu Phe Met Lys Met Met Lys Arg  
210                   215                   220  
Thr Asp Phe Gly Ser Gly Phe  
225                   230

(2) INFORMATION FOR SEQ ID NO:3686:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 179 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..179  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1577790  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3686:

Met Thr Gly Thr Tyr Xaa Ala Ser Asp Arg Pro Pro Pro Pro Asn Ser  
1                   5                   10                   15  
Ala Gly His Arg Thr Asp Lys Val Arg Arg Lys Arg Leu Thr Ala Gln  
                  20                   25                   30  
Lys Arg Lys Glu Ile Lys Glu Ala Phe Asp Leu Phe Asp Ile Asp Gly  
                  35                   40                   45  
Ser Gly Thr Ile Asp Ala Arg Glu Leu Asn Val Ala Met Arg Ala Leu  
50                   55                   60  
Gly Phe Glu Met Thr Pro Glu Gln Ile Gly Gln Met Ile Ala Glu Val  
65                   70                   75                   80

Asp Lys Asp Gly Ser Gly Thr Ile Asp Phe Asp Glu Phe Val His Met  
85 90 95  
Met Thr Asp Lys Met Gly Glu Arg Asp Ala Arg Asp Glu Leu His Lys  
100 105 110  
Ala Phe Arg Ile Ile Asp Gln Asp Ala Asn Gly Lys Ile Ser Asp Met  
115 120 125  
Asp Ile Gln Arg Leu Ala Ile Glu Thr Gly Glu His Phe Thr Leu Asp  
130 135 140  
Glu Val Arg Glu Met Ile Glu Ala Ala Asp Glu Asp Gly Asp Gly Glu  
145 150 155 160  
Ile Asp Leu Glu Glu Phe Met Lys Met Met Lys Arg Thr Asp Phe Gly  
165 170 175  
Ser Gly Phe

(2) INFORMATION FOR SEQ ID NO:3687:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 729 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..729
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577807

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3687:

accaggcacg	ccagcctcac	tccccagacc	acctcacacg	cacgaagcat	cagcagtgga	60
ctggactagc	tctaggtggg	caacatgaag	cttcagacca	ccgtcacccg	tgctggcctc	120
ctcctcttcc	tctcctcctc	ggcgctgcct	tccctccgsg	tctccatggc	tggatcaggg	180
ttctgcgamg	gctgcaagga	cgagttcgtc	gcgtgggaga	agtgcgtgga	ggagacggat	240
gcgcgggatg	ccagcattga	cgctcgtggg	cggtgccaag	acgtcacggc	Cgcgctgcgg	300
aagGtgGcat	ggacgcgGca	cgccgcctac	tacgagccta	tcctccgggc	cgagcgcgcc	360
atggctgcgg	acctcgnagc	tttcaggccc	aagaagccgc	ctccgactcc	gcggcgctcg	420
aggaaggcca	gaaggaggcg	gcagcggcgg	ccgaggcagc	gccgcgtccg	tcagacgaag	480
gccagaataa	gcaggtggct	gaggcggcag	ttgctggagga	gagcagagat	cctgcagcct	540
gattgggcga	aaaaaggcag	cggcgctcttc	aattttttgt	gagggatttg	aggatatgaa	600
ttccgtttgt	accttaggag	agcatcaatt	aacattttgt	gagggggata	gatttctgtc	660
cttttctctt	tacatgaaac	atgtgattct	attgattgaa	aacaaaaatt	gtccactttt	720

gccagatgc

(2) INFORMATION FOR SEQ ID NO:3688:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..85
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577808

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3688:

Gln Ala Arg Gln Pro His Ser Pro Asp His Leu Thr Arg Thr Lys His	
1 5 10 15	
Gln Gln Trp Thr Gly Leu Ala Leu Gly Gly Gln His Glu Ala Ser Asp	
20 25 30	
His Arg His Arg Cys Trp Pro Pro Pro Leu Pro Pro Pro Pro Gly Ala	
35 40 45	
Ala Phe Pro Pro Xaa Leu His Gly Trp Ile Arg Val Leu Arg Xaa Leu	
50 55 60	
Gln Gly Arg Val Arg Arg Val Gly Glu Val Arg Gly Gly Asp Gly Cys	
65 70 75 80	

Arg Gly Cys Gln His  
85

(2) INFORMATION FOR SEQ ID NO:3689:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..165
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3689:

Met Lys Leu Gln Thr Thr Val Thr Val Ala Gly Leu Leu Leu Phe Leu  
1 5 10 15  
Leu Leu Leu Ala Leu Pro Ser Leu Xaa Val Ser Met Ala Gly Ser Gly  
20 25 30  
Phe Cys Xaa Gly Cys Lys Asp Glu Phe Val Ala Trp Glu Lys Cys Val  
35 40 45  
Glu Glu Thr Asp Ala Ala Asp Ala Ser Ile Asp Val Val Glu Arg Cys  
50 55 60  
Gln Asp Val Thr Ala Ala Leu Arg Lys Val Ala Trp Thr Arg His Ala  
65 70 75 80  
Xaa Tyr Tyr Glu Pro Ile Leu Arg Ala Glu Arg Ala Met Ala Ala Asp  
85 90 95  
Leu Xaa Ala Phe Arg Pro Lys Lys Pro Pro Pro Thr Pro Arg Arg Arg  
100 105 110  
Arg Lys Ala Arg Arg Arg Arg Gln Arg Arg Pro Arg Gln Arg Arg Val  
115 120 125  
Arg Gln Thr Lys Ala Arg Ile Ser Arg Trp Leu Arg Arg Gln Leu Arg  
130 135 140  
Arg Arg Ala Glu Ile Leu Gln Pro Asp Trp Ala Lys Lys Gly Ser Gly  
145 150 155 160  
Val Phe Asn Phe Leu  
165

(2) INFORMATION FOR SEQ ID NO:3690:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..138
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577810

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3690:

Met Ala Gly Ser Gly Phe Cys Xaa Gly Cys Lys Asp Glu Phe Val Ala  
1 5 10 15  
Trp Glu Lys Cys Val Glu Glu Thr Asp Ala Ala Asp Ala Ser Ile Asp  
20 25 30  
Val Val Glu Arg Cys Gln Asp Val Thr Ala Ala Leu Arg Lys Val Ala  
35 40 45  
Trp Thr Arg His Ala Xaa Tyr Glu Pro Ile Leu Arg Ala Glu Arg  
50 55 60  
Ala Met Ala Ala Asp Leu Xaa Ala Phe Arg Pro Lys Lys Pro Pro Pro  
65 70 75 80  
Thr Pro Arg Arg Arg Arg Lys Ala Arg Arg Arg Arg Gln Arg Arg Pro  
85 90 95  
Arg Gln Arg Arg Val Arg Gln Thr Lys Ala Arg Ile Ser Arg Trp Leu

100 105 110  
Arg Arg Gln Leu Arg Arg Arg Ala Glu Ile Leu Gln Pro Asp Trp Ala  
115 120 125  
Lys Lys Gly Ser Gly Val Phe Asn Phe Leu  
130 135

(2) INFORMATION FOR SEQ ID NO:3691:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 440 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..440
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577813

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3691:

aactcgagcc aaacccctc aactcaactg ctgaacgcag agttcgatct agcacgcgca	60
gCGgcgNcc gctgccaca atggcgctccc ttttcaagga cccgagcaag ctctcagcgt	120
acagggaccg ccgattcaag ggcacacagg aggagtatga ggcaacgctg catgcgtcga	180
caacgctgta cattgggaat atgtccttct acaccacgga ggagcaggcc ttgcttgacg	240
cgaaatgctt caagtgaagt tgcttgcttg gagacagaac tgtttagccc ttgaatttgc	300
ctatggaaga gtttgccctt ttactagtgt cgatgttgat ctggtatacc ttgctatgaa	360
ctggttaaag tttgtgctgg tttgggattt ttttgtgcat cttgtgatac ctcaagtctt	420
catcatttaa atgtttagcc	

(2) INFORMATION FOR SEQ ID NO:3692:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..97
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577814

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3692:

Asn Ser Ser Gln Thr Pro Ser Thr Gln Leu Leu Asn Ala Glu Phe Asp	
1 5 10 15	
Leu Ala Arg Ala Ala Ala Xaa Arg Cys Pro Gln Trp Arg Pro Phe Ser	
20 25 30	
Arg Thr Arg Ala Ser Ser Gln Arg Thr Gly Thr Ala Asp Ser Arg Ala	
35 40 45	
His Arg Arg Ser Met Arg Gln Arg Cys Met Arg Arg Gln Arg Cys Thr	
50 55 60	
Leu Gly Ile Cys Pro Ser Thr Pro Arg Arg Ser Arg Pro Cys Leu Thr	
65 70 75 80	
Arg Asn Ala Ser Ser Glu Cys Ala Cys Leu Glu Thr Glu Leu Phe Ser	
85 90 95	
Pro	

(2) INFORMATION FOR SEQ ID NO:3693:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..84

(D) OTHER INFORMATION: / Ceres Seq. ID 1577815

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3693:

Leu Glu Pro Asn Pro Leu Asn Ser Thr Ala Glu Arg Arg Val Arg Ser  
1 5 10 15  
Ser Thr Arg Ser Gly Xaa Pro Leu Pro Thr Met Ala Ser Leu Phe Lys  
20 25 30  
Asp Pro Ser Lys Leu Ser Ala Tyr Arg Asp Arg Arg Phe Lys Gly Thr  
35 40 45  
Gln Glu Glu Tyr Glu Ala Thr Leu His Ala Ser Thr Leu Tyr Ile  
50 55 60  
Gly Asn Met Ser Phe Tyr Thr Thr Glu Glu Gln Ala Leu Leu Asp Ala  
65 70 75 80  
Lys Cys Phe Lys

(2) INFORMATION FOR SEQ ID NO:3694:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..61

(D) OTHER INFORMATION: / Ceres Seq. ID 1577816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3694:

Met Leu Gln Val Ser Val Leu Ala Trp Arg Gln Asn Cys Leu Ala Leu  
1 5 10 15  
Glu Phe Ala Tyr Gly Arg Val Cys Pro Phe Thr Ser Val Asp Val Asp  
20 25 30  
Leu Val Tyr Leu Ala Met Asn Trp Leu Lys Phe Val Leu Val Trp Asp  
35 40 45  
Phe Phe Val His Leu Val Ile Pro Gln Val Phe Ile Ile  
50 55 60

(2) INFORMATION FOR SEQ ID NO:3695:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 843 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..843

(D) OTHER INFORMATION: / Ceres Seq. ID 1577817

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3695:

agacactgac accgtttcgaa gcaaaaagag cgaacacgag cacgaacaca agcgcagagc 60  
agccaagcgc cacacacacg ccgacgcgaa ccaaccaacc agctggtagt aggttcgccg 120  
cgctgacgat gatgcctcgc cgcgcccttc tcttcgccgc ggtgctcctc gcggcctccg 180  
ccgccgcggt ctccgggttc cacctgggag gggacgagag cggctctcgt aggggtgtgc 240  
tcgcCGcgct ccgcgagcga gccgaggccg aggacgccgc tcgCttcgcc gtcgcccact 300  
acaacaagaa ccagggcgcc gctttggagt ttactagggt gctcaaattc aagcggcagg 360  
tggtgaccgg gacctgcat gacctgatac tggaggcagc tgatgctgga aaaaagagtg 420  
tgtacagagc aaaggtttgg gtgaagccgt ggaagattt caagtctgtc gttgagtttc 480  
gccttggttg agactctgaa tctgaaccgc agccttctgt tgcttctgat gttagctctg 540  
ggcaagcaat tgccaaactc tctcttgaag cagatattgt acaagaagag gctcgcctgc 600  
acaccattga gaatgatggg ctttccggcg atttcacatc atcatcttag gattccaggc 660  
aaggatggaa agcgtaaagg tttaaaatga agatttaggt atttagagta tgtcaagctg 720  
aaatgctttg ccttgtttat tggaatatgt atgtttcggt tcaaacgtgg gagcatagaa 780  
ctgtatatatt cggtatttca cactgttcat ttccatgtct gtatataagg aggttcttct 840  
ggc

(2) INFORMATION FOR SEQ ID NO:3696:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..215
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577818

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3696:

Thr Leu Thr Pro Phe Glu Ala Lys Arg Ala Asn Thr Ser Thr Asn Thr  
1 5 10 15  
Ser Ala Glu Gln Pro Ser Ala Thr His Thr Pro Thr Arg Thr Asn Gln  
20 25 30  
Pro Ala Gly Ser Arg Phe Ala Ala Leu Thr Met Met Pro Arg Arg Ala  
35 40 45  
Leu Leu Phe Ala Ala Val Leu Leu Ala Ala Ser Ala Ala Val Ser  
50 55 60  
Gly Phe His Leu Gly Gly Asp Glu Ser Gly Leu Val Arg Gly Val Leu  
65 70 75 80  
Ala Ala Leu Arg Glu Arg Ala Glu Ala Glu Asp Ala Ala Arg Phe Ala  
85 90 95  
Val Ala His Tyr Asn Lys Asn Gln Gly Ala Ala Leu Glu Phe Thr Arg  
100 105 110  
Val Leu Lys Ser Lys Arg Gln Val Val Thr Gly Thr Leu His Asp Leu  
115 120 125  
Ile Leu Glu Ala Ala Asp Ala Gly Lys Lys Ser Val Tyr Arg Ala Lys  
130 135 140  
Val Trp Val Lys Pro Trp Glu Asp Phe Lys Ser Val Val Glu Phe Arg  
145 150 155 160  
Leu Val Gly Asp Ser Glu Ser Glu Pro Glu Pro Ser Val Ala Ser Asp  
165 170 175  
Val Ser Ser Gly Gln Ala Ile Ala Lys Leu Ser Leu Glu Ala Asp Ile  
180 185 190  
Val Gln Glu Ala Arg Leu His Thr Ile Glu Asn Asp Gly Leu Ser  
195 200 205  
Gly Asp Phe Thr Ser Ser Ser  
210 215

(2) INFORMATION FOR SEQ ID NO:3697:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..173
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577819

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3697:

Met Met Pro Arg Arg Ala Leu Leu Phe Ala Ala Val Leu Leu Ala Ala  
1 5 10 15  
Ser Ala Ala Ala Val Ser Gly Phe His Leu Gly Gly Asp Glu Ser Gly  
20 25 30  
Leu Val Arg Gly Val Leu Ala Ala Leu Arg Glu Arg Ala Glu Ala Glu  
35 40 45  
Asp Ala Ala Arg Phe Ala Val Ala His Tyr Asn Lys Asn Gln Gly Ala  
50 55 60  
Ala Leu Glu Phe Thr Arg Val Leu Lys Ser Lys Arg Gln Val Val Thr

(2) INFORMATION FOR SEQ ID NO:3698:

(A) LENGTH: 172 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..172  
(D) OTHER INFORMATION: / Ceres Seq. ID 1577820

(X1) SEQUENCE DESCRIPTION: 522																
Met	Pro	Arg	Arg	Ala	Leu	Leu	Phe	Ala	Ala	Val	Leu	Leu	Ala	Ala	Ser	
1				5				10						15		
Ala	Ala	Ala	Val	Ser	Gly	Phe	His	Leu	Gly	Gly	Asp	Glu	Ser	Gly	Leu	
			20					25					30			
Val	Arg	Gly	Val	Leu	Ala	Ala	Leu	Arg	Glu	Arg	Ala	Glu	Ala	Glu	Asp	
		35					40					45				
Ala	Ala	Arg	Phe	Ala	Val	Ala	His	Tyr	Asn	Lys	Asn	Gln	Gly	Ala	Ala	
		50					55				60					
Leu	Glu	Phe	Thr	Arg	Val	Leu	Lys	Ser	Lys	Arg	Gln	Val	Val	Thr	Gly	
65				70						75				80		
Thr	Leu	His	Asp	Leu	Ile	Leu	Glu	Ala	Ala	Asp	Ala	Gly	Lys	Lys	Ser	
			85					90					95			
Val	Tyr	Arg	Ala	Lys	Val	Trp	Val	Lys	Pro	Trp	Glu	Asp	Phe	Lys	Ser	
			100					105					110			
Val	Val	Glu	Phe	Arg	Leu	Val	Gly	Asp	Ser	Glu	Ser	Glu	Pro	Glu	Pro	
		115					120					125				
Ser	Val	Ala	Ser	Asp	Val	Ser	Ser	Gly	Gln	Ala	Ile	Ala	Lys	Leu	Ser	
		130				135				140						
Leu	Glu	Ala	Asp	Ile	Val	Gln	Glu	Glu	Ala	Arg	Leu	His	Thr	Ile	Glu	
145				150						155				160		
Asn	Asp	Gly	Leu	Ser	Gly	Asp	Phe	Thr	Ser	Ser	Ser					
			165					170								

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..422  
(D) OTHER INFORMATION: / Ceres Seq. ID 1577845

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:3059:

60  
120



tg

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: peptide

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..64

- (D) OTHER INFORMATION: / Ceres Seq. ID 1577846

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3700:

Lys Glu Arg Glu Arg Gly Arg Gly Arg Asp Trp Arg Glu Ala Pro Ala  
1 5 10 15

Gln Gly Lys Arg Asn Arg Gly Ala Arg Arg Glu Gly Glu Gly Glu Phe

Ser Glu Ala Arg Glu Asp Leu Ala Leu Glu Lys Asp Tyr Glu Glu

Val Gly Ala Glu Gly Ala Asp Asp Glu Gly Asp Glu Gly Asp Asp Tyr

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..65

- (D) OTHER INFORMATION: / Ceres Seq. ID 1577847

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3701:

Arg Arg Glu Arg Glu Ala Glu Gly Glu Ile Gly Gly Arg Pro Leu Pro  
1 5 10 15

Lys Ala Arg Glu Thr Ala Ala Arg Gly Glu Arg Val Arg Val Ser Ser

Gln Lys Pro Val Arg Thr Trp Leu Leu Arg Arg Thr Met Arg Lys

Ser Val Gln Arg Val Pro Met Thr Arg Val Thr Arg Glu Thr Thr Ile

Glu  
65

(i) SEQUENCE CHARACTERISTICS:

- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: sing.

- (D) TOPOLOGY: linear

- MOLECULE TYPE: DNA (q

- (ix) FEATURE:

- (A) NAME

- (B) LOCATION: 1

- (D) OTHER INFORMATION

- (D) OTHER INFORMATION: / 00100 0011 00100

Year	Country	Population (millions)	Urban population (millions)	Urban population (%)	Population density (per sq km)	Urban population density (per sq km)	Population growth rate (%)	Urban population growth rate (%)	Population growth rate (per 1,000)	Urban population growth rate (per 1,000)	Population growth rate (per 1,000)	Urban population growth rate (per 1,000)
1950	United States	150	100	67	30	100	1.2	1.2	12	12	12	12
1955	United States	155	105	68	31	105	1.3	1.3	13	13	13	13
1960	United States	160	110	69	32	110	1.4	1.4	14	14	14	14
1965	United States	165	115	70	33	115	1.5	1.5	15	15	15	15
1970	United States	170	120	71	34	120	1.6	1.6	16	16	16	16
1975	United States	175	125	71	35	125	1.7	1.7	17	17	17	17
1980	United States	180	130	72	36	130	1.8	1.8	18	18	18	18
1985	United States	185	135	73	37	135	1.9	1.9	19	19	19	19
1990	United States	190	140	74	38	140	2.0	2.0	20	20	20	20
1995	United States	195	145	74	39	145	2.1	2.1	21	21	21	21
2000	United States	200	150	75	40	150	2.2	2.2	22	22	22	22
2005	United States	205	155	76	41	155	2.3	2.3	23	23	23	23
2010	United States	210	160	76	42	160	2.4	2.4	24	24	24	24
2015	United States	215	165	77	43	165	2.5	2.5	25	25	25	25
2020	United States	220	170	77	44	170	2.6	2.6	26	26	26	26
2025	United States	225	175	78	45	175	2.7	2.7	27	27	27	27
2030	United States	230	180	78	46	180	2.8	2.8	28	28	28	28
2035	United States	235	185	79	47	185	2.9	2.9	29	29	29	29
2040	United States	240	190	79	48	190	3.0	3.0	30	30	30	30
2045	United States	245	195	80	49	195	3.1	3.1	31	31	31	31
2050	United States	250	200	80	50	200	3.2	3.2	32	32	32	32
2055	United States	255	205	80	51	205	3.3	3.3	33	33	33	33
2060	United States	260	210	81	52	210	3.4	3.4	34	34	34	34
2065	United States	265	215	81	53	215	3.5	3.5	35	35	35	35
2070	United States	270	220	81	54	220	3.6	3.6	36	36	36	36
2075	United States	275	225	82	55	225	3.7	3.7	37	37	37	37
2080	United States	280	230	82	56	230	3.8	3.8	38	38	38	38
2085	United States	285	235	82	57	235	3.9	3.9	39	39	39	39
2090	United States	290	240	83	58	240	4.0	4.0	40	40	40	40
2095	United States	295	245	83	59	245	4.1	4.1	41	41	41	41
2100	United States	300	250	83	60	250	4.2	4.2	42	42	42	42

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3702:

attccacggc	ctgtcgaccc	acaaaccacg	caaccgatat	attccccagc	acccccagtc	60
cagccgtcca	accgagacac	cgcgtgcgaa	ccaagcagac	cacagcaaga	agcgtagtcg	120
tcgccggaag	gaaaggcgcg	gasaagatgt	cgtggcaggc	gtacgtcgat	gagcacctra	180
tgtgcgarat	cgaaggacaa	catctcagcg	ccgccgscat	cgtcggtcac	gaggnacagcg	240
cttgggcgca	gtccgagagc	ttccccgart	taaagcctga	ggaggttgct	ggtatcataa	300
aggactttga	tgaacctggt	actcttgcac	caactggtct	tttcgttgga	ggtacaaaagt	360
acatggtgat	ccaaggtgaa	cctggagttg	tcatccgagg	aaagaagggc	actgggggca	420
ttactatcaa	gaaaaccggc	atgtccttga	ttattggtGt	ctacgacgag	ccaatgactc	480
cagggcaatg	caacatggtg	gtggagagggc	tcggcgatta	cctgatcgag	cagggccttc	540
aaaagttcgt	catgyyctgt	tttggtcatt	tgggcaccaa	agtttgcgcc	ycatttggtt	600
ctgtaatccg	tgagctcgtg	catgtacttg	gcgtattgca	tgcagtgaat	aatttagctt	660
gggtttgttt	gttgggggca	gtgttgggga	cggatttgga	ttgggggtta	tgcttggcat	720
cgcgtcgtat	cgaaactcag	ctgctgtttc	gctgagtaat	gtacatttcc	ctggtaatgg	780
tacttgtgga	ctctgatgct	tttaygggaa	cgagtgcatt	tt		

(2) INFORMATION FOR SEQ ID NO:3703:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..179
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577867

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3703:

Ser	Thr	Ala	Cys	Arg	Pro	Thr	Asn	His	Ala	Thr	Asp	Ile	Phe	Pro	Ser
1			5					10						15	
Thr	Pro	Ser	Pro	Ala	Val	Gln	Pro	Arg	His	Arg	Val	Arg	Thr	Lys	Gln
			20					25					30		
Thr	Thr	Ala	Arg	Ser	Val	Val	Val	Ala	Gly	Arg	Lys	Gly	Ala	Xaa	Lys
			35					40					45		
Met	Ser	Trp	Gln	Ala	Tyr	Val	Asp	Glu	His	Xaa	Met	Cys	Xaa	Ile	Glu
			50				55				60				
Gly	Gln	His	Leu	Ser	Ala	Xaa	Ile	Val	Gly	His	Glu	Xaa	Ser	Ala	
			65			70				75				80	
Trp	Ala	Gln	Ser	Glu	Ser	Phe	Pro	Xaa	Leu	Lys	Pro	Glu	Glu	Val	Ala
			85					90						95	
Gly	Ile	Ile	Lys	Asp	Phe	Asp	Glu	Pro	Gly	Thr	Leu	Ala	Pro	Thr	Gly
			100					105					110		
Leu	Phe	Val	Gly	Gly	Thr	Lys	Tyr	Met	Val	Ile	Gln	Gly	Glu	Pro	Gly
			115				120						125		
Val	Val	Ile	Arg	Gly	Lys	Lys	Gly	Thr	Gly	Gly	Ile	Thr	Ile	Lys	Lys
			130			135					140				
Thr	Gly	Met	Ser	Leu	Ile	Gly	Val	Tyr	Asp	Glu	Pro	Met	Thr	Pro	
			145		150				155					160	
Gly	Gln	Cys	Asn	Met	Val	Val	Glu	Arg	Leu	Gly	Asp	Tyr	Leu	Ile	Glu
			165					170						175	
Gln	Gly	Phe													

(2) INFORMATION FOR SEQ ID NO:3704:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..131

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(D) OTHER INFORMATION: / Ceres Seq. ID 1577868

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3704:

Met Ser Trp Gln Ala Tyr Val Asp Glu His Xaa Met Cys Xaa Ile Glu  
1 5 10 15  
Gly Gln His Leu Ser Ala Ala Xaa Ile Val Gly His Glu Xaa Ser Ala  
20 25 30  
Trp Ala Gln Ser Glu Ser Phe Pro Xaa Leu Lys Pro Glu Glu Val Ala  
35 40 45  
Gly Ile Ile Lys Asp Phe Asp Glu Pro Gly Thr Leu Ala Pro Thr Gly  
50 55 60  
Leu Phe Val Gly Gly Thr Lys Tyr Met Val Ile Gln Gly Glu Pro Gly  
65 70 75 80  
Val Val Ile Arg Gly Lys Lys Gly Thr Gly Gly Ile Thr Ile Lys Lys  
85 90 95  
Thr Gly Met Ser Leu Ile Ile Gly Val Tyr Asp Glu Pro Met Thr Pro  
100 105 110  
Gly Gln Cys Asn Met Val Val Glu Arg Leu Gly Asp Tyr Leu Ile Glu  
115 120 125  
Gln Gly Phe  
130

(2) INFORMATION FOR SEQ ID NO:3705:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..120

(D) OTHER INFORMATION: / Ceres Seq. ID 1577869

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3705:

Met Cys Xaa Ile Glu Gly Gln His Leu Ser Ala Ala Xaa Ile Val Gly  
1 5 10 15  
His Glu Xaa Ser Ala Trp Ala Gln Ser Glu Ser Phe Pro Xaa Leu Lys  
20 25 30  
Pro Glu Glu Val Ala Gly Ile Ile Lys Asp Phe Asp Glu Pro Gly Thr  
35 40 45  
Leu Ala Pro Thr Gly Leu Phe Val Gly Gly Thr Lys Tyr Met Val Ile  
50 55 60  
Gln Gly Glu Pro Gly Val Val Ile Arg Gly Lys Lys Gly Thr Gly Gly  
65 70 75 80  
Ile Thr Ile Lys Lys Thr Gly Met Ser Leu Ile Ile Gly Val Tyr Asp  
85 90 95  
Glu Pro Met Thr Pro Gly Gln Cys Asn Met Val Val Glu Arg Leu Gly  
100 105 110  
Asp Tyr Leu Ile Glu Gln Gly Phe  
115 120

(2) INFORMATION FOR SEQ ID NO:3706:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..371
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577881

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3706:

atataaaagg atcgccctcc gcgcgcgcgc gctccttcgc aaaccctcct accccattcc

(2) INFORMATION FOR SEQ ID NO:3707:

(A) LENGTH: 95 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..95

(D) OTHER INFORMATION: / Ceres Seq. ID 1577882

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3707:

(2) INFORMATION FOR SEQ ID NO:3708:

(A) LENGTH: 52 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

MOLECULE TYPE: peptid

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..52

(D) OTHER INFORMATION: / Ceres Seq. ID 1577883

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3708:

(2) INFORMATION FOR SEQ ID NO:3709:

(A) LENGTH: 800 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

MOLECULE TYPE: DNA (g

(ix) FEATURE:

(B) LOCATION: 1

(D) OTHER INFORMATION

(D) OTHER INFORMATION: / SERIALIZED: 11-11-68

(X1)	SEQUENCE	DESCRIPTION	SEQ ID NO			
ttttgatgaa	aacgtcgact	ctttttttgtc	gaatgatgat	gtagacggaa	gaggcatggt	60
tgacgacact	gaaaaagggt	cttcagagca	caatacacag	tccttaaagg	gtctctcttt	120
gagtgaagtt	ggtaacaacc	gtacaagtaa	caacaaagtt	gtttgctgtc	acttctcttc	180
agatgggaag	ttactcgcta	gtgcggcca	tgagaagaag	gtcttcctct	ggaatatgga	240
caatttttaag	atggatacca	aaatagaaga	ccatacaaac	tttatcacag	acataagatt	300
cagaactaat	tcaactcagt	tggctacatc	atcttctgtac	ggaactgttc	gactttggaa	360
tgctgctgat	gaaagtggcg	ctttacaaac	ttttcatggg	cataggtctc	atgtaacatc	420
agtagatttt	cacccaagat	tgacagaggt	tctttgctct	tgcgacgaca	atggagAaaa	480
ttctcttctg	gacagttggt	cagactacat	ctactcatgt	tttgcgggtg	aagcagggtg	540
gaactggaag	agtcaggttt	gaacctcgaa	gtgggcagct	cctcgctgtg	gcagctggaa	600
gcatggtgaa	cattttttgat	gttgaaaagc	aatccagctt	acctgcttc	gtgattcaga	660
tgctgctttc	tttcaagtga	tatgtcgatg	tagtgtcgca	gcaatgtatt	tggtttggct	720
acagctgttc	tgtcgtctgt	gcgtaaaaa	ttagctatgt	atctatccat	atctgcatat	780
ttgaatgtat	ggtcgttttc					

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(D) OTHER INFORMATION: / Ceres Seq. ID 1577906

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 1																
Phe 1	Asp 2	Glu 3	Asn 4	Val 5	Asp 6	Ser 7	Phe 8	Leu 9	Ser 10	Asn 11	Asp 12	Asp 13	Val 14	Asp 15	Gly 16	
Arg	Gly	Met	Phe 20	Ala	Ala	Leu	Glu	Lys 25	Gly	Ser	Ser	Glu	His 30	Asn	Thr	
Glu	Ser	Leu	Lys 35	Gly	Leu	Ser	Leu 40	Ser	Glu	Val	Gly	Asn 45	Asn	Arg	Thr	
Ser	Asn 50	Asn	Lys	Val	Val	Cys 55	Cys	His	Phe	Ser	Ser	Asp 60	Gly	Lys	Leu	
Leu 65	Ala	Ser	Ala	Gly	His 70	Glu	Lys	Lys	Val	Phe 75	Leu	Trp	Asn	Met	Asp 80	
Asn	Phe	Lys	Met	Asp 85	Thr	Lys	Ile	Glu	Asp 90	His	Thr	Asn	Phe	Ile 95	Thr	
Asp	Ile	Arg	Phe 100	Arg	Thr	Asn	Ser	Thr 105	Gln	Leu	Ala	Thr	Ser 110	Ser	Ser	
Asp	Gly	Thr	Val 115	Arg	Leu	Trp	Asn 120	Ala	Ala	Asp	Glu	Ser 125	Gly	Ala	Leu	
Gln	Thr 130	Phe	His	Gly	His	Arg 135	Ser	His	Val	Thr	Ser 140	Val	Asp	Phe	His	
Pro 145	Arg	Leu	Thr	Glu	Val 150	Leu	Cys	Ser	Cys	Asp 155	Asp	Asn	Gly	Glu	Asn 160	
Ser	Leu	Leu	Asp 165	Ser	Trp	Ser	Asp	Tyr	Ile 170	Tyr	Ser	Cys	Phe	Ala 175	Gly	
Glu	Ala	Gly	Trp 180	Asn	Trp	Lys	Ser	Gln 185	Val							

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..168

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3711:

(2) INFORMATION FOR SEQ ID NO:3712:

(A) LENGTH: 108 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..108

(D) OTHER INFORMATION: / Ceres Seq. ID 1577908

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3712:

(2) INFORMATION FOR SEQ ID NO:3713:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 774 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..774

(D) OTHER INFORMATION: / Ceres Seq. ID 1577940

Variable	Mean	SD	Min	Max
Age	34.5	10.2	21	55
Gender	0.48	0.50	0	1
Marital status	0.62	0.49	0	1
Education	12.5	1.8	9	16
Income	15.2	3.5	10	25
Occupation	1.2	0.8	0	2
Health status	1.8	0.9	1	3
Stress level	2.5	1.2	1	4
Life satisfaction	3.2	1.5	1	5
Resilience	2.8	1.1	1	4
Optimism	3.5	1.3	1	5
Self-efficacy	3.8	1.4	1	5
Emotional stability	3.1	1.2	1	5
Prosocial behavior	3.4	1.3	1	5
Empathy	3.6	1.4	1	5
Agreeableness	3.7	1.5	1	5
Conscientiousness	3.9	1.6	1	5
Neuroticism	2.9	1.1	1	5
Openness	3.3	1.2	1	5
Extraversion	3.5	1.3	1	5
Intelligence	110.5	15.2	85	145
Memory	15.8	2.5	10	25
Attention	14.2	2.2	10	25
Processing speed	13.5	2.0	10	25
Verbal ability	12.8	1.8	10	25
Non-verbal ability	12.5	1.7	10	25
Fluid intelligence	12.2	1.6	10	25
Crystalline intelligence	12.5	1.7	10	25
Executive function	13.8	2.1	10	25
Working memory	14.5	2.3	10	25
Inhibition	15.2	2.5	10	25
Planning	15.8	2.7	10	25
Flexibility	16.5	2.9	10	25
Problem solving	17.2	3.1	10	25
Decision making	18.5	3.5	10	25
Emotional regulation	19.2	3.8	10	25
Impulse control	20.5	4.2	10	25
Stress management	21.8	4.5	10	25
Resilience (repeated)	22.5	4.8	10	25
Optimism (repeated)	23.2	5.1	10	25
Self-efficacy (repeated)	24.5	5.5	10	25
Emotional stability (repeated)	25.8	5.8	10	25
Prosocial behavior (repeated)	26.5	6.2	10	25
Empathy (repeated)	27.2	6.5	10	25
Agreeableness (repeated)	28.5	6.8	10	25
Conscientiousness (repeated)	29.2	7.1	10	25
Neuroticism (repeated)	30.5	7.5	10	25
Openness (repeated)	31.8	7.8	10	25
Extraversion (repeated)	32.5	8.1	10	25
Intelligence (repeated)	33.2	8.5	10	25
Memory (repeated)	34.5	8.8	10	25
Attention (repeated)	35.8	9.2	10	25
Processing speed (repeated)	36.5	9.5	10	25
Verbal ability (repeated)	37.2	9.8	10	25
Non-verbal ability (repeated)	38.5	10.2	10	25
Fluid intelligence (repeated)	39.2	10.5	10	25
Crystalline intelligence (repeated)	40.5	10.8	10	25
Executive function (repeated)	41.8	11.2	10	25
Working memory (repeated)	42.5	11.5	10	25
Inhibition (repeated)	43.2	11.8	10	25
Planning (repeated)	44.5	12.2	10	25
Flexibility (repeated)	45.8	12.5	10	25
Problem solving (repeated)	46.5	12.8	10	25
Decision making (repeated)	47.2	13.2	10	25
Emotional regulation (repeated)	48.5	13.5	10	25
Impulse control (repeated)	49.2	13.8	10	25
Stress management (repeated)	50.5	14.2	10	25
Resilience (repeated)	51.8	14.5	10	25
Optimism (repeated)	52.5	14.8	10	25
Self-efficacy (repeated)	53.2	15.2	10	25
Emotional stability (repeated)	54.5	15.5	10	25
Prosocial behavior (repeated)	55.8	15.8	10	25
Empathy (repeated)	56.5	16.2	10	25
Agreeableness (repeated)	57.2	16.5	10	25
Conscientiousness (repeated)	58.5	16.8	10	25
Neuroticism (repeated)	59.2	17.2	10	25
Openness (repeated)	60.5	17.5	10	25
Extraversion (repeated)	61.8	17.8	10	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3713:

atatattcaa	gcgcgcgcat	cagcgcgtgcc	cccaaatagt	acatctccct	ccatgatgct	60
cgcaactcct	cctagcatca	ctcaccgccca	ccttcacagc	ggcatcatcc	cgccaccggg	120
tccggggccac	cgcaggagac	tcgtctccac	tgcacgcgcc	gccgtgaagc	gagatggtgc	180
caccacggag	gtagcaggcg	atgaggggcg	gtcgtcgtcg	tcgtcgtcgc	cgccgCccgc	240
cggaaagctc	gaggggtgact	aaggctgccg	cgacggcgac	cccggcgggcg	ttttcgttgc	300
ccaaggacta	cagccatacg	ctgttccact	ccgagttcct	ggaggtgctg	ggcctgatcg	360
acctcgagtc	gctgcggaag	cgcccgaggc	tcaccgtagg	ggtgaacggtg	aaggcgtccc	420
tgcgcgtccc	ggtgctcgtg	gtcctggcgg	ccctgtacct	cgcggacgtg	accagcGggt	480
cttgttgact	ggacgcacat	tcacctggag	ggcgacgcgc	acgacgtagg	ggactagtga	540
agaagggacg	ccctcactgc	cbtgccctgc	catgcccccg	ctctccattg	tagcggatgc	600
aggcatgcag	cagcctcaac	ttgcttggtg	aaacaatcag	cttcaggaca	taaactgact	660
tttagtttag	tggtgtgctt	tgtaaaccct	gcttttatct	tactcgtctt	atttctaact	720
attagatata	atgtattcaa	acacatcttt	gaataagaaa	cgatttttagt	ctct	

(2) INFORMATION FOR SEQ ID NO:3714:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..86
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577941

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3714:

Tyr	Ile	Gln	Ala	Arg	Ala	Ser	Ala	Leu	Pro	Pro	Asn	Ser	Thr	Ser	Pro
1			5					10						15	
Ser	Met	Met	Leu	Ala	Thr	Pro	Pro	Ser	Ile	Thr	His	Arg	His	Leu	His
			20					25					30		
Ser	Gly	Ile	Ile	Pro	Pro	Pro	Gly	Pro	Gly	His	Arg	Arg	Arg	Leu	Val
		35					40					45			
Ser	Thr	Ala	Arg	Ala	Ala	Val	Lys	Arg	Asp	Gly	Ala	Thr	Thr	Glu	Val
	50					55				60					
Ala	Gly	Asp	Glu	Gly	Ala	Ser	Ser	Ser	Ser	Ser	Ser	Pro	Pro	Pro	Ala
65						70				75					80
Gly	Lys	Leu	Glu	Gly	Asp										
						85									

(2) INFORMATION FOR SEQ ID NO:3715:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..69
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577942

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3715:

Met	Met	Leu	Ala	Thr	Pro	Pro	Ser	Ile	Thr	His	Arg	His	Leu	His	Ser
1			5					10					15		
Gly	Ile	Ile	Pro	Pro	Pro	Gly	Pro	Gly	His	Arg	Arg	Arg	Leu	Val	Ser
			20					25					30		
Thr	Ala	Arg	Ala	Ala	Val	Lys	Arg	Asp	Gly	Ala	Thr	Thr	Glu	Val	Ala
		35				40					45				
Gly	Asp	Glu	Gly	Ala	Ser	Ser	Ser	Ser	Ser	Ser	Pro	Pro	Pro	Ala	Gly
	50					55					60				
Lys	Leu	Glu	Gly	Asp											
65															

(2) INFORMATION FOR SEQ ID NO:3716:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 95 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..95  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1577943  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3716:

Met Arg Ala Arg Arg Arg Arg Arg Arg Arg Arg Pro Pro Glu Ser  
1                    5                    10                    15  
Ser Arg Val Thr Lys Ala Ala Ala Thr Ala Thr Pro Ala Ala Phe Ser  
                    20                    25                    30  
Leu Pro Lys Asp Tyr Ser His Thr Leu Phe His Ser Glu Phe Leu Glu  
                    35                    40                    45  
Val Leu Gly Leu Ile Asp Leu Glu Ser Leu Arg Lys Arg Pro Arg Leu  
50                    55                    60  
Thr Val Gly Val Thr Val Lys Ala Ser Leu Pro Leu Pro Val Leu Val  
65                    70                    75                    80  
Val Leu Ala Ala Leu Tyr Leu Ala Asp Val Thr Ser Gly Ser Cys  
                    85                    90                    95

(2) INFORMATION FOR SEQ ID NO:3717:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 674 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..674  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1577969  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3717:

ctcgctataa aacatgcccg cwccctgcact accactacta caaccagcgg tagtgccgg 60  
catcatccgt ctcgtctcgt ctcgtctcgc ctctcctctc cttttccccc ctccctgcac 120  
agcgccgctc accgtcaccg taccacagca gcgatcgatg gctgaggtag acaacgagcg 180  
gcccgtgatg gtgggcgacg tccgggacgc gccgggtggg cgcgagaacg acctcgaggc 240  
catcgagctC Gcgcgcttcg Cggctgcgca gcacaacagc aagaccaacg cgatgctgga 300  
attcgagagg ctggtgaagg tgaggcacca ggtcgtggcc gggaccctgc accacttcac 360  
cgctcagagg aaggaggccg gcggcggcga aaagaagctg tacgaggcca aggtGgtggg 420  
agaaggcgtg ggagaacttc aagcagctgc agagcttcga gctcgtcgga gaNcgccgcg 480  
gtcgccctgag gcgcacaggc ttttcgctgg aggctggagc acaacaatga aagaatttaa 540  
ctgtcatccc actggaaaag tatgatataa tgaataaacc agcgtcttac ccacatgtat 600  
tgtaccctaa tgagatatatt gaccactgta atagaatgag atgtgctaag gaatctgaaa 660  
gccttcttgc tttt

(2) INFORMATION FOR SEQ ID NO:3718:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 183 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..183  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1577970  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3718:

Met Pro Xaa Pro Ala Leu Pro Leu Leu Gln Pro Ala Val Val Ala Gly  
1                    5                    10                    15



Ile Ile Arg Leu Val Ser Ser Arg Leu Ala Ser Pro Leu Leu Phe Pro  
20 25 30  
Pro Pro Cys Thr Ala Pro Leu Thr Val Thr Val Pro Gln Gln Arg Ser  
35 40 45  
Met Ala Glu Val His Asn Glu Arg Pro Val Met Val Gly Asp Val Arg  
50 55 60  
Asp Ala Pro Val Gly Arg Glu Asn Asp Leu Glu Ala Ile Glu Leu Ala  
65 70 75 80  
Arg Phe Ala Val Ala Glu His Asn Ser Lys Thr Asn Ala Met Leu Glu  
85 90 95  
Phe Glu Arg Leu Val Lys Val Arg His Gln Val Val Ala Gly Thr Leu  
100 105 110  
His His Phe Thr Val Glu Val Lys Glu Ala Gly Gly Gly Glu Lys Lys  
115 120 125  
Leu Tyr Glu Ala Lys Val Val Gly Glu Gly Val Gly Glu Leu Gln Ala  
130 135 140  
Ala Ala Glu Leu Arg Ala Arg Arg Arg Xaa Pro Arg Ser Pro Glu Ala  
145 150 155 160  
His Arg Leu Phe Ala Gly Gly Trp Ser Thr Thr Met Lys Glu Phe Asn  
165 170 175  
Cys His Pro Thr Gly Lys Val  
180

(2) INFORMATION FOR SEQ ID NO:3719:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..135
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577971

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3719:

Met Ala Glu Val His Asn Glu Arg Pro Val Met Val Gly Asp Val Arg  
1 5 10 15  
Asp Ala Pro Val Gly Arg Glu Asn Asp Leu Glu Ala Ile Glu Leu Ala  
20 25 30  
Arg Phe Ala Val Ala Glu His Asn Ser Lys Thr Asn Ala Met Leu Glu  
35 40 45  
Phe Glu Arg Leu Val Lys Val Arg His Gln Val Val Ala Gly Thr Leu  
50 55 60  
His His Phe Thr Val Glu Val Lys Glu Ala Gly Gly Gly Glu Lys Lys  
65 70 75 80  
Leu Tyr Glu Ala Lys Val Val Gly Glu Gly Val Gly Glu Leu Gln Ala  
85 90 95  
Ala Ala Glu Leu Arg Ala Arg Arg Arg Xaa Pro Arg Ser Pro Glu Ala  
100 105 110  
His Arg Leu Phe Ala Gly Gly Trp Ser Thr Thr Met Lys Glu Phe Asn  
115 120 125  
Cys His Pro Thr Gly Lys Val  
130 135

(2) INFORMATION FOR SEQ ID NO:3720:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

000001-13566666

(B) LOCATION: 1..125

(D) OTHER INFORMATION: / Ceres Seq. ID 1577972

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3720:

Met	Val	Gly	Asp	Val	Arg	Asp	Ala	Pro	Val	Gly	Arg	Glu	Asn	Asp	Leu
1				5					10					15	
Glu	Ala	Ile	Glu	Leu	Ala	Arg	Phe	Ala	Val	Ala	Glu	His	Asn	Ser	Lys
			20					25					30		
Thr	Asn	Ala	Met	Leu	Glu	Phe	Glu	Arg	Leu	Val	Lys	Val	Arg	His	Gln
		35					40					45			
Val	Val	Ala	Gly	Thr	Leu	His	His	Phe	Thr	Val	Glu	Val	Lys	Glu	Ala
	50					55					60				
Gly	Gly	Gly	Glu	Lys	Lys	Leu	Tyr	Glu	Ala	Lys	Val	Val	Gly	Glu	Gly
65				70						75				80	
Val	Gly	Glu	Leu	Gln	Ala	Ala	Ala	Glu	Leu	Arg	Ala	Arg	Arg	Arg	Xaa
				85					90					95	
Pro	Arg	Ser	Pro	Glu	Ala	His	Arg	Leu	Phe	Ala	Gly	Gly	Trp	Ser	Thr
			100					105						110	
Thr	Met	Lys	Glu	Phe	Asn	Cys	His	Pro	Thr	Gly	Lys	Val			
			115				120					125			

(2) INFORMATION FOR SEQ ID NO:3721:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 800 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..800

(D) OTHER INFORMATION: / Ceres Seq. ID 1577981

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3721:

aaaaaacctc	ctgcagtcgt	tttcaacctc	tccctctctc	acggcggcgtt	ttctggcgac	60
ggcggcggcg	gcgacgacga	gcagccacct	ggggaagagc	aggtagcagg	aaatggcggc	120
gttctctgagg	tcaaaatgtt	caccagtttg	acgtactttg	atgggaagcc	ttggaaatag	180
tttgtttgagg	gctgccaaact	cttctgtttg	ggcaataaca	aggccttctc	attgcatgac	240
tatcagtcag	cAaaatcaga	acattcatcc	agatgaggac	taacctgaag	gtggtcgata	300
actccggggc	caagcgggtg	atgtgcatcc	agtccctgag	ggggaagaaa	ggagcaaggc	360
tcggggacat	gatcatcgga	tccgtaaagg	aggcccagcc	tcgtggcaag	gtcaagaaa	420
gagacgtagt	ctacggcgtg	gtcgtccgtg	cgcctatgaa	gaaaggacgc	agcgtatggc	480
gcgaggtcca	gttcgacgac	aacgcgggtg	tcctcgtgaa	caagaagggc	gagctgatcg	540
gcacccgcgt	ctttggcccc	gtccccacg	agctgaggaa	gaagaagcac	ctcaagatcc	600
tggccctggc	tgaacacatt	gtttgaggtg	tgtcgcatag	ccaagtgttt	gtgggaatgt	660
ttttttttgt	gtgttctctg	tttgaataat	gcattgtgaa	acgatagcat	ggaccgtttg	720
aactattttg	atgacattgc	tcgtccattt	ggatggccaa	tacgtgtcgt	gatcgattct	780
ggagttccat	tttttttgtt					

(2) INFORMATION FOR SEQ ID NO:3722:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 129 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..129

(D) OTHER INFORMATION: / Ceres Seq. ID 1577982

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3722:

Met	Leu	Ser	Val	Ser	Lys	Ile	Arg	Thr	Phe	Ile	Gln	Met	Arg	Thr	Asn
1				5					10					15	
Leu	Lys	Val	Val	Asp	Asn	Ser	Gly	Ala	Lys	Arg	Val	Met	Cys	Ile	Gln
				20				25					30		

Ser Leu Arg Gly Lys Lys Gly Ala Arg Leu Gly Asp Met Ile Ile Gly  
35 40 45  
Ser Val Lys Glu Ala Gln Pro Arg Gly Lys Val Lys Lys Gly Asp Val  
50 55 60  
Val Tyr Gly Val Val Val Arg Ala Ala Met Lys Lys Gly Arg Ser Asp  
65 70 75 80  
Gly Ser Glu Val Gln Phe Asp Asp Asn Ala Val Val Leu Val Asn Lys  
85 90 95  
Lys Gly Glu Leu Ile Gly Thr Arg Val Phe Gly Pro Val Pro His Glu  
100 105 110  
Leu Arg Lys Lys Lys His Leu Lys Ile Leu Ala Leu Ala Glu His Ile  
115 120 125  
Val

(2) INFORMATION FOR SEQ ID NO:3723:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..117
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577983

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3723:

Met Arg Thr Asn Leu Lys Val Val Asp Asn Ser Gly Ala Lys Arg Val  
1 5 10 15  
Met Cys Ile Gln Ser Leu Arg Gly Lys Lys Gly Ala Arg Leu Gly Asp  
20 25 30  
Met Ile Ile Gly Ser Val Lys Glu Ala Gln Pro Arg Gly Lys Val Lys  
35 40 45  
Lys Gly Asp Val Val Tyr Gly Val Val Val Arg Ala Ala Met Lys Lys  
50 55 60  
Gly Arg Ser Asp Gly Ser Glu Val Gln Phe Asp Asp Asn Ala Val Val  
65 70 75 80  
Leu Val Asn Lys Lys Gly Glu Leu Ile Gly Thr Arg Val Phe Gly Pro  
85 90 95  
Val Pro His Glu Leu Arg Lys Lys Lys His Leu Lys Ile Leu Ala Leu  
100 105 110  
Ala Glu His Ile Val  
115

(2) INFORMATION FOR SEQ ID NO:3724:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..101
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577984

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3724:

Met Cys Ile Gln Ser Leu Arg Gly Lys Lys Gly Ala Arg Leu Gly Asp  
1 5 10 15  
Met Ile Ile Gly Ser Val Lys Glu Ala Gln Pro Arg Gly Lys Val Lys  
20 25 30  
Lys Gly Asp Val Val Tyr Gly Val Val Val Arg Ala Ala Met Lys Lys  
35 40 45  
Gly Arg Ser Asp Gly Ser Glu Val Gln Phe Asp Asp Asn Ala Val Val

50 55 60  
Leu Val Asn Lys Lys Gly Glu Leu Ile Gly Thr Arg Val Phe Gly Pro  
65 70 75 80  
Val Pro His Glu Leu Arg Lys Lys Lys His Leu Lys Ile Leu Ala Leu  
85 90 95  
Ala Glu His Ile Val  
100

(2) INFORMATION FOR SEQ ID NO:3725:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 747 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..747
- (D) OTHER INFORMATION: / Ceres Seq. ID 1577999

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3725:

accaaccacc gtggccccg caaattactc aaatttgccc ttctgtctc ggttccctct 60  
tcccggcgca ccagcctacc tcgccgacgc caggccgcca cgccgccgga gacatgaacc 120  
agcccgtgca gaagaacacc ctctacgtcg gtgggctggc ggaggaggtg gacgagaaga 180  
tcctgcacgc cgcgttcgtg ccctttggtg aggtcaagga cgtcaagacg ccgctcgatc 240  
agtccacgca gaagcaccgc tCcttcggct tcgtcacctt cctggagcgc gaggacgccg 300  
ccgctgccat ggacaacatg gacggcgccg agctcttcgg ccgcgtgctt accgtcaact 360  
acgccttccc cgagcgcacg aagggagggg agcagggatg ggctgcccag ccaatctggg 420  
ccgatgcgga cacttggttc gagaggcagc agcaggaaga ggagatgcag cggctgcagg 480  
cagagcaccg tgcagcgatg caggcagcag agaagctgca cagggagaaa ctggccgctg 540  
aaaggggaagg cgagaaagaa gaagatccca tggctgccgc agaggcccag gctgtgaaac 600  
aaagttctta agaaccgat atcaactcat aactcatgtg ctacgttgot gcctgtttgt 660  
cagatatgac taaacgaatc ttgcgaatgc tgtttgtttt gctgaaagaa ccctatttct 720  
cacctgacgt gggattctta ttggttt

(2) INFORMATION FOR SEQ ID NO:3726:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..202
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3726:

Gln Pro Pro Trp Pro Arg Gln Ile Thr Gln Ile Cys Pro Ser Cys Leu  
1 5 10 15  
Gly Ser Leu Phe Pro Ala His Gln Pro Thr Ser Pro Thr Pro Gly Arg  
20 25 30  
His Ala Ala Gly Asp Met Asn Gln Pro Val Gln Lys Asn Thr Leu Tyr  
35 40 45  
Val Gly Gly Leu Ala Glu Glu Val Asp Glu Lys Ile Leu His Ala Ala  
50 55 60  
Phe Val Pro Phe Gly Glu Val Lys Asp Val Lys Thr Pro Leu Asp Gln  
65 70 75 80  
Ser Thr Gln Lys His Arg Ser Phe Gly Phe Val Thr Phe Leu Glu Arg  
85 90 95  
Glu Asp Ala Ala Ala Ala Met Asp Asn Met Asp Gly Ala Glu Leu Phe  
100 105 110  
Gly Arg Val Leu Thr Val Asn Tyr Ala Phe Pro Glu Arg Ile Lys Gly  
115 120 125  
Gly Glu Gln Gly Trp Ala Ala Gln Pro Ile Trp Ala Asp Ala Asp Thr

130 135 140  
Trp Phe Glu Arg Gln Gln Glu Glu Glu Met Gln Arg Leu Gln Ala  
145 150 155 160  
Glu His Arg Ala Ala Met Gln Ala Ala Glu Lys Leu His Arg Glu Lys  
165 170 175  
Leu Ala Ala Glu Arg Glu Gly Glu Lys Glu Glu Asp Pro Met Ala Ala  
180 185 190  
Ala Glu Ala Gln Ala Val Lys Gln Ser Ser  
195 200

(2) INFORMATION FOR SEQ ID NO:3727:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..165
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3727:

Met Asn Gln Pro Val Gln Lys Asn Thr Leu Tyr Val Gly Gly Leu Ala  
1 5 10 15  
Glu Glu Val Asp Glu Lys Ile Leu His Ala Ala Phe Val Pro Phe Gly  
20 25 30  
Glu Val Lys Asp Val Lys Thr Pro Leu Asp Gln Ser Thr Gln Lys His  
35 40 45  
Arg Ser Phe Gly Phe Val Thr Phe Leu Glu Arg Glu Asp Ala Ala Ala  
50 55 60  
Ala Met Asp Asn Met Asp Gly Ala Glu Leu Phe Gly Arg Val Leu Thr  
65 70 75 80  
Val Asn Tyr Ala Phe Pro Glu Arg Ile Lys Gly Gly Glu Gln Gly Trp  
85 90 95  
Ala Ala Gln Pro Ile Trp Ala Asp Ala Asp Thr Trp Phe Glu Arg Gln  
100 105 110  
Gln Gln Glu Glu Met Gln Arg Leu Gln Ala Glu His Arg Ala Ala  
115 120 125  
Met Gln Ala Ala Glu Lys Leu His Arg Glu Lys Leu Ala Ala Glu Arg  
130 135 140  
Glu Gly Glu Lys Glu Glu Asp Pro Met Ala Ala Ala Glu Ala Gln Ala  
145 150 155 160  
Val Lys Gln Ser Ser  
165

(2) INFORMATION FOR SEQ ID NO:3728:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 967 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..967
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578004

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3728:

aaaactaacc ccaaacccca atccacccca tcccctctc atccactcgg ggcggccatg 60  
gcctgctcct tctccgccc catcacccgtc tottccgcc ctaccccggc cgccagaccc 120  
ctcgtctgtg ccccgagtc cgtctgcac gctcgtccg cggtcgccac cactgccagg 180  
ccgctccgcc tcgccgctc aaggtccgc cgggctacca gactcgttg ccgcgccagg 240  
tangtcgatg acttgccgt ggtcggaac aaggcgccag acttagaagc cgaggctgtg 300  
ttcgaccagg agttcatcaa cgtgaagctc tctgattaca ttgggaagaa gtacgtcatt 360

```
ctgtttcttct accccttgga tttcaccttc gtctgcmcga ccgagattAc tgcgttttagt 420
gacagatacg aggaatttga gaagttgaac actgagggttc ttggtgtttc cattgacagt 480
gtgtttctccc accttgcatg ggtgcagaca gacaggaagt cgggtgggct cggcgatctt 540
aaatacccac ttgtttctga tgtgacaaa tcaatttcaa aggccttttg tgttctgac 600
cctgaccagg gtattgcttt gagaggactg ttcattcattg acaaggaggg agtgattcag 660
cactctacca ttaacaacct tgccattggt cgtagtgtgg atgagaccat gaggaccctt 720
caggcattgc agtacgtcca ggagaacca gacgagggtg gcccggccg atggaaacca 780
ggggagaggt cgatgaagcc cgaccccaag ggaagcaaag agtacttcgc ggccatctag 840
attcgtcgtc attgagaagc aggtgcccg taagtgtcc agcagtaggt tctcgtgttc 900
agcggagctc gcgttttgac aagtgtattg tgctgatgtg catcccgatt tgagtgtctg 960
tctttgc
```

(2) INFORMATION FOR SEQ ID NO:3729:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..279
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578005

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3729:

```
Lys Thr Asn Pro Lys Pro Gln Ser Thr Pro Ser Pro Pro His Pro Leu
1          5          10          15
Arg Ala Ala Met Ala Cys Ser Phe Ser Ala Ala Ile Thr Val Ser Ser
20          25          30
Ala Pro Thr Pro Ala Ala Arg Pro Leu Ala Ala Ala Pro Gln Ser Val
35          40          45
Cys Ile Ala Arg Ser Ala Val Ala Thr Thr Ala Arg Pro Leu Arg Leu
50          55          60
Ala Ala Ser Arg Ser Ala Arg Ala Thr Arg Leu Val Ala Arg Ala Arg
65          70          75          80
Xaa Val Asp Asp Leu Pro Leu Val Gly Asn Lys Ala Pro Asp Leu Glu
85          90          95
Ala Glu Ala Val Phe Asp Gln Glu Phe Ile Asn Val Lys Leu Ser Asp
100         105         110
Tyr Ile Gly Lys Lys Tyr Val Ile Leu Phe Phe Tyr Pro Leu Asp Phe
115         120         125
Thr Phe Val Cys Xaa Thr Glu Ile Thr Ala Phe Ser Asp Arg Tyr Glu
130         135         140
Glu Phe Glu Lys Leu Asn Thr Glu Val Leu Gly Val Ser Ile Asp Ser
145         150         155         160
Val Phe Ser His Leu Ala Trp Val Gln Thr Asp Arg Lys Ser Gly Gly
165         170         175
Leu Gly Asp Leu Lys Tyr Pro Leu Val Ser Asp Val Thr Lys Ser Ile
180         185         190
Ser Lys Ala Phe Gly Val Leu Ile Pro Asp Gln Gly Ile Ala Leu Arg
195         200         205
Gly Leu Phe Ile Ile Asp Lys Glu Gly Val Ile Gln His Ser Thr Ile
210         215         220
Asn Asn Leu Ala Ile Gly Arg Ser Val Asp Glu Thr Met Arg Thr Leu
225         230         235         240
Gln Ala Leu Gln Tyr Val Gln Glu Asn Pro Asp Glu Val Cys Pro Ala
245         250         255
Gly Trp Lys Pro Gly Glu Arg Ser Met Lys Pro Asp Pro Lys Gly Ser
260         265         270
Lys Glu Tyr Phe Ala Ala Ile
275
```

(2) INFORMATION FOR SEQ ID NO:3730:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 260 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..260  
(D) OTHER INFORMATION: / Ceres Seq. ID 1578006  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3730:

Met Ala Cys Ser Phe Ser Ala Ala Ile Thr Val Ser Ser Ala Pro Thr  
1 5 10 15  
Pro Ala Ala Arg Pro Leu Ala Ala Ala Pro Gln Ser Val Cys Ile Ala  
20 25 30  
Arg Ser Ala Val Ala Thr Thr Ala Arg Pro Leu Arg Leu Ala Ala Ser  
35 40 45  
Arg Ser Ala Arg Ala Thr Arg Leu Val Ala Arg Ala Arg Xaa Val Asp  
50 55 60  
Asp Leu Pro Leu Val Gly Asn Lys Ala Pro Asp Leu Glu Ala Glu Ala  
65 70 75 80  
Val Phe Asp Gln Glu Phe Ile Asn Val Lys Leu Ser Asp Tyr Ile Gly  
85 90 95  
Lys Lys Tyr Val Ile Leu Phe Phe Tyr Pro Leu Asp Phe Thr Phe Val  
100 105 110  
Cys Xaa Thr Glu Ile Thr Ala Phe Ser Asp Arg Tyr Glu Glu Phe Glu  
115 120 125  
Lys Leu Asn Thr Glu Val Leu Gly Val Ser Ile Asp Ser Val Phe Ser  
130 135 140  
His Leu Ala Trp Val Gln Thr Asp Arg Lys Ser Gly Gly Leu Gly Asp  
145 150 155 160  
Leu Lys Tyr Pro Leu Val Ser Asp Val Thr Lys Ser Ile Ser Lys Ala  
165 170 175  
Phe Gly Val Leu Ile Pro Asp Gln Gly Ile Ala Leu Arg Gly Leu Phe  
180 185 190  
Ile Ile Asp Lys Glu Gly Val Ile Gln His Ser Thr Ile Asn Asn Leu  
195 200 205  
Ala Ile Gly Arg Ser Val Asp Glu Thr Met Arg Thr Leu Gln Ala Leu  
210 215 220  
Gln Tyr Val Gln Glu Asn Pro Asp Glu Val Cys Pro Ala Gly Trp Lys  
225 230 235 240  
Pro Gly Glu Arg Ser Met Lys Pro Asp Pro Lys Gly Ser Lys Glu Tyr  
245 250 255  
Phe Ala Ala Ile  
260

(2) INFORMATION FOR SEQ ID NO:3731:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 828 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..828  
(D) OTHER INFORMATION: / Ceres Seq. ID 1578007

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3731:

agaaacagac	ctgcacggct	ccactccaac	tccctcccaa	gccccaaagcc	ggcaagcccc	60
caaccacctt	ccttttccac	atccacaccg	ccccgggttt	cctcacgcct	ccgccctccc	120
accgcgtcac	tcccgctcct	atccaccgcg	atggcctccc	gcctcgccgt	cgccgtcgcc	180
gtcgccgcgc	ccgcgtogtc	tccttccccg	gtcggcaccg	tcgccccgcm	ccgcgtcgcc	240
ctccgccgag	gcctccccgc	gacgtggcac	gctctccgcg	ccctccctcg	atcccggtggc	300

gcggccgctcg tgtgccaggc ccagggcggc caggacaccg ccatccaagt tcctgatgtg 360  
agcaaatacca catggcaatc acttgtggtg gagagcgagc ttcccgCcc tcgttcagtt 420  
ctgggcctca tgggtgtggac cgtgtaagat gatagacccc atcgttggca agctctcgaa 480  
ggagtacgaa ggaaagctga agtgttacaa gctaaacacc gacgagaacc ctgacatcgc 540  
gacccaattc ggcattccgga gcatcccccac catgatgata ttcaagaatg gtgagaagaa 600  
ggacgcggtg attggagccg tgccagagag caccctggtc acctgcatcg acaagtacgt 660  
tgggtgggagg tgaaatctca atctgggcca ctagccttgg acttccatat gtagacggat 720  
gggtatgtgt ataccgttca tatcgaactg ctgttgagta gttgtatgta gataataatg 780  
tgatgctcac tccaataaat gcgattcaag gatgggcaag tcattctgg

(2) INFORMATION FOR SEQ ID NO:3732:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..148
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578008

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3732:

Arg Asn Arg Pro Ala Arg Leu His Ser Asn Ser Leu Pro Ser Pro Lys  
1 5 10 15  
Pro Ala Ser Pro Gln Pro Pro Ser Phe Ser Thr Ser Thr Pro Pro Arg  
20 25 30  
Val Ser Ser Arg Leu Arg Pro Pro Thr Arg Ser Leu Pro Ser Leu Ser  
35 40 45  
Thr Ala Met Ala Ser Arg Leu Ala Val Ala Val Ala Ala Pro  
50 55 60  
Ala Ser Ser Pro Ser Pro Val Gly Thr Val Ala Pro Xaa Arg Val Ala  
65 70 75 80  
Leu Arg Arg Gly Leu Pro Pro Thr Trp His Ala Leu Arg Ala Leu Pro  
85 90 95  
Arg Ser Arg Gly Ala Ala Val Val Cys Gln Ala Gln Gly Gly Gln Asp  
100 105 110  
Thr Ala Ile Gln Val Pro Asp Val Ser Lys Ser Thr Trp Gln Ser Leu  
115 120 125  
Val Val Glu Ser Glu Leu Pro Val Pro Arg Ser Val Leu Gly Leu Met  
130 135 140  
Val Trp Thr Val  
145

(2) INFORMATION FOR SEQ ID NO:3733:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..119
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578009

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3733:

Glu Thr Asp Leu His Gly Ser Thr Pro Thr Pro Ser Gln Ala Pro Ser  
1 5 10 15  
Arg Gln Ala Pro Asn His Leu Pro Phe Pro His Pro His Arg Pro Gly  
20 25 30  
Phe Pro His Ala Ser Ala Leu Pro Pro Ala His Ser Arg Pro Tyr Pro  
35 40 45  
Pro Arg Trp Pro Pro Ala Ser Pro Ser Pro Ser Pro Arg Pro  
50 55 60



Arg Arg Leu Leu Pro Arg Ser Ala Pro Ser Pro Arg Xaa Ala Ser Pro  
65 70 75 80  
Ser Ala Glu Ala Ser Arg Arg Arg Gly Thr Leu Ser Ala Pro Ser Leu  
85 90 95  
Asp Pro Val Ala Arg Pro Ser Cys Ala Arg Pro Arg Ala Ala Arg Thr  
100 105 110  
Pro Pro Ser Lys Phe Leu Met  
115

(2) INFORMATION FOR SEQ ID NO:3734:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..117

(D) OTHER INFORMATION: / Ceres Seq. ID 1578010

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3734:

Lys Gln Thr Cys Thr Ala Pro Leu Gln Leu Pro Pro Lys Pro Gln Ala  
1 5 10 15  
Gly Lys Pro Pro Thr Thr Phe Leu Phe His Ile His Thr Ala Pro Gly  
20 25 30  
Phe Leu Thr Pro Pro Pro Ser His Pro Leu Thr Pro Val Pro Ile His  
35 40 45  
Arg Asp Gly Leu Pro Pro Arg Arg Arg Arg Arg Arg Ala Arg  
50 55 60  
Val Val Ser Phe Pro Gly Arg His Arg Arg Pro Xaa Pro Arg Arg Pro  
65 70 75 80  
Pro Pro Arg Pro Pro Ala Asp Val Ala Arg Ser Pro Arg Pro Pro Ser  
85 90 95  
Ile Pro Trp Arg Gly Arg Arg Val Pro Gly Pro Gly Arg Pro Gly His  
100 105 110  
Arg His Pro Ser Ser  
115

(2) INFORMATION FOR SEQ ID NO:3735:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 628 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..628

(D) OTHER INFORMATION: / Ceres Seq. ID 1578015

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3735:

atatatttga tttggaagga aaataactta agactcgtaa aggtcgtgga ggacgaggtg 60  
tttcccgaag ggacggtgct gaagaagggc accaaggtgg tctacgccat gtactccatg 120  
grgcgatgg agagcatctg gggcgacgac tgccgggagt acaggccgga gcggtggctc 180  
cgggacggcc gcttcatgag cgagtcgcc tacaagttca Cgccttcaa cggcgggccc 240  
cgctgtgcc tcggcaagga cttcgcctac taccagatga agttcgccgc cgcctccatc 300  
ctNccgCggy taccgcgtcg acgtcgtcga gggccacccc gtcgcgcccc agatggcgct 360  
caccatgtac atgaagcaag gcctcaaggt cacgctgacc aagagagaca agaccaagct 420  
ctgaactgtt ggtgccgagc cgagcttgcc aataagactc tgagactgaa gagagatata 480  
cagtatgaaa gaagcagggc ttttcatgtt tttcatgtac atctagtata gaacttttat 540  
atatatgtat agatacatat gtatatgtgt tggcaaaacg cttgaccttc aggtgatgta 600  
accgtaata ttgtagcagt attatttc

(2) INFORMATION FOR SEQ ID NO:3736:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..176  
(D) OTHER INFORMATION: / Ceres Seq. ID 1578016  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3736:

Ile Tyr Leu Ile Trp Lys Glu Asn Asn Leu Arg Leu Val Lys Val Val  
1 5 10 15  
Glu Asp Glu Val Phe Pro Asp Gly Thr Val Leu Lys Lys Gly Thr Lys  
20 25 30  
Val Val Tyr Ala Met Tyr Ser Met Xaa Arg Met Glu Ser Ile Trp Gly  
35 40 45  
Asp Asp Cys Arg Glu Tyr Arg Pro Glu Arg Trp Leu Arg Asp Gly Arg  
50 55 60  
Phe Met Ser Glu Ser Ala Tyr Lys Phe Thr Ala Phe Asn Gly Gly Pro  
65 70 75 80  
Arg Leu Cys Leu Gly Lys Asp Phe Ala Tyr Tyr Gln Met Lys Phe Ala  
85 90 95  
Ala Ala Ser Ile Xaa Pro Pro Xaa Pro Arg Arg Arg Arg Arg Gly Pro  
100 105 110  
Pro Arg Arg Ala Gln Asp Gly Ala His His Val His Glu Ala Arg Pro  
115 120 125  
Gln Gly His Ala Asp Gln Glu Arg Gln Asp Gln Ala Leu Asn Cys Trp  
130 135 140  
Cys Arg Ala Glu Leu Ala Asn Lys Thr Leu Arg Leu Lys Arg Asp Ile  
145 150 155 160  
Gln Tyr Glu Arg Ser Arg Ala Leu His Leu Phe His Leu His Leu Val  
165 170 175

(2) INFORMATION FOR SEQ ID NO:3737:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 140 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..140  
(D) OTHER INFORMATION: / Ceres Seq. ID 1578017  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3737:

Met Tyr Ser Met Xaa Arg Met Glu Ser Ile Trp Gly Asp Asp Cys Arg  
1 5 10 15  
Glu Tyr Arg Pro Glu Arg Trp Leu Arg Asp Gly Arg Phe Met Ser Glu  
20 25 30  
Ser Ala Tyr Lys Phe Thr Ala Phe Asn Gly Gly Pro Arg Leu Cys Leu  
35 40 45  
Gly Lys Asp Phe Ala Tyr Tyr Gln Met Lys Phe Ala Ala Ser Ile  
50 55 60  
Xaa Pro Pro Xaa Pro Arg Arg Arg Arg Gly Pro Pro Arg Arg Ala  
65 70 75 80  
Gln Asp Gly Ala His His Val His Glu Ala Arg Pro Gln Gly His Ala  
85 90 95  
Asp Gln Glu Arg Gln Asp Gln Ala Leu Asn Cys Trp Cys Arg Ala Glu  
100 105 110  
Leu Ala Asn Lys Thr Leu Arg Leu Lys Arg Asp Ile Gln Tyr Glu Arg

115 120 125  
Ser Arg Ala Leu His Leu Phe His Leu His Leu Val  
130 135 140

(2) INFORMATION FOR SEQ ID NO:3738:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..137
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578018

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3738:

Met Xaa Arg Met Glu Ser Ile Trp Gly Asp Asp Cys Arg Glu Tyr Arg  
1 5 10 15  
Pro Glu Arg Trp Leu Arg Asp Gly Arg Phe Met Ser Glu Ser Ala Tyr  
20 25 30  
Lys Phe Thr Ala Phe Asn Gly Gly Pro Arg Leu Cys Leu Gly Lys Asp  
35 40 45  
Phe Ala Tyr Tyr Gln Met Lys Phe Ala Ala Ala Ser Ile Xaa Pro Pro  
50 55 60  
Xaa Pro Arg Arg Arg Arg Arg Gly Pro Pro Arg Arg Ala Gln Asp Gly  
65 70 75 80  
Ala His His Val His Glu Ala Arg Pro Gln Gly His Ala Asp Gln Glu  
85 90 95  
Arg Gln Asp Gln Ala Leu Asn Cys Trp Cys Arg Ala Glu Leu Ala Asn  
100 105 110  
Lys Thr Leu Arg Leu Lys Arg Asp Ile Gln Tyr Glu Arg Ser Arg Ala  
115 120 125  
Leu His Leu Phe His Leu His Leu Val  
130 135

(2) INFORMATION FOR SEQ ID NO:3739:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 922 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..922
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578031

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3739:

ctttccctcc ccatcccgtg aggcgtgagc gccacaccca cacgaaggat cccgaagccg 60  
aagagaaccc taccgaggag gcagaaaatc cgtagcgcgc ctcatacgat tccgagatcc 120  
gtgcctctta tcggcagcca tgatgctgcg cgcngcgggc aggcgactcc tcggcgtagg 180  
aggcggcgat ccagcgcccc cggtcgtctg tgctgtggcg gcgagcagga gcagaggata 240  
ccacgagcgg gtggtggacc actacaacaa cccgcgcaac gtggggtcct tggacaagga 300  
cgacacggac gtcggaacgg ggatcgtcgg cgcgcggcgg tcgggggacg tcatgaagct 360  
gcagatccgc gtcgacgagg ggtccggcag gatcgctgac gcgcgcttca agaCcttcgg 420  
ctgcRgctcc gccatcgctt cctcctccgt cgcttccgaa tgggtcaagg gcaagcaagt 480  
ggaggaagtg gtggccatca agaacaccga gattgcgaag cacctgtctc ttccaccagt 540  
gaagctccac tgcagcatgc tcgctgagga agcaatcaag gccgccgtga aggattacga 600  
ggcaaagaaa gggaagaaga tggccaaggc agaggagcag gacaccccat gcccgtaaga 660  
gcgacagcta gtaaaactgaa gcgagcagag agtactgtat gtagtatgta acggctaacg 720  
agcgaggtag tcgtgtcgtg tgtgccaaaa gaagcatgta tgtaatgtaa agctaggtaa 780  
caacgatgtt tgggtttcat agaataagcg aacttgccgc agtggttttt ttatctgctc 840  
tgcacatgaa taaggctctg ccattgctct ttatctgttt agtcggagca tgtatgctta 900  
gtttgatcaa gcaatgctgt tg

(2) INFORMATION FOR SEQ ID NO:3740:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 172 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..172

(D) OTHER INFORMATION: / Ceres Seq. ID 1578032

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3740:

Met Met Leu Arg Xaa Ala Gly Arg Arg Leu Leu Gly Val Gly Gly Gly  
1 5 10 15  
Asp Pro Ala Pro Ala Val Ala Ala Ala Val Ala Ala Ser Arg Ser Arg  
20 25 30  
Gly Tyr His Glu Arg Val Val Asp His Tyr Asn Asn Pro Arg Asn Val  
35 40 45  
Gly Ser Leu Asp Lys Asp Asp Thr Asp Val Gly Thr Gly Ile Val Gly  
50 55 60  
Ala Pro Ala Cys Gly Asp Val Met Lys Leu Gln Ile Arg Val Asp Glu  
65 70 75 80  
Gly Ser Gly Arg Ile Val Asp Ala Arg Phe Lys Thr Phe Gly Cys Xaa  
85 90 95  
Ser Ala Ile Ala Ser Ser Ser Val Ala Ser Glu Trp Val Lys Gly Lys  
100 105 110  
Gln Val Glu Glu Val Val Ala Ile Lys Asn Thr Glu Ile Ala Lys His  
115 120 125  
Leu Ser Leu Pro Pro Val Lys Leu His Cys Ser Met Leu Ala Glu Asp  
130 135 140  
Ala Ile Lys Ala Ala Val Lys Asp Tyr Glu Ala Lys Lys Gly Lys Lys  
145 150 155 160  
Met Ala Lys Ala Glu Glu Gln Asp Thr Pro Cys Pro  
165 170

(2) INFORMATION FOR SEQ ID NO:3741:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 171 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..171

(D) OTHER INFORMATION: / Ceres Seq. ID 1578033

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3741:

Met Leu Arg Xaa Ala Gly Arg Arg Leu Leu Gly Val Gly Gly Gly Asp  
1 5 10 15  
Pro Ala Pro Ala Val Ala Ala Ala Val Ala Ala Ser Arg Ser Arg Gly  
20 25 30  
Tyr His Glu Arg Val Val Asp His Tyr Asn Asn Pro Arg Asn Val Gly  
35 40 45  
Ser Leu Asp Lys Asp Asp Thr Asp Val Gly Thr Gly Ile Val Gly Ala  
50 55 60  
Pro Ala Cys Gly Asp Val Met Lys Leu Gln Ile Arg Val Asp Glu Gly  
65 70 75 80  
Ser Gly Arg Ile Val Asp Ala Arg Phe Lys Thr Phe Gly Cys Xaa Ser  
85 90 95  
Ala Ile Ala Ser Ser Ser Val Ala Ser Glu Trp Val Lys Gly Lys Gln  
100 105 110  
Val Glu Glu Val Val Ala Ile Lys Asn Thr Glu Ile Ala Lys His Leu

115 120 125  
Ser Leu Pro Pro Val Lys Leu His Cys Ser Met Leu Ala Glu Asp Ala  
130 135 140  
Ile Lys Ala Ala Val Lys Asp Tyr Glu Ala Lys Lys Gly Lys Lys Met  
145 150 155 160  
Ala Lys Ala Glu Glu Gln Asp Thr Pro Cys Pro  
165 170

(2) INFORMATION FOR SEQ ID NO:3742:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..101

(D) OTHER INFORMATION: / Ceres Seq. ID 1578034

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3742:

Met Lys Leu Gln Ile Arg Val Asp Glu Gly Ser Gly Arg Ile Val Asp  
1 5 10 15  
Ala Arg Phe Lys Thr Phe Gly Cys Xaa Ser Ala Ile Ala Ser Ser Ser  
20 25 30  
Val Ala Ser Glu Trp Val Lys Gly Lys Gln Val Glu Glu Val Val Ala  
35 40 45  
Ile Lys Asn Thr Glu Ile Ala Lys His Leu Ser Leu Pro Pro Val Lys  
50 55 60  
Leu His Cys Ser Met Leu Ala Glu Asp Ala Ile Lys Ala Ala Val Lys  
65 70 75 80  
Asp Tyr Glu Ala Lys Lys Gly Lys Lys Met Ala Lys Ala Glu Glu Gln  
85 90 95  
Asp Thr Pro Cys Pro  
100

(2) INFORMATION FOR SEQ ID NO:3743:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 753 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..753

(D) OTHER INFORMATION: / Ceres Seq. ID 1578035

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3743:

aaatgacgcc atgccggcgc caccgagggc gaaagctgtc cagatcgtgt gattttgcat 60  
cccattccgc agcgcgacac gsstgacctc ctgcacggcc tccacctccg tcttgaggcg 120  
aacgtangtg cgaaggacca actctttcga agggaaatta tatctcaggt gcttaggagt 180  
ctgccatggc cagcgagaat aaggtattta ggttcgagga agtcgccaag cacaacgtca 240  
ccaaggactg ctggatcatc atcgccggca aggtgtatga tgtcactcct tttatggatg 300  
agcatcctgg tggagatgag gttttgctag ctgtaactgg gaaagatgct acagctgatt 360  
ttgaagatat tggccacagt gattccgcaa gggacatgat ggagaagtac cacatcgggc 420  
agatagatgc ttcaacaatc ccagcaaagc gaacttatgt gcacccccag caagcgcca 480  
gccactcaga caagaataat gatctcctca tcaagatcct gcagttcctt gtgCccatta 540  
tgatcctggg ccttgcatct ggtatacgtc agtacagcaa atcagagtag tactgttctt 600  
gaagacttgc ctttgagtc tgttttatgg taatggtttg gatgagaaca gttcagtaat 660  
tgcttagtgt atttgtcagg tggatgttat ctcatgggtc atatactatg tattatggac 720  
atccatgtgt tgccgaaatg tgctcttttc ccc

(2) INFORMATION FOR SEQ ID NO:3744:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids

- (B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..134  
(D) OTHER INFORMATION: / Ceres Seq. ID 1578036  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3744:

Met Ala Ser Glu Asn Lys Val Phe Arg Phe Glu Glu Val Ala Lys His  
1 5 10 15  
Asn Val Thr Lys Asp Cys Trp Ile Ile Ala Gly Lys Val Tyr Asp  
20 25 30  
Val Thr Pro Phe Met Asp Glu His Pro Gly Gly Asp Glu Val Leu Leu  
35 40 45  
Ala Val Thr Gly Lys Asp Ala Thr Ala Asp Phe Glu Asp Ile Gly His  
50 55 60  
Ser Asp Ser Ala Arg Asp Met Met Glu Lys Tyr His Ile Gly Gln Ile  
65 70 75 80  
Asp Ala Ser Thr Ile Pro Ala Lys Arg Thr Tyr Val His Pro Gln Gln  
85 90 95  
Ala Pro Ser His Ser Asp Lys Asn Asn Asp Leu Leu Ile Lys Ile Leu  
100 105 110  
Gln Phe Leu Val Pro Ile Met Ile Leu Gly Leu Ala Phe Gly Ile Arg  
115 120 125  
Gln Tyr Ser Lys Ser Glu  
130

(2) INFORMATION FOR SEQ ID NO:3745:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 98 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..98  
(D) OTHER INFORMATION: / Ceres Seq. ID 1578037

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3745:

Met Asp Glu His Pro Gly Gly Asp Glu Val Leu Leu Ala Val Thr Gly  
1 5 10 15  
Lys Asp Ala Thr Ala Asp Phe Glu Asp Ile Gly His Ser Asp Ser Ala  
20 25 30  
Arg Asp Met Met Glu Lys Tyr His Ile Gly Gln Ile Asp Ala Ser Thr  
35 40 45  
Ile Pro Ala Lys Arg Thr Tyr Val His Pro Gln Gln Ala Pro Ser His  
50 55 60  
Ser Asp Lys Asn Asn Asp Leu Leu Ile Lys Ile Leu Gln Phe Leu Val  
65 70 75 80  
Pro Ile Met Ile Leu Gly Leu Ala Phe Gly Ile Arg Gln Tyr Ser Lys  
85 90 95  
Ser Glu

(2) INFORMATION FOR SEQ ID NO:3746:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 803 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:

002104-1578036

(A) NAME/KEY: -

(B) LOCATION: 1..803

(D) OTHER INFORMATION: / Ceres Seq. ID 1578042

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3746:

aatccccaca	acaccagaat	cgcggaatca	cagacgcgtc	tatctcagct	tgctgcactg	60
cactaccctg	ccctgccatc	atatcgtaag	tgagcccggc	cgagcgagag	crngggagag	120
gcatggctgc	tccgaagctc	gcgacgctgg	cgctggccgt	gctcctggcg	gcgaccgtgg	180
tggctcccc	ggcgcggtg	cgcgcggcga	tgctgtgctc	caccgtgtac	agcacgctga	240
tgccgtgcct	gccgttcgtc	cagatgggcg	gggccatgcc	gccccagccg	tgctgcggcg	300
gcatccgcag	cctgctgcag	cagccaacaa	cacccccgac	cgccgcacta	tctgcggctg	360
cctcaagaac	gtcgccaacg	gCgccaacgg	gagcggcacc	tacatcagcc	scgcccgcgc	420
gctgcccagc	aagtgcggcg	tcgCcctgcc	gtacaagatc	agcaccaacg	ttaactgcaa	480
cacgattaat	taagtgatga	ggcgctcctgt	gcgcgtccgg	gcgaggaatg	catgcatggc	540
gctggcggag	agtaataaaa	taatgctact	ggtattttaa	gctatatcga	ggtgtgcctg	600
tctctagtca	tttattatgg	tgtttaggaa	tggtctacac	agttcgtaac	ggtgtatcgt	660
ggatgcatgt	tgccgcgagc	agagtacgta	ggcatgaacc	gatgtgtgog	cttctgtctg	720
tttactctct	ctatgtagta	atgtgtgggt	gctttgatcc	agatgtattc	gctcgtgagt	780
cgtggaagta	gatcgtttca	gtg				

(2) INFORMATION FOR SEQ ID NO:3747:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 163 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..163

(D) OTHER INFORMATION: / Ceres Seq. ID 1578043

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3747:

Ile	Pro	Thr	Thr	Pro	Glu	Ser	Ala	Asn	His	Arg	Arg	Val	Tyr	Leu	Ser
1				5					10					15	
Leu	Leu	His	Cys	Thr	Thr	Leu	Pro	Cys	His	His	Ile	Val	Arg	Glu	Pro
				20				25					30		
Gly	Arg	Ala	Arg	Xaa	Xaa	Glu	Arg	His	Gly	Cys	Ser	Glu	Ala	Arg	Asp
				35				40				45			
Ala	Gly	Ala	Gly	Arg	Ala	Pro	Gly	Gly	Asp	Arg	Gly	Gly	Ser	Pro	Gly
				50			55				60				
Arg	Gly	Ala	Arg	Gly	Asp	Val	Val	Leu	His	Arg	Val	Gln	His	Ala	Asp
				65			70			75				80	
Ala	Val	Pro	Ala	Val	Arg	Pro	Asp	Gly	Arg	Gly	His	Ala	Ala	Pro	Ala
				85				90						95	
Val	Leu	Arg	Arg	His	Pro	Gln	Pro	Ala	Ala	Ala	Ala	Asn	Asn	Thr	Pro
				100				105						110	
Asp	Arg	Arg	Thr	Ile	Cys	Gly	Cys	Leu	Lys	Asn	Val	Ala	Asn	Gly	Ala
				115			120					125			
Asn	Gly	Ser	Gly	Thr	Tyr	Ile	Ser	Xaa	Ala	Ala	Ala	Leu	Pro	Ser	Lys
				130			135				140				
Cys	Gly	Val	Ala	Leu	Pro	Tyr	Lys	Ile	Ser	Thr	Asn	Val	Asn	Cys	Asn
				145			150			155				160	
Thr	Ile	Asn													

(2) INFORMATION FOR SEQ ID NO:3748:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 164 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

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(B) LOCATION: 1..164

(D) OTHER INFORMATION: / Ceres Seq. ID 1578044

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3748:

Ser Pro Gln His Gln Asn Pro Arg Ile Thr Asp Ala Ser Ile Ser Ala  
1 5 10 15  
Cys Cys Thr Ala Leu Pro Cys Pro Ala Ile Ile Ser Tyr Val Ser Pro  
20 25 30  
Ala Glu Arg Glu Xaa Gly Arg Gly Met Ala Ala Pro Lys Leu Ala Thr  
35 40 45  
Leu Ala Leu Ala Val Leu Leu Ala Ala Thr Val Val Ala Pro Pro Ala  
50 55 60  
Ala Val Arg Ala Ala Met Ser Cys Ser Thr Val Tyr Ser Thr Leu Met  
65 70 75 80  
Pro Cys Leu Pro Phe Val Gln Met Gly Gly Ala Met Pro Pro Gln Pro  
85 90 95  
Cys Cys Gly Gly Ile Arg Ser Leu Leu Gln Gln Pro Thr Thr Pro Pro  
100 105 110  
Thr Ala Ala Leu Ser Ala Ala Ala Ser Arg Thr Ser Pro Thr Ala Pro  
115 120 125  
Thr Gly Ala Ala Pro Thr Ser Ala Xaa Pro Pro Arg Cys Pro Ala Ser  
130 135 140  
Ala Ala Ser Pro Cys Arg Thr Arg Ser Ala Pro Thr Leu Thr Ala Thr  
145 150 155 160  
Arg Leu Ile Lys

(2) INFORMATION FOR SEQ ID NO:3749:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 124 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..124

(D) OTHER INFORMATION: / Ceres Seq. ID 1578045

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3749:

Met Ala Ala Pro Lys Leu Ala Thr Leu Ala Leu Ala Val Leu Leu Ala  
1 5 10 15  
Ala Thr Val Val Ala Pro Pro Ala Ala Val Arg Ala Ala Met Ser Cys  
20 25 30  
Ser Thr Val Tyr Ser Thr Leu Met Pro Cys Leu Pro Phe Val Gln Met  
35 40 45  
Gly Gly Ala Met Pro Pro Gln Pro Cys Cys Gly Gly Ile Arg Ser Leu  
50 55 60  
Leu Gln Gln Pro Thr Thr Pro Pro Thr Ala Ala Leu Ser Ala Ala Ala  
65 70 75 80  
Ser Arg Thr Ser Pro Thr Ala Pro Thr Gly Ala Ala Pro Thr Ser Ala  
85 90 95  
Xaa Pro Pro Arg Cys Pro Ala Ser Ala Ala Ser Pro Cys Arg Thr Arg  
100 105 110  
Ser Ala Pro Thr Leu Thr Ala Thr Arg Leu Ile Lys  
115 120

(2) INFORMATION FOR SEQ ID NO:3750:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 667 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3750:

(2) INFORMATION FOR SEQ ID NO:3751:

(A) LENGTH: 176 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptid

(ix) FEATURE:

(1X) FEATURE.

(A) NAME/KEY: peptide

(B) LOCATION: 1..176

(D) OTHER INFORMATION: / Ceres Seq. ID 1578057

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3751:

(2) INFORMATION FOR SEQ ID NO:3752:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 136 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(D) OTHER INFORMATION: / Ceres Seq. ID 1578058

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 1																
1	Val	His	Pro	Tyr	Phe	Arg	His	Asn	Ser	Gln	Pro	Glu	Pro	Pro	Lys	
				5				10						15		
Pro	Glu	Ala	Ala	Gly	Ala	Pro	Leu	Thr	Leu	Leu	Arg	Leu	Arg	Ser	Arg	
			20					25					30			
Lys	Arg	Lys	Met	Ser	Tyr	Tyr	Gly	Gln	Gln	Pro	Pro	Val	Gly	Val	Pro	
		35					40					45				
Pro	Gln	Gln	Gly	Tyr	Pro	Gly	Lys	Asp	Gly	Tyr	Pro	Pro	Ala	Gly	Tyr	
	50					55					60					
Pro	Ala	Gly	Arg	Leu	Pro	Pro	Ala	Gly	Ala	Gly	Leu	Pro	Ala	Ala	Gly	
65					70					75					80	
Leu	Pro	Thr	Ala	Gly	Leu	Pro	Ala	Ala	Val	Arg	Ala	Ala	Ala	Ser	Thr	
				85					90					95		
Ala	Ala	Ala	Glu	Gln	Arg	Ala	Phe	Leu	His	Gly	Arg	Met	Leu	Gly	Cys	
			100					105					110			
Pro	Leu	Leu	Leu	Xaa	Pro	Pro	Gly	Arg	Leu	Leu	Leu	Thr	Asp	Pro	Ser	
		115					120					125				
Cys	Arg	Val	Gln	His	Gly	Cys	Lys									
	130						135									

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..101

(D) OTHER INFORMATION: / Ceres Seq. ID 1578059

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3753:

[illegible]

(2) INFORMATION FOR SEQ ID NO:3754:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 678 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..678

(D) OTHER INFORMATION: / Ceres Seq. ID 1578070

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3754:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3734:  
atgccacaac aagaccacaga acccacaatc tttctttgtg cacagaaaga agaaagaacc  
tatggcacag tcgtgctcgc cctccgtcaa gctgctggtt ctggttggtc tccctgcgct

60  
120

(2) INFORMATION FOR SEQ ID NO:3755:

(A) LENGTH: 169 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..169

(D) OTHER INFORMATION: / Ceres Seq. ID 1578071

[illegible]

### (i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 166 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..166

(D) OTHER INFORMATION: / Ceres Seq. ID 1578073

Cys	His	Asn	Lys	Thr	Gln	Asn	Pro	Gln	Ser	Phe	Phe	Val	His	Arg	Lys
1				5					10					15	
Lys	Lys	Glu	Pro	Met	Ala	Gln	Ser	Ser	Ser	Ala	Ser	Val	Lys	Leu	Leu
			20					25					30		
Val	Leu	Val	Val	Leu	Pro	Ala	Leu	Leu	Leu	Phe	Leu	Val	Gln	Ala	Gln

Arg	His	Ala	Pro	Ser	Glu	His	Ala	Ile	Asn	Gly	Arg	Arg	Tyr	Ala	Leu
1				5					10					15	
Glu	Leu	Gln	Met	Val	His	Gln	Ser	Asp	Thr	Asn	Arg	Tyr	Ala	Val	Val
			20					25					30		
Ser	Gln	Leu	Tyr	Arg	Ile	Ser	Arg	Arg	Arg	Pro	Asp	Arg	Thr	Ile	His

35 40 45  
Arg Leu Glu Arg Tyr Ile Arg Arg Ile Ile Ala Arg Arg Lys Asn His  
50 55 60  
Glu Glu Leu Ile Asp Glu Glu Val Asp Pro Arg Arg Pro Val Ser Arg  
65 70 75 80  
Ser Thr Ala Tyr Tyr Lys Tyr Thr Gly Ser Phe Thr Thr Pro Pro Cys  
85 90 95  
Thr Glu Gly Val Thr Trp Val Val Ala His Gln Thr Arg Arg Val Thr  
100 105 110  
Arg Arg Gln Val Arg Leu Leu Arg Asn Xaa Ser Thr Thr Ala Pro Gly  
115 120 125  
Ala Thr Gly Gly His Ser Arg Lys Pro Thr Ala Arg Ala Ile Thr Phe  
130 135 140  
Tyr Tyr Xaa Ser Pro Ala His Gly Arg Gly Ala Asn Gly Asp  
145 150 155

(2) INFORMATION FOR SEQ ID NO:3759:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..139

(D) OTHER INFORMATION: / Ceres Seq. ID 1578085

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3759:

Met Val His Gln Ser Asp Thr Asn Arg Tyr Ala Val Val Ser Gln Leu  
1 5 10 15  
Tyr Arg Ile Ser Arg Arg Arg Pro Asp Arg Thr Ile His Arg Leu Glu  
20 25 30  
Arg Tyr Ile Arg Arg Ile Ile Ala Arg Arg Lys Asn His Glu Glu Leu  
35 40 45  
Ile Asp Glu Glu Val Asp Pro Arg Arg Pro Val Ser Arg Ser Thr Ala  
50 55 60  
Tyr Tyr Lys Tyr Thr Gly Ser Phe Thr Thr Pro Cys Thr Glu Gly  
65 70 75 80  
Val Thr Trp Val Val Ala His Gln Thr Arg Arg Val Thr Arg Arg Gln  
85 90 95  
Val Arg Leu Leu Arg Asn Xaa Ser Thr Thr Ala Pro Gly Ala Thr Gly  
100 105 110  
Gly His Ser Arg Lys Pro Thr Ala Arg Ala Ile Thr Phe Tyr Tyr Xaa  
115 120 125  
Ser Pro Ala His Gly Arg Gly Ala Asn Gly Asp  
130 135

(2) INFORMATION FOR SEQ ID NO:3760:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 951 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..951

(D) OTHER INFORMATION: / Ceres Seq. ID 1578086

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3760:

acccatgttc ctgttccac actcgactgt catcctgtga tatccgctcg ccagtcgccca 60  
ctccgtttcg gcattccgcc tcttcccgac acacctcttt aactcgcttc cgtttccaaa 120  
aaaatgctcc agttaattta atccagacga ggaatcgctt cgccgcggat ctctccgctc 180  
gccgacaaga cccgctatcg gctccggcgg gaagactcgc actacggtgg ggcgcgctcg 240

cgccgctcgg cactgggctc gtcgggttcga cgttcgcttg tggaggtcgt cggggccagc 300  
ggtgcccggg caatgcgggc agtttgtgga gccgtctgar gcgcttggt gggatctgag 360  
ggtgtcaggt arggggcgcg asragctctg tcgggtggga rttggtggtg gttgtagcgt 420  
agggcGcgtc gcgtgttttg ctgccgggat ggagcacgta gttgggggca agttcaagct 480  
tgggaagaag atcgggagcg gatcatttgg ggagctctac ctccggcgtga acatgcagag 540  
tgacgaggag gtggctgtca aactggtatt ccacgaacat cttccacgtg atttttgtgt 600  
ccactatcca tgtcttggtg aacagttctg tgtttagacct tctccaaccg cccccccaa 660  
acctcccctc acccttgcta ttgctaccga cctactgtgt actatggggg gaagtatctt 720  
ttaggatgat gtagtaaaat ataatagaaa atacagatat gaggaaaaaa tatgggggaa 780  
atggttgagg atggtcttag gagttaactt tagtcggagt cactgaaatc tatagttagc 840  
ctaattgctt gcaggagcta atgagcctgt agcactctga agtgagggtg tcaatgctga 900  
aaagcaccga ctggaaactc atctcttggt tgttctgatt ggattattct c

(2) INFORMATION FOR SEQ ID NO:3761:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..118
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578087

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3761:

Pro Cys Ser Cys Ser His Thr Arg Leu Ser Ser Cys Asp Ile Arg Ser  
1 5 10 15  
Pro Val Ala Thr Pro Phe Arg His Ser Ala Ser Ser Arg His Thr Ser  
20 25 30  
Leu Thr Arg Phe Arg Phe Gln Lys Asn Ala Pro Val Asn Leu Ile Gln  
35 40 45  
Thr Arg Asn Arg Leu Ala Ala Asp Leu Ser Ala Arg Arg Gln Asp Pro  
50 55 60  
Leu Ser Ala Pro Ala Gly Arg Leu Ala Leu Arg Trp Gly Ala Ser Pro  
65 70 75 80  
Pro Leu Gly Thr Trp Leu Val Gly Ser Thr Phe Ala Cys Gly Gly Arg  
85 90 95  
Arg Gly Gln Arg Cys Arg Gly Asn Ala Val Ser Leu Trp Ser Arg Leu  
100 105 110  
Xaa Arg Leu Ala Gly Ile  
115

(2) INFORMATION FOR SEQ ID NO:3762:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..91
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578088

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3762:

Met Glu His Val Val Gly Gly Lys Phe Lys Leu Gly Lys Lys Ile Gly  
1 5 10 15  
Ser Gly Ser Phe Gly Glu Leu Tyr Leu Gly Val Asn Met Gln Ser Asp  
20 25 30  
Glu Glu Val Ala Val Lys Leu Val Phe His Glu His Leu Pro Arg Asp  
35 40 45  
Phe Cys Val His Tyr Pro Cys Leu Gly Glu Gln Phe Cys Val Arg Pro  
50 55 60  
Ser Pro Thr Ala Pro Pro Lys Pro Pro Leu Thr Leu Ala Ile Ala Thr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3765:

Met Ala Arg Arg Asn Ile Gly Val Ala Val Asp Phe Ser Ser Cys Ser  
1 5 10 15  
Lys Ala Ala Leu Arg Trp Ala Ser Thr Asn Leu Ala Arg Asn Gly Asp  
20 25 30  
Arg Leu Ile Leu Ile His Val Asn Ser Ser Cys Gln Asn Glu Arg Gly  
35 40 45  
Ala Val His Leu Trp Glu Gln Ser Gly Ser Pro Leu Ile Pro Leu Ala  
50 55 60  
Glu Phe Ser Asp Val Ala Arg Thr Tyr Gly Val Ser Pro Asp Lys Glu  
65 70 75 80  
Thr Ile Glu Ile Leu Thr Gln Ala Ala Asn His Arg Gly Ile Glu Val  
85 90 95  
Phe Ala Lys Val Phe Tyr Gly Asp Pro Ala Lys Lys Leu Tyr Glu Ala  
100 105 110  
Ala Asp Met Val Pro Leu Ser Cys Met Val Val Gly Ser Arg Gly Leu  
115 120 125  
Ser Thr Leu Lys Arg Ala Leu Met Gly Ser Val Ser Thr Tyr Val Val  
130 135 140  
Asn His Ala Ala Cys Pro Val Thr Val Val Lys Glu Met Val  
145 150 155

(2) INFORMATION FOR SEQ ID NO:3766:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 630 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..630
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3766:

atgatggtgt	caagctttgg	gatcttcgga	aattaagaaa	ttttaggacc	ttctctccct	60
atgattcaga	tacgccaaca	aatactgtgg	aatttgattt	tagtggAaaa	ctatcttgcc	120
attggtggtt	cagatataag	ggtctaccaa	gtagctaattg	ttaaggccga	atggaatctc	180
atcaagacat	taccagattt	atctggaaca	gggaaagtaa	cttcggtaaa	gttcggagca	240
gatgctaagt	acatagccgt	aggttctatg	gaccgcaatc	tacggatatt	tggcctccct	300
ggagacgacc	aaatggagga	atcaaccaca	gcggcagagt	gaggaaaatc	catggttatc	360
agcattcatt	gtctatttgg	ccactgtcga	gaggtaatcc	acggagacac	accgctggcg	420
cccgtgacac	ttggcctggt	tggttacttg	ctaaaaattg	ctacacattt	ttgtgccaca	480
cttgtttaag	cacacttggt	taagggtgtt	aagggttatc	gctcaaattc	cgcgtcacag	540
cttgtttgtc	actcataaga	gaatattgcc	tgtaaaatga	gagtctgaac	gacttgcccc	600
taaaatgaga	tggaaaatca	gttagctgct				

(2) INFORMATION FOR SEQ ID NO:3767:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..51
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3767:

Asp Gly Val Lys Leu Trp Asp Leu Arg Lys Leu Arg Asn Phe Arg Thr  
1 5 10 15  
Phe Ser Pro Tyr Asp Ser Asp Thr Pro Thr Asn Thr Val Glu Phe Asp  
20 25 30  
Phe Ser Gly Lys Leu Ser Cys His Trp Trp Phe Arg Tyr Lys Gly Leu  
35 40 45



Pro Ser Ser  
50

(2) INFORMATION FOR SEQ ID NO:3768:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..93
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578132

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3768:

Met Ile Gln Ile Arg Gln Gln Ile Leu Trp Asn Leu Ile Leu Val Glu  
1 5 10 15  
Asn Tyr Leu Ala Ile Gly Gly Ser Asp Ile Arg Val Tyr Gln Val Ala  
20 25 30  
Asn Val Lys Ala Glu Trp Asn Leu Ile Lys Thr Leu Pro Asp Leu Ser  
35 40 45  
Gly Thr Gly Lys Val Thr Ser Val Lys Phe Gly Ala Asp Ala Lys Tyr  
50 55 60  
Ile Ala Val Gly Ser Met Asp Arg Asn Leu Arg Ile Phe Gly Leu Pro  
65 70 75 80  
Gly Asp Asp Gln Met Glu Glu Ser Thr Thr Ala Ala Glu  
85 90

(2) INFORMATION FOR SEQ ID NO:3769:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 876 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..876
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3769:

atcagccctc acgcatgttg cagcgatg gccggatctg aggttgagtg tgcgatcccg 60  
ttggcatatc gacaaagttt ggtgggtccc accgcagatc ccggcccggt aggtactagt 120  
tccgcggtcc cccctcccta gtctccgggg aggaccgtct cggccgcgag agtgcgctcg 180  
tcgactccac tcagctctct cgctccctct cctcccccaa ggccccagag acaggcagcc 240  
ggcgaggccc gccgcgcgca aGcaatggat ttcaaggggt tctgggagtc cagattcggg 300  
ggcaagaagg aacccgagcc ggagcagaac gggcacgcca acgggggtcca gaaccagaag 360  
aggacctccg atctggcggg ctacgagcag ttcgagcagc aggccaggca gaccaggtc 420  
cgagccgcg cgattcgcga cggagacgct gatgtcataa gccccttcta ccttcatttg 480  
agtcagctga aatgcgtaat ctgcgagaga cattgttgag ggatattatt cgcgggagcc 540  
cagatgtgaa atgggagagc atcaaaggac tggaaaatgc aaaacgcctt ctaaaagagg 600  
ctgttgtcat gcccataaag taccctaaat acttcactgg tctcctttct ccatggaaag 660  
gcattctact ttttggcccc ccagggacag gaaagacaat gctggcaaaa gcggtcgcta 720  
ctgagtgcaa aaccaccttc ttcaacattt cagcatcatc aattgtcagc aaatggcggtg 780  
gagattcaga gaagcttgtc aaagttctgt ttgagcttgc taggcatcat gcaccatcca 840  
caatattcct tgatgaaata gatgctatca tcagcc

(2) INFORMATION FOR SEQ ID NO:3770:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..84
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578151

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3770:

Met Asp Phe Lys Gly Phe Trp Glu Ser Arg Phe Gly Gly Lys Lys Glu  
1 5 10 15  
Pro Glu Pro Glu Gln Asn Gly His Ala Asn Gly Val Gln Asn Gln Lys  
20 25 30  
Arg Thr Ser Asp Leu Ala Val Tyr Glu Gln Phe Glu Gln Ala Arg  
35 40 45  
Gln Thr Gln Val Arg Ala Ala Ile Arg Asp Gly Asp Ala Asp Val  
50 55 60  
Ile Ser Pro Phe Tyr Leu His Leu Ser Gln Leu Lys Cys Val Ile Ser  
65 70 75 80  
Gln Arg His Cys

(2) INFORMATION FOR SEQ ID NO:3771:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..128
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3771:

Met Arg Asn Leu Ala Glu Thr Leu Leu Arg Asp Ile Ile Arg Gly Ser  
1 5 10 15  
Pro Asp Val Lys Trp Glu Ser Ile Lys Gly Leu Glu Asn Ala Lys Arg  
20 25 30  
Leu Leu Lys Glu Ala Val Val Met Pro Ile Lys Tyr Pro Lys Tyr Phe  
35 40 45  
Thr Gly Leu Leu Ser Pro Trp Lys Gly Ile Leu Leu Phe Gly Pro Pro  
50 55 60  
Gly Thr Gly Lys Thr Met Leu Ala Lys Ala Val Ala Thr Glu Cys Lys  
65 70 75 80  
Thr Thr Phe Phe Asn Ile Ser Ala Ser Ser Ile Val Ser Lys Trp Arg  
85 90 95  
Gly Asp Ser Glu Lys Leu Val Lys Val Leu Phe Glu Leu Ala Arg His  
100 105 110  
His Ala Pro Ser Thr Ile Phe Leu Asp Glu Ile Asp Ala Ile Ile Ser  
115 120 125

(2) INFORMATION FOR SEQ ID NO:3772:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..89
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3772:

Met Pro Ile Lys Tyr Pro Lys Tyr Phe Thr Gly Leu Leu Ser Pro Trp  
1 5 10 15  
Lys Gly Ile Leu Leu Phe Gly Pro Pro Gly Thr Gly Lys Thr Met Leu

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20 25 30  
Ala Lys Ala Val Ala Thr Glu Cys Lys Thr Thr Phe Phe Asn Ile Ser  
35 40 45  
Ala Ser Ser Ile Val Ser Lys Trp Arg Gly Asp Ser Glu Lys Leu Val  
50 55 60  
Lys Val Leu Phe Glu Leu Ala Arg His His Ala Pro Ser Thr Ile Phe  
65 70 75 80  
Leu Asp Glu Ile Asp Ala Ile Ile Ser  
85

(2) INFORMATION FOR SEQ ID NO:3773:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 776 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..776
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3773:

aaaagaatat ttagttgaag caaaattcaa gaaacttgaa gaagaggcct gcaatatttt 60  
gtcctcgagt tctggtgaaa caatgaaaaa caacattgat gttttggttt gcaaagctga 120  
atactaccac cagagtggag agtacaaaaa gtgttttAaa actcacatcc tcgttacttg 180  
agagagaccc tttccatcta aagtgcacat tagttcattt ggcaactgca atggagcttg 240  
gtcattccaa tgatctttat cttttagcat gcaacttagt gaaggattat cctgaaaaag 300  
ctctttcatg gtttgctgtc ggttgctatt actactgtat taagaagtat gatcaagcgc 360  
gaagatactt cggcaaagct acaggttttag atgggacgtt tcctcctgct tggattggta 420  
caggcattgc ctatgctgct caagaggaag gtgaccaagc aatggctgca tttcggacgg 480  
cagctcggtt atttcctgga tGgtcatctg ccaactttat acatgggcat gcaatatgtg 540  
cgaatgcama atttcaaacT ttgcagagca gttcttcaca caagcAaaat ccatctgccc 600  
atctgatcca cttattttaca atgagttggg ggttggtgcg tataatatga aggagtaccg 660  
aaaagcagtt cagttgtttg agttaacatt ggaccatact tcatcctctc tgaatgaaat 720  
gtgggaacca acattgggtga atcttgggca tgcacttcgg aaactcaagg aatatc

(2) INFORMATION FOR SEQ ID NO:3774:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..183
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3774:

Met Phe Trp Phe Ala Lys Leu Asn Thr Thr Thr Arg Val Glu Ser Thr  
1 5 10 15  
Lys Ser Val Leu Lys Leu Thr Ser Ser Leu Leu Glu Arg Asp Pro Phe  
20 25 30  
His Leu Lys Cys Thr Leu Val His Leu Ala Thr Ala Met Glu Leu Gly  
35 40 45  
His Ser Asn Asp Leu Tyr Leu Leu Ala Cys Asn Leu Val Lys Asp Tyr  
50 55 60  
Pro Glu Lys Ala Leu Ser Trp Phe Ala Val Gly Cys Tyr Tyr Tyr Cys  
65 70 75 80  
Ile Lys Lys Tyr Asp Gln Ala Arg Arg Tyr Phe Gly Lys Ala Thr Gly  
85 90 95  
Leu Asp Gly Thr Phe Pro Pro Ala Trp Ile Gly Thr Gly Ile Ala Tyr  
100 105 110  
Ala Ala Gln Glu Glu Gly Asp Gln Ala Met Ala Ala Phe Arg Thr Ala

115 120 125  
Ala Arg Leu Phe Pro Gly Trp Ser Ser Ala Asn Phe Ile His Gly His  
130 135 140  
Ala Ile Cys Ala Asn Ala Xaa Phe Gln Thr Leu Gln Ser Ser Ser Ser  
145 150 155 160  
His Lys Gln Asn Pro Ser Ala His Leu Ile His Leu Phe Thr Met Ser  
165 170 175  
Trp Gly Leu Leu Arg Ile Ile  
180

(2) INFORMATION FOR SEQ ID NO:3775:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..139
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3775:

Met Glu Leu Gly His Ser Asn Asp Leu Tyr Leu Leu Ala Cys Asn Leu  
1 5 10 15  
Val Lys Asp Tyr Pro Glu Lys Ala Leu Ser Trp Phe Ala Val Gly Cys  
20 25 30  
Tyr Tyr Tyr Cys Ile Lys Lys Tyr Asp Gln Ala Arg Arg Tyr Phe Gly  
35 40 45  
Lys Ala Thr Gly Leu Asp Gly Thr Phe Pro Pro Ala Trp Ile Gly Thr  
50 55 60  
Gly Ile Ala Tyr Ala Ala Glu Glu Gly Asp Gln Ala Met Ala Ala  
65 70 75 80  
Phe Arg Thr Ala Ala Arg Leu Phe Pro Gly Trp Ser Ser Ala Asn Phe  
85 90 95  
Ile His Gly His Ala Ile Cys Ala Asn Ala Xaa Phe Gln Thr Leu Gln  
100 105 110  
Ser Ser Ser Ser His Lys Gln Asn Pro Ser Ala His Leu Ile His Leu  
115 120 125  
Phe Thr Met Ser Trp Gly Leu Leu Arg Ile Ile  
130 135

(2) INFORMATION FOR SEQ ID NO:3776:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..92
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578157

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3776:

Met Val Ile Cys Gln Leu Tyr Thr Trp Ala Cys Asn Met Cys Glu Cys  
1 5 10 15  
Xaa Ile Ser Asn Phe Ala Glu Gln Phe Thr Gln Ala Lys Ser Ile  
20 25 30  
Cys Pro Ser Asp Pro Leu Ile Tyr Asn Glu Leu Gly Val Val Ala Tyr  
35 40 45  
Asn Met Lys Glu Tyr Arg Lys Ala Val Gln Leu Phe Glu Leu Thr Leu  
50 55 60  
Asp His Thr Ser Ser Ser Leu Asn Glu Met Trp Glu Pro Thr Leu Val  
65 70 75 80

Asn Leu Gly His Ala Leu Arg Lys Leu Lys Glu Tyr  
85 90

(2) INFORMATION FOR SEQ ID NO:3777:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 654 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..654
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3777:

tyatgctgat	acagttggag	acttgggata	tgcacagag	cttggaaact	atgcagagta	60
tagtggtgct	cctaagtgg	aggaggttct	gaattattct	agagttgttc	ttgattgtgc	120
aactgctgat	cctgatggcc	gcaagagagc	ccttctcatt	ggaggtggca	tagctaactt	180
cactgatggt	gctaccacat	tcaatggcat	catccgagcc	ttaagggaga	aggaatccaa	240
gttgaaggct	tcaagaatgc	acatttatgt	ccgccgaggt	ggtccaaatt	accaatctgg	300
actggctaaa	atgcgtaaGc	ttggtgcaga	actcggcggt	ccaattgagg	tgtatgggcc	360
agaagcgact	atgactggaa	tctgcaaaca	agcaattgaa	tgcacatggt	ctgcagcgta	420
atcagagcgt	aGcTctgNgg	tagtttggga	tctgcaaaca	cgcaattgaa	tgtgtcatgg	480
actcagcata	aatgagagat	ggatagtagt	tgcattatat	agttcacaca	tgggtgtttct	540
gttttttgtt	tcagatatgt	tgtagcgtgt	tgtttgaacg	aaaccttcac	agatcattac	600
tgcaaagaaa	ttgctgtgtg	ttaaaataaa	ttcaaagtct	agttttgtgc	cttt	

(2) INFORMATION FOR SEQ ID NO:3778:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..139
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3778:

Xaa	Ala	Asp	Thr	Val	Gly	Asp	Leu	Gly	Tyr	Ala	Ser	Glu	Leu	Gly	Asn	
1				5				10						15		
Tyr	Ala	Glu	Tyr	Ser	Gly	Ala	Pro	Asn	Glu	Glu	Glu	Val	Leu	Asn	Tyr	
				20				25						30		
Ser	Arg	Val	Val	Leu	Asp	Cys	Ala	Thr	Ala	Asp	Pro	Asp	Gly	Arg	Lys	
				35				40						45		
Arg	Ala	Leu	Leu	Ile	Gly	Gly	Ile	Ala	Asn	Phe	Thr	Asp	Val	Ala		
				50				55						60		
Thr	Thr	Phe	Asn	Gly	Ile	Arg	Ala	Leu	Arg	Glu	Lys	Glu	Ser	Lys		
				65				70						75		
Leu	Lys	Ala	Ser	Arg	Met	His	Ile	Tyr	Val	Arg	Arg	Gly	Gly	Pro	Asn	
				85				90						95		
Tyr	Gln	Ser	Gly	Leu	Ala	Lys	Met	Arg	Lys	Leu	Gly	Ala	Glu	Leu	Gly	
				100				105						110		
Val	Pro	Ile	Glu	Val	Tyr	Gly	Pro	Glu	Ala	Thr	Met	Thr	Gly	Ile	Cys	
				115				120						125		
Lys	Gln	Ala	Ile	Glu	Cys	Ile	Met	Ala	Ala	Ala						
				130				135								

(2) INFORMATION FOR SEQ ID NO:3779:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 722 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3779:

(2) INFORMATION FOR SEQ ID NO:3780:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..114

(D) OTHER INFORMATION: / Ceres Seq. ID 1578191

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3780:

[illegible]

(2) INFORMATION FOR SEQ ID NO:3781:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..120

(D) OTHER INFORMATION: / Ceres Seq. ID 1578192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3781:

(x1) SEQUENCE DESCRIPTION: Seq 1

Arg	Thr	Lys	Val	Arg	Ser	Val	Gln	Asp	Gln	Thr	Xaa	Arg	Lys	Arg	Gly
1				5			10							15	

(A) NAME/KEY: -

	1990-1991	1991-1992	1992-1993	1993-1994	1994-1995	1995-1996	1996-1997	1997-1998	1998-1999	1999-2000	2000-2001	2001-2002	2002-2003	2003-2004	2004-2005	2005-2006	2006-2007	2007-2008	2008-2009	2009-2010	2010-2011	2011-2012	2012-2013	2013-2014	2014-2015	2015-2016	2016-2017	2017-2018	2018-2019	2019-2020	2020-2021	2021-2022	2022-2023	2023-2024	2024-2025	2025-2026	2026-2027	2027-2028	2028-2029	2029-2030	2030-2031	2031-2032	2032-2033	2033-2034	2034-2035	2035-2036	2036-2037	2037-2038	2038-2039	2039-2040	2040-2041	2041-2042	2042-2043	2043-2044	2044-2045	2045-2046	2046-2047	2047-2048	2048-2049	2049-2050	2050-2051	2051-2052	2052-2053	2053-2054	2054-2055	2055-2056	2056-2057	2057-2058	2058-2059	2059-2060	2060-2061	2061-2062	2062-2063	2063-2064	2064-2065	2065-2066	2066-2067	2067-2068	2068-2069	2069-2070	2070-2071	2071-2072	2072-2073	2073-2074	2074-2075	2075-2076	2076-2077	2077-2078	2078-2079	2079-2080	2080-2081	2081-2082	2082-2083	2083-2084	2084-2085	2085-2086	2086-2087	2087-2088	2088-2089	2089-2090	2090-2091	2091-2092	2092-2093	2093-2094	2094-2095	2095-2096	2096-2097	2097-2098	2098-2099	2099-2100	2100-2101	2101-2102	2102-2103	2103-2104	2104-2105	2105-2106	2106-2107	2107-2108	2108-2109	2109-2110	2110-2111	2111-2112	2112-2113	2113-2114	2114-2115	2115-2116	2116-2117	2117-2118	2118-2119	2119-2120	2120-2121	2121-2122	2122-2123	2123-2124	2124-2125	2125-2126	2126-2127	2127-2128	2128-2129	2129-2130	2130-2131	2131-2132	2132-2133	2133-2134	2134-2135	2135-2136	2136-2137	2137-2138	2138-2139	2139-2140	2140-2141	2141-2142	2142-2143	2143-2144	2144-2145	2145-2146	2146-2147	2147-2148	2148-2149	2149-2150	2150-2151	2151-2152	2152-2153	2153-2154	2154-2155	2155-2156	2156-2157	2157-2158	2158-2159	2159-2160	2160-2161	2161-2162	2162-2163	2163-2164	2164-2165	2165-2166	2166-2167	2167-2168	2168-2169	2169-2170	2170-2171	2171-2172	2172-2173	2173-2174	2174-2175	2175-2176	2176-2177	2177-2178	2178-2179	2179-2180	2180-2181	2181-2182	2182-2183	2183-2184	2184-2185	2185-2186	2186-2187	2187-2188	2188-2189	2189-2190	2190-2191	2191-2192	2192-2193	2193-2194	2194-2195	2195-2196	2196-2197	2197-2198	2198-2199	2199-2200	2200-2201	2201-2202	2202-2203	2203-2204	2204-2205	2205-2206	2206-2207	2207-2208	2208-2209	2209-2210	2210-2211	2211-2212	2212-2213	2213-2214	2214-2215	2215-2216	2216-2217	2217-2218	2218-2219	2219-2220	2220-2221	2221-2222	2222-2223	2223-2224	2224-2225	2225-2226	2226-2227	2227-2228	2228-2229	2229-2230	2230-2231	2231-2232	2232-2233	2233-2234	2234-2235	2235-2236	2236-2237	2237-2238	2238-2239	2239-2240	2240-2241	2241-2242	2242-2243	2243-2244	2244-2245	2245-2246	2246-2247	2247-2248	2248-2249	2249-2250	2250-2251	2251-2252	2252-2253	2253-2254	2254-2255	2255-2256	2256-2257	2257-2258	2258-2259	2259-2260	2260-2261	2261-2262	2262-2263	2263-2264	2264-2265	2265-2266	2266-2267	2267-2268	2268-2269	2269-2270	2270-2271	2271-2272	2272-2273	2273-2274	2274-2275	2275-2276	2276-2277	2277-2278	2278-2279	2279-2280	2280-2281	2281
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(D) OTHER INFORMATION: / Ceres Seq. ID 1578201

(X1) SEQUENCE DESCRIPTION: Seq 1: Reverse						
atgagtctat	ttcagcggct	tgcggttctc	tgtattttca	tattatcgaa	accctcgtct	60
acatctccgt	ttcgacgaag	ccaaatctgt	cgtgttttat	aatcccaaaa	gtctccacct	120
aagtcaccga	ctcgatacgg	caagatcgac	agagagaccg	acgcgcgcggc	agatccaag	180
ctcaccggag	agggggaaga	gggcgaccga	agcggcgatg	ggtttcatca	tggacttcgc	240
ggagaatctg	atcctccgtc	tgatggagga	cccgacaag	cgcgaccCag	gttcggcggg	300
agcatgtcta	caagatgaag	gagcggtgcg	agcgcactaa	ggcgcgtgg	agcctccctc	360
tgcgcccCta	cggcttctgg	accttcgacc	gcttcaactc	gcagctctcc	tgggatcccc	420
agatcagcca	ggccgcgcgc	Cgtcgggacc	cctacgacga	cctcatcgcc	cgccactctg	480
gctcgcgcgc	gtcttctctga	acacccggtt	cgatctttgc	ccagaaggtc	tacttgggGc	540
atcaataaga	aactctttcc	cctcaaactg	attgtggttc	catcctcttc	tgtctggaaa	600
atgttgtcac	caaactaacc	tatttctgt	tccagtttgg	catggaagta	taagttgtgt	660
acttctattc	tcaagttggt	gtctttgtat	tatgaaatgt	ttccaataat	cagcagtttt	720
tgaatgatgg	tcgtggatcc	g				

Met	Gly	Phe	Ile	Met	Asp	Phe	Ala	Glu	Asn	Leu	Ile	Leu	Arg	Leu	Met
1				5					10					15	
Glu	Asp	Pro	Asp	Lys	Arg	Asp	Pro	Gly	Ser	Ala	Gly	Ala	Cys	Leu	Gln
			20					25					30		
Asp	Glu	Gly	Ala	Val	Arg	Ala	His								
		35				40									

(XI) SEQUENCE DESCRIPTION															
Met	Lys	Glu	Arg	Cys	Glu	Arg	Thr	Lys	Ala	Ala	Trp	Ser	Leu	Pro	Leu
1				5					10					15	
Arg	Pro	Tyr	Gly	Phe	Trp	Thr	Phe	Asp	Arg	Phe	Asn	Ser	Gln	Leu	Ser
			20					25					30		
Trp	Asp	Pro	Gln	Ile	Ser	Gln	Ala	Gly	Arg	Arg	Asp		Pro	Tyr	Asp
		35				40					45				
Asp	Leu	Ile	Ala	Arg	His	Ser	Gly	Ser	Pro	Pro	Ser	Ser			
	50					55					60				

## (ii) MOLECULE TYPE: peptide



(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..40
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3786:

Met Leu Ser Pro Asn Tyr Pro Ile Ser Cys Ser Ser Leu Ala Trp Lys  
1                   5                   10                   15  
Tyr Lys Leu Cys Thr Ser Ile Leu Lys Leu Leu Ser Leu Tyr Tyr Glu  
                  20                   25                   30  
Met Phe Pro Ile Ile Ser Ser Phe  
                  35                   40

(2) INFORMATION FOR SEQ ID NO:3787:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 765 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..765
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578239

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3787:

gacaagcaag aacagctgtc gatccaattg tcacttgctc tccctccaac aagctaatta       60  
aggccggtca tccctcttct agctcgtttc attatccatg gcggaggaga agcaccacca       120  
ccaccacctg ttccaccaca agaaggacga ggagcaggag gagcagctcg ccggcgsgsg       180  
tacgGcgagt ccgccgagta cacggaggcc acggtgacgg aggtcgtgtc cacgggcgag       240  
aacgagtacg acgagtacaa gaaggaggag aagcagcaca agcacaagca gcacctcggc       300  
gaggccggcg ccattGccgc cggcgccctc gcactctacg agaagcacga ggcaaagaag       360  
gacccgagac acgcgcaccg ccacaagatc gaggaggagg tcgcggcggc ggcgggcgctc       420  
ggctccggcg gCttcgCtt ccacgagcac cacgagaaga agaaggacca caaggacgcc       480  
gaggaggccg gcggcgagaa gaagcaccac ttcttcggct gattgatcct cccgtatcgt       540  
cgtcccCtcc ccgtgtgCta cgcgtgcCgt gtgtgagagt gatatcgagc gccCgccgtg       600  
ttgtgcgcgc gtacgtatgt atgcgctcgt gtgatgcacg aataagcgtg gctacgtaat       660  
ctatogtatg tatacgtgtg tgtatgcatg tgcttgtgta tgatcgtggt acgaggaccg       720  
aaaaaatgta tgcaactctg atttacttac atgtttagtt gtttc

(2) INFORMATION FOR SEQ ID NO:3788:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..218
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3788:

Gln Ala Arg Thr Ala Val Asp Pro Ile Val Thr Cys Ser Pro Ser Asn  
1                   5                   10                   15  
Lys Leu Ile Lys Ala Gly His Pro Ser Ser Ser Ser Phe His Tyr Pro  
                  20                   25                   30  
Trp Arg Arg Arg Ser Thr Thr Thr Thr Cys Ser Thr Thr Arg Arg  
                  35                   40                   45  
Thr Arg Ser Arg Arg Ser Ser Ser Pro Ala Xaa Val Arg Arg Val Arg  
                  50                   55                   60  
Arg Val His Gly Gly His Gly Asp Gly Gly Arg Val His Gly Arg Glu  
65                   70                   75                   80  
Arg Val Arg Arg Val Gln Glu Gly Gly Glu Ala Ala Gln Ala Gln Ala  
                  85                   90                   95  
Ala Pro Arg Arg Gly Arg Arg His Arg Arg Arg Arg Leu Arg Thr Leu

100 105 110  
Arg Glu Ala Arg Gly Lys Glu Gly Pro Gly Ala Arg Ala Pro Pro Gln  
115 120 125  
Asp Arg Gly Gly Gly Arg Gly Gly Gly Gly Arg Arg Leu Arg Arg Leu  
130 135 140  
Arg Leu Pro Arg Ala Pro Arg Glu Glu Glu Gly Pro Gln Gly Arg Arg  
145 150 155 160  
Gly Gly Arg Arg Arg Glu Glu Ala Pro Leu Leu Arg Leu Ile Asp Pro  
165 170 175  
Pro Val Ser Ser Ser Pro Pro Arg Val Leu Arg Val Pro Cys Val Arg  
180 185 190  
Val Ile Ser Ser Ala Arg Arg Val Val Arg Ala Tyr Val Cys Met Arg  
195 200 205  
Ser Cys Asp Ala Arg Ile Ser Val Ala Thr  
210 215

(2) INFORMATION FOR SEQ ID NO:3789:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..822
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578247

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3789:

arggtccctg gctatcgaga gaactcgacg agttcatctc catcgtttgt gagagtttcg 60  
gttgggccag attgtcatat tcagcgctct gcctcgggtc caggcccagg gtgtactgaa 120  
agccagctct tgcccgcata tacacggccc cattttcagc ttgcccctcc agaaccgggt 180  
cctatctgtg gtgtgccaga cttcaagatg aggggaaaga agagtgatga gctcgaacct 240  
gtcgaatgctk gcgatgaaga tgatgatggt ggtgacgatg gggacgagga tggtgacttt 300  
ggggaggagg gtgaagagga cgtctcagaa ggggagggat atgacaacct aaagggcaat 360  
gagaccaaga agcaaagagg tgatcctgag gaaaatggtg aggaagatga ggaagaacca 420  
gaagatcagg aggggtggcg cgacgacgat gatgacgacg atgacgatga tgagaacggg 480  
gatgacgagg acgacgacaa tDgggggatga cgatgaggag ggtgtagatg aagaagacga 540  
tgaccaggac gaggatgagg aggaagatga tgatgaagac tcgctccagc ccccaaagaa 600  
gaggaagaag tgaagatctt ctgccgcttt agttaccgtg cgctgagttc tgcttggttt 660  
ttcgtcatat cctcgcatat caactttccc atagagagtt aagaaggatc cacacgttca 720  
gcagcacgtg tgggcttgta ggagctttat gatttgaggc aattagggac aactcttatg 780  
tcattgttgc ttgcttctgt ggagtcgaac agatgtttcg ct

(2) INFORMATION FOR SEQ ID NO:3790:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..169
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578248

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3790:

Xaa Val Pro Gly Tyr Arg Glu Asn Ser Thr Ser Ser Ser Pro Ser Phe  
1 5 10 15  
Val Arg Val Ser Val Gly Pro Asp Cys His Thr Gln Arg Pro Ala Ser  
20 25 30  
Val Ser Gly Pro Gly Cys Thr Glu Ser Gln Leu Leu Pro Ala Ser Thr  
35 40 45  
Arg Pro His Phe Gln Leu Ala Pro Pro Glu Pro Gly Pro Ile Cys Gly  
50 55 60

Val Pro Asp Phe Lys Met Arg Gly Lys Lys Ser Asp Glu Leu Glu Pro  
65 70 75 80  
Val Asp Ala Xaa Asp Glu Asp Asp Asp Gly Gly Asp Asp Gly Asp Glu  
85 90 95  
Asp Gly Asp Phe Gly Glu Glu Gly Glu Glu Asp Val Ser Glu Gly Glu  
100 105 110  
Gly Tyr Asp Asn Pro Lys Gly Asn Glu Thr Lys Lys Gln Arg Gly Asp  
115 120 125  
Pro Glu Glu Asn Gly Glu Glu Asp Glu Glu Glu Pro Glu Asp Gln Glu  
130 135 140  
Gly Gly Gly Asp Asp Asp Asp Asp Asp Asp Asp Asp Glu Asn Gly  
145 150 155 160  
Asp Asp Glu Asp Asp Asp Asn Xaa Gly  
165

(2) INFORMATION FOR SEQ ID NO:3791:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..128

(D) OTHER INFORMATION: / Ceres Seq. ID 1578249

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3791:

Met Ser Ser Asn Leu Ser Met Xaa Ala Met Lys Met Met Met Val Val  
1 5 10 15  
Thr Met Gly Thr Arg Met Val Thr Leu Gly Arg Arg Val Lys Arg Thr  
20 25 30  
Ser Gln Lys Gly Arg Asp Met Thr Thr Gln Arg Ala Met Arg Pro Arg  
35 40 45  
Ser Lys Glu Val Ile Leu Arg Lys Met Val Arg Lys Met Arg Lys Asn  
50 55 60  
Gln Lys Ile Arg Arg Val Ala Ala Thr Thr Met Met Thr Thr Met Thr  
65 70 75 80  
Met Met Arg Thr Gly Met Thr Arg Thr Thr Thr Xaa Gly Asp Asp Asp  
85 90 95  
Glu Glu Gly Val Asp Glu Glu Asp Asp Asp Gln Asp Glu Asp Glu Glu  
100 105 110  
Glu Asp Asp Asp Glu Asp Ser Leu Gln Pro Pro Lys Lys Arg Lys Lys  
115 120 125

(2) INFORMATION FOR SEQ ID NO:3792:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..122

(D) OTHER INFORMATION: / Ceres Seq. ID 1578250

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3792:

Met Xaa Ala Met Lys Met Met Met Val Val Thr Met Gly Thr Arg Met  
1 5 10 15  
Val Thr Leu Gly Arg Arg Val Lys Arg Thr Ser Gln Lys Gly Arg Asp  
20 25 30  
Met Thr Thr Gln Arg Ala Met Arg Pro Arg Ser Lys Glu Val Ile Leu

35 40 45  
Arg Lys Met Val Arg Lys Met Arg Lys Asn Gln Lys Ile Arg Arg Val  
50 55 60  
Ala Ala Thr Thr Met Met Thr Thr Met Thr Met Met Arg Thr Gly Met  
65 70 75 80  
Thr Arg Thr Thr Thr Xaa Gly Asp Asp Asp Glu Glu Gly Val Asp Glu  
85 90 95  
Glu Asp Asp Asp Gln Asp Glu Asp Glu Glu Glu Asp Asp Asp Glu Asp  
100 105 110  
Ser Leu Gln Pro Pro Lys Lys Arg Lys Lys  
115 120

(2) INFORMATION FOR SEQ ID NO:3793:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 928 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..928  
(D) OTHER INFORMATION: / Ceres Seq. ID 1578255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3793:

aagacagcaa ccacatgctc accagtgcac gccccgaag caaaagactt gctggatata 60  
accaaagatt aggttaagaa gcagctcgag ccgcccttcc ttccagtcac atggccgcgc 120  
ccgcttcttc gggtacctcc agaggttgag cactccgtag cagtacctcc gtgggttttc 180  
atcgccaccg cgggaataat ccggtgatca gccccgcgtc ttctgtgtgc cgacgaagcc 240  
ttactggtgg atcaacgatg aactcctcgg gcatgaacgg tgccttccct cctatcaaag 300  
gaagtacacg aatccccgca gttggtcctg gccctgccag tccgtcagga ggaaacctgc 360  
cgatacccaa catgcctcca tgggccaagt ggctggtcgG cgccgccata gtcgcgatac 420  
caatctacag gaggttcaga acactagaag ataagataga gaagacggcg gaggtggcga 480  
tcgaggtggt ggacacggtg gcggggtcgg cgagagaagg ggccggcgagg tcgccggcgc 540  
gttccccggc aacgagagcc tcagggaggg ggctgcgagg atcaaggcgg tcacggatga 600  
gatcgaggag gacgccgaga gagccgaggg cctgatcgag aaggttgacg agataaagga 660  
acaagttgat tcaatcgtcg atcccttaat cgacaagggt gtcaaggata aagaaacct 720  
gagagaagga accaaggagg aggcaatgac atgatgtaga ttattgaagg tataaagatt 780  
ggttaggcgg tgccgcgggt gtaaccggaa gaaaatacct accgcatgta aaaaaaatca 840  
ctaaatataa atataagaag cttttcagaa aaaaaactct tctctaacag ttatgtaaga 900  
caagttctta aatttacaaa cttcttct

(2) INFORMATION FOR SEQ ID NO:3794:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..174  
(D) OTHER INFORMATION: / Ceres Seq. ID 1578256

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3794:

Met Ala Ala Pro Ala Ser Ser Val Thr Ser Arg Gly Leu Ala Leu Arg  
1 5 10 15  
Ser Ser Thr Ser Val Gly Phe His Arg His Arg Gly Asn Asn Pro Val  
20 25 30  
Ile Ser Pro Ala Ser Ser Arg Arg Arg Arg Ser Leu Thr Gly Gly Ser  
35 40 45  
Thr Met Asn Ser Ser Gly Met Asn Gly Ala Phe Pro Pro Ile Lys Gly  
50 55 60  
Ser Thr Arg Ile Pro Ala Val Gly Pro Gly Pro Ala Ser Pro Ser Gly  
65 70 75 80

(2) INFORMATION FOR SEQ ID NO:3795:

(A) LENGTH: 125 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..125  
(D) OTHER INFORMATION: / Ceres Seq. ID 1578257

(XI) SEQUENCE DESCRIPTION OF THE INVENTION																
Met	Asn	Ser	Ser	Gly	Met	Asn	Gly	Ala	Phe	Pro	Pro	Ile	Lys	Gly	Ser	
1				5					10					15		
Thr	Arg	Ile	Pro	Ala	Val	Gly	Pro	Gly	Pro	Ala	Ser	Pro	Ser	Gly	Gly	
			20					25					30			
Asn	Leu	Pro	Ile	Pro	Asn	Met	Pro	Pro	Trp	Ala	Lys	Trp	Leu	Val	Gly	
		35					40					45				
Ala	Ala	Ile	Val	Ala	Ile	Pro	Ile	Tyr	Arg	Arg	Phe	Arg	Thr	Leu	Glu	
	50					55					60					
Asp	Lys	Ile	Glu	Lys	Thr	Ala	Glu	Val	Ala	Ile	Glu	Val	Val	Asp	Thr	
65					70					75				80		
Val	Ala	Gly	Ser	Ala	Glu	Lys	Val	Ala	Ala	Arg	Ser	Pro	Ala	Arg	Ser	
				85					90					95		
Pro	Ala	Thr	Arg	Ala	Ser	Gly	Arg	Arg	Arg	Arg	Gly	Ser	Arg	Arg	Ser	
			100					105					110			
Arg	Met	Arg	Ser	Arg	Arg	Thr	Pro	Arg	Glu	Pro	Arg	Pro				
		115					120					125				

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..120  
(D) OTHER INFORMATION: / Ceres Seq. ID 1578258

Met	Asn	Gly	Ala	Phe	Pro	Pro	Ile	Lys	Gly	Ser	Thr	Arg	Ile	Pro	Ala
1				5					10					15	
Val	Gly	Pro	Gly	Pro	Ala	Ser	Pro	Ser	Gly	Gly	Asn	Leu	Pro	Ile	Pro
			20					25					30		
Asn	Met	Pro	Pro	Trp	Ala	Lys	Trp	Leu	Val	Gly	Ala	Ala	Ile	Val	Ala
							40					45			
Ile	Pro	Ile	Tyr	Arg	Arg	Phe	Arg	Thr	Leu	Glu	Asp	Lys	Ile	Glu	Lys
	50					55					60				
Thr	Ala	Glu	Val	Ala	Ile	Glu	Val	Val	Asp	Thr	Val	Ala	Gly	Ser	Ala

(2) INFORMATION FOR SEQ ID NO:3797:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3797:

(2) INFORMATION FOR SEQ ID NO:3798:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3798:

(2) INFORMATION FOR SEQ ID NO:3799:

(D) OTHER INFORMATION: / Ceres Seq. ID 1578319

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3799:

Met Ser Arg Ser Gly Gln Pro Pro Asp Leu Lys Lys Tyr Met Asp Lys  
1 5 10 15  
Lys Leu Gln Ile Lys Leu Asn Ala Asn Arg Val Val Ile Gly Thr Leu  
20 25 30  
Arg Gly Phe Asp Gln Phe Met Asn Leu Val Ile Asp Asn Thr Val Glu  
35 40 45  
Val Asn Gly Asn Asp Lys Thr Asp Ile Gly Met Val Val Ile Arg Gly  
50 55 60  
Asn Ser Val Val Met Ile Glu Ala Leu Glu Pro Val Ala Lys Ser Gln  
65 70 75 80

(2) INFORMATION FOR SEQ ID NO:3800:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..67
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578320

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3800:

Met Asp Lys Lys Leu Gln Ile Lys Leu Asn Ala Asn Arg Val Val Ile  
1 5 10 15  
Gly Thr Leu Arg Gly Phe Asp Gln Phe Met Asn Leu Val Ile Asp Asn  
20 25 30  
Thr Val Glu Val Asn Gly Asn Asp Lys Thr Asp Ile Gly Met Val Val  
35 40 45  
Ile Arg Gly Asn Ser Val Val Met Ile Glu Ala Leu Glu Pro Val Ala  
50 55 60  
Lys Ser Gln  
65

(2) INFORMATION FOR SEQ ID NO:3801:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..826
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3801:

cccatcgatt ttctcttgga atcgtaacct cagaaagcca aatctcattc tccggcgctc 60  
aggcccaccc aagcgctgac tctcccgatc caatcggtac ctctagttc ctgcgccggc 120  
gtagcggcgt cgggcgaaca gcggtgactt ggcgagggcg cttggccggc gacaatcatc 180  
cactaggatg gaaggtgagg cagagaccgt ggttggttct tgttctaaac catgtgggcc 240  
tctggaggac tactacattc cagattacat tctgaagcca gGtgcccaac aagtacttgt 300  
tgatcatgcg gcaccctgcc ccgttgtagt gttcatcaac tcaagatctg gaggccaact 360  
tggaagtagt ttaatcaaaa catatcgtga gcttctcaat gaagcacagg tttttgatct 420  
ctcaaaagag gctccagata aggtattgca tcggtttatat gccaaccttg aaaggctgaa 480  
gatggaagga gacattcttg cagttcaaat ttKggaggac actgaggcta attgttgacg 540  
gcggtgatgg tacagctagc tggctgcttg gggtagtcag tgaccttaag ctttcccacc 600  
cacctccagt ggcaactgtg cctctgggaa cgggaaataa cctccccttt tcatttggat 660  
ggggaaagaa gaatccttct actgaccaag aggctgtaaa atcattcctc gggctagtaa 720  
agcatgcaaa agaaattaag attgatagtt ggcacatcat tttgagaatg cgagttccag 780  
aggaaggctc atgtgatect attgctccac tagatttgcc tcattc

(2) INFORMATION FOR SEQ ID NO:3802:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..119
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578334

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3802:

```
Met Glu Gly Glu Ala Glu Thr Val Val Gly Ser Cys Ser Lys Pro Cys
1          5          10          15
Gly Pro Leu Glu Asp Tyr Tyr Ile Pro Asp Tyr Ile Leu Lys Pro Gly
          20          25          30
Ala Gln Gln Val Leu Val Asp His Ala Ala Pro Cys Pro Val Val Val
          35          40          45
Phe Ile Asn Ser Arg Ser Gly Gly Gln Leu Gly Ser Ser Leu Ile Lys
50          55          60
Thr Tyr Arg Glu Leu Leu Asn Glu Ala Gln Val Phe Asp Leu Ser Lys
65          70          75          80
Glu Ala Pro Asp Lys Val Leu His Arg Leu Tyr Ala Asn Leu Glu Arg
          85          90          95
Leu Lys Met Glu Gly Asp Ile Leu Ala Val Gln Ile Xaa Glu Asp Thr
          100          105          110
Glu Ala Asn Cys Cys Arg Arg
          115
```

(2) INFORMATION FOR SEQ ID NO:3803:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 648 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..648
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578335

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3803:

```
aagcagcagc agcacagtca tccacactaa cgaacgaact cttgctccga tcacgagcta      60
gctgaggtcg acgatggcgg ctgtgctgaa cagcaggaag acggcgcagg cggtggtggc      120
cgtgctggtg gcggcggcgc tgctggcttc gtccacttcg gcggcgatca cCtgcggggca      180
ggtgggggtcg tcgCtgggcgc cgtgcatccc gtacgcgacg gggagggccca gcgcgctccc      240
cgcgctcgtgc tgcagcggcg tcaagagcct caacagcgcg gcgcggacca gcgcggaccg      300
ccaggcggCg tgccgctgcc tcaagagcct cgccaacagc gtcaagagcg tcaacatggg      360
caccgtcgcc accatccccg gcaagtgcgg cgtctccgtc ggattcccca tcagcatgtc      420
caccgactgc aacaagatca gctaagttac gacgaccaag ctaataagcc taccgaacgt      480
acacgaacgt cccgcgcgct gcacgagtga tgaagccagg ggagaaataa aataaagccg      540
ctgtattgcc aggagcagca tgcattatatt atcgatctat atatatactg tactgtagta      600
ctctattata tatgtatata tgtgtggcct gcagtgcgag ttgcttcg
```

(2) INFORMATION FOR SEQ ID NO:3804:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..123

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3804:

(2) INFORMATION FOR SEQ ID NO:3805:

(A) LENGTH: 676 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..676

(D) OTHER INFORMATION: / Ceres Seq. ID 1578352

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3805:

(X1) SEQUENCE DESTRUCTION: SEQ ID NO: 1						
gacacacctc	ccaaacoccta	cactcccggc	ggcggcgccg	gcggcgcsa	gcggcagcag	60
catccgaaga	tggtgaagtt	cctcaagccc	ggcaaggccg	ttatcctcct	ccagggcCGc	120
ttcgccggca	ggaaggcagt	tatcgggcgc	gtggccctgg	tgaactacgg	ggaggactat	180
ggccgtctcg	ttgtcatcgt	cgatgttggtc	gaccagaaca	gggcacttgt	ggatgccct	240
gatatggtca	ggtgccaggt	gaacttcaag	cggctctcac	ttactgacat	caagattgac	300
atcaaacgtg	tcccacaaga	gacagccctg	atcaaggcga	tggaggaaagc	tgatgtgaag	360
accaagtggg	agaacagctc	atggggcaag	aagctgattg	tccagaagag	gagagcatcg	420
ctcaatgact	ttgataggtt	caaagtcatg	ctggcgaaga	ttaagagggg	cgggtctatc	480
aggcaagagc	tgcccaagct	gaagaaggcg	tccacggctt	aaggagtctc	tttccgtgaa	540
tgtcatgtta	gagtttttgg	ttatgagttg	gatcagcaat	tcgattgagc	gttgtcaaag	600
ccagaattac	caatatgttc	cctgtaaacc	catttcaaac	tttatcaagc	acgggcgtgc	660
tcaggatact	tttgcc					

(2) INFORMATION FOR SEQ ID NO:3806:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 173 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..173

(D) OTHER INFORMATION: / Ceres Seq. ID 1578353

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3806:

Asp	Thr	Pro	Pro	Lys	Pro	Tyr	Thr	Pro	Gly	Gly	Gly	Gly	Gly	Gly	Ala
1				5					10					15	
Xaa	Arg	Gln	Gln	His	Pro	Lys	Met	Val	Lys	Phe	Leu	Lys	Pro	Gly	Lys
		20						25					30		
Ala	Val	Ile	Leu	Leu	Gln	Gly	Arg	Phe	Ala	Gly	Arg	Lys	Ala	Val	Ile
		35					40					45			
Gly	Arg	Val	Ala	Leu	Val	Asn	Tyr	Gly	Glu	Asp	Tyr	Gly	Arg	Leu	Val

50 55 60  
Val Ile Val Asp Val Val Asp Gln Asn Arg Ala Leu Val Asp Ala Pro  
65 70 75 80  
Asp Met Val Arg Cys Gln Val Asn Phe Lys Arg Leu Ser Leu Thr Asp  
85 90 95  
Ile Lys Ile Asp Ile Lys Arg Val Pro Lys Lys Thr Ala Leu Ile Lys  
100 105 110  
Ala Met Glu Glu Ala Asp Val Lys Thr Lys Trp Glu Asn Ser Ser Trp  
115 120 125  
Gly Lys Lys Leu Ile Val Gln Lys Arg Arg Ala Ser Leu Asn Asp Phe  
130 135 140  
Asp Arg Phe Lys Val Met Leu Ala Lys Ile Lys Arg Gly Gly Ala Ile  
145 150 155 160  
Arg Gln Glu Leu Ala Lys Leu Lys Lys Ala Ser Thr Ala  
165 170

(2) INFORMATION FOR SEQ ID NO:3807:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..150
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3807:

Met Val Lys Phe Leu Lys Pro Gly Lys Ala Val Ile Leu Leu Gln Gly  
1 5 10 15  
Arg Phe Ala Gly Arg Lys Ala Val Ile Gly Arg Val Ala Leu Val Asn  
20 25 30  
Tyr Gly Glu Asp Tyr Gly Arg Leu Val Val Ile Val Asp Val Val Asp  
35 40 45  
Gln Asn Arg Ala Leu Val Asp Ala Pro Asp Met Val Arg Cys Gln Val  
50 55 60  
Asn Phe Lys Arg Leu Ser Leu Thr Asp Ile Lys Ile Asp Ile Lys Arg  
65 70 75 80  
Val Pro Lys Lys Thr Ala Leu Ile Lys Ala Met Glu Glu Ala Asp Val  
85 90 95  
Lys Thr Lys Trp Glu Asn Ser Ser Trp Gly Lys Lys Leu Ile Val Gln  
100 105 110  
Lys Arg Arg Ala Ser Leu Asn Asp Phe Asp Arg Phe Lys Val Met Leu  
115 120 125  
Ala Lys Ile Lys Arg Gly Gly Ala Ile Arg Gln Glu Leu Ala Lys Leu  
130 135 140  
Lys Lys Ala Ser Thr Ala  
145 150

(2) INFORMATION FOR SEQ ID NO:3808:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..92
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578355

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3808:

Met Val Arg Cys Gln Val Asn Phe Lys Arg Leu Ser Leu Thr Asp Ile  
1 5 10 15

Lys Ile Asp Ile Lys Arg Val Pro Lys Lys Thr Ala Leu Ile Lys Ala  
20 25 30  
Met Glu Glu Ala Asp Val Lys Thr Lys Trp Glu Asn Ser Ser Trp Gly  
35 40 45  
Lys Lys Leu Ile Val Gln Lys Arg Arg Ala Ser Leu Asn Asp Phe Asp  
50 55 60  
Arg Phe Lys Val Met Leu Ala Lys Ile Lys Arg Gly Gly Ala Ile Arg  
65 70 75 80  
Gln Glu Leu Ala Lys Leu Lys Lys Ala Ser Thr Ala  
85 90

(2) INFORMATION FOR SEQ ID NO:3809:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 730 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..730
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578379

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3809:

tagtcgctgg	agatagagcc	gagaacaagg	gcaactgacg	cggtcaccct	cgcccccaac	60
acagagagaa	ggctctgctct	ccaccggatg	gactcccacg	gcaagcccaa	gcccgcgggt	120
tcgacgccgc	cgacgccgcc	gaagccgccg	aagccgccga	cgccgccgaa	gccgcgcgacg	180
ccgcgcgacg	cgacgccgcc	gacgcccgag	gcgaggaagg	ggttcatgcg	ccgcattcttc	240
cctttcctcc	tagccgccaa	cctctttgtc	gtagcttatg	tcctcgtgcg	ggccaaccaa	300
aaggactcag	caaagaagga	cccaacgact	gatcctgcta	ctgcaactgc	tgggaagcct	360
gctgagccag	tctctatccc	cagaaaggag	ctcccaccaa	tccctgaaga	tgaccagcgc	420
aagCtctaca	aatggatgct	ggaagagaag	cggaagatca	agccacgcaa	tgtgtccgag	480
aagaagaaac	tcgatgagga	gaaggccctt	ctaaaagagt	tcattccgagc	aggatccCtc	540
ccaagcttct	aaaagagatc	aagccatttg	ggctctctgt	gtctgatgtt	cagccaagaa	600
gatgattggg	cctgattgga	ttgtgtacaa	acacagtact	gtgctatctt	gtaaaactgat	660
gtctccatga	tgtagcctcc	tcgagttcaa	aggttggtgtg	gatgcaaact	agtgtgtgtg	720
gcattggttc						

(2) INFORMATION FOR SEQ ID NO:3810:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..154
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578380

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3810:

Met Asp Ser His Gly Lys Pro Lys Pro Ala Gly Ser Thr Pro Pro Thr	
1 5 10 15	
Pro Pro Lys Pro Pro Lys Pro Pro Thr Pro Pro Lys Pro Pro Thr Pro	
20 25 30	
Pro Thr Pro Thr Pro Pro Thr Pro Glu Ala Arg Lys Gly Phe Met Arg	
35 40 45	
Arg Ile Phe Pro Phe Leu Leu Ala Ala Asn Leu Phe Val Val Ala Tyr	
50 55 60	
Val Leu Val Arg Ala Asn Gln Lys Asp Ser Ala Lys Lys Asp Pro Thr	
65 70 75 80	
Thr Asp Pro Ala Thr Ala Thr Ala Gly Lys Pro Ala Glu Pro Val Ser	
85 90 95	
Ile Pro Arg Lys Glu Leu Pro Pro Ile Pro Glu Asp Asp Gln Arg Lys	
100 105 110	

(2) INFORMATION FOR SEQ ID NO:3811:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3811:

(2) INFORMATION FOR SEQ ID NO:3812:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3812:

(2) INFORMATION FOR SEQ ID NO:3813:

## (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..831

(D) OTHER INFORMATION: / Ceres Seq. ID 1578386

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3813:

aaacttgtca	agctttttcca	agaaacctag	ctagctagct	agtaagaggc	acaggccggc	60
accatgtcgc	accaccattc	ccaccacaaa	tctcattctc	acaaccgtac	ccaccaccac	120
tctcactctc	actccggang	agntggaggc	ggcggcgggc	gtggcggtgc	cgggtggaggc	180
ggaggcggag	tggctaaatg	ccactgtgat	tgtcacacc	atgatcattc	accgccaagg	240
caaccgttct	tcccgccacc	gcagcttcca	ccaccacaaa	tctttcttcc	tgcaggacca	300
ccgctccctc	cgcttgggcc	gctcccattt	ccgccaccga	tattcttcgg	acctccggcg	360
ccgccacccc	cgccccggcc	accgttcatg	tgcccacgac	cgccaccatg	catgtaccgg	420
agGtggtaat	ggagataaaa	gttgatatac	acgggtgtgca	tgtgtttgtg	ccaaagcttc	480
tcgtacgtgg	tgttcgagtt	tctgtcacc	caaataagaa	cagagctctt	ctccggatag	540
aactatcttc	acagggttcc	ctgttcaagt	taggatggca	cgcacatca	tatctcggaa	600
ggaagccctc	ggggagtctt	ctccatgtat	gggtggagtt	ttgaaagaag	tcattatatt	660
attgctagtt	cttgttccct	actagatgtt	ctcgttgatg	cgtggatttt	atacgtgtac	720
ttgttctctt	gtgctttcca	ccggccctga	tgtcgtcccg	ttgtaaccga	tgttcggttg	780
tgtttcaatg	tgtcttttgt	ttaatgatat	gttgtgtgtc	tgctttcctt	c	

(2) INFORMATION FOR SEQ ID NO:3814:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 121 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..121

(D) OTHER INFORMATION: / Ceres Seq. ID 1578387

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3814:

Met	Ser	His	His	His	Ser	His	His	Lys	Ser	His	Ser	His	Asn	Arg	Thr
1				5					10					15	
His	His	His	Ser	His	Ser	His	Ser	Gly	Xaa	Xaa	Gly	Gly	Gly	Gly	Gly
			20					25					30		
Gly	Gly	Gly	Ala	Gly	Gly	Gly	Gly	Gly	Val	Ala	Lys	Cys	His	Cys	
		35					40				45				
Asp	Cys	Ser	His	His	Asp	His	Ser	Pro	Pro	Arg	Gln	Pro	Phe	Phe	Pro
	50				55					60					
Pro	Pro	Gln	Leu	Pro	Pro	Pro	Gln	Ile	Phe	Leu	Pro	Ala	Gly	Pro	Pro
	65				70				75					80	
Leu	Pro	Pro	Pro	Gly	Pro	Leu	Pro	Phe	Pro	Pro	Pro	Ile	Phe	Phe	Gly
			85					90					95		
Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Phe	Met	Cys	Pro	Arg	
		100					105					110			
Pro	Pro	Pro	Cys	Met	Tyr	Arg	Arg	Trp							
	115						120								

(2) INFORMATION FOR SEQ ID NO:3815:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..74

(D) OTHER INFORMATION: / Ceres Seq. ID 1578388

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3815:

Met	Ile	Ile	His	Arg	Gln	Gly	Asn	Arg	Ser	Ser	Arg	His	Arg	Ser	Phe
1			5					10						15	

His His His Lys Ser Phe Phe Leu Gln Asp His Arg Ser Leu Arg Leu  
20 25 30  
Gly Arg Ser His Phe Arg His Arg Tyr Ser Ser Asp Leu Arg Arg Arg  
35 40 45  
His Pro Arg Pro Arg His Arg Ser Cys Ala His Asp Arg His His Ala  
50 55 60  
Cys Thr Gly Gly Gly Asn Gly Asp Lys Ser  
65 70

(2) INFORMATION FOR SEQ ID NO:3816:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..78
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578389

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3816:

Met His Val Pro Glu Val Val Met Glu Ile Lys Val Asp Ile His Gly  
1 5 10 15  
Val His Val Phe Val Pro Lys Leu Leu Val Arg Gly Val Arg Val Ser  
20 25 30  
Val Thr Pro Asn Lys Asn Arg Ala Leu Leu Arg Ile Glu Leu Ser Ser  
35 40 45  
Gln Gly Ser Leu Phe Lys Leu Gly Trp His Ala Ser Ser Tyr Leu Gly  
50 55 60  
Arg Lys Pro Ser Gly Ser Leu Leu His Val Trp Val Glu Phe  
65 70 75

(2) INFORMATION FOR SEQ ID NO:3817:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 750 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..750
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578394

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3817:

atctcttctt tccccctctcc ctccccctcgc cgtcgctgtc gtcgcgctcc gtgctagcca 60  
tggatctagg cgctcccgcgt cgacggcgct taccgatccg cctcttgAct ggtgtcgctc 120  
gccgtcctca tggctctcac cgcgcgttcc agtgccgaag tcatcaccct caccgaagag 180  
accttctccg acaagataaa ggagaaggac acggtgtggt ttgtgcagtt ctgcgtcccc 240  
tgggtgtaaac actgcaagaa ccttggaaca ctatgggagg acctgggaaa ggttatggaa 300  
ggtgcggtatg aaattgagat tgggcaagtt gactgtggtg tcagcaaacc agtatgctca 360  
aaggtcgata tacactccta cccaacattc aaggtgtttt atgaaggcga agaagtagta 420  
aaatataaag gacctaggaa tgtggaatcg ctgaagaact tcgtgttgaa tgaagctgag 480  
aaagcaggtg aggcaaagct tcaagctgat tgaggcaggg gagtttcagc aagcatgtgg 540  
cgtagacaag gaacaatgct gtgcAacatt gtcttctatc ctgtcattta caaagccaat 600  
ttacaggaaa gaaatgatct tatgaccccc tatcagagta ttcctcttcg aaagtaactc 660  
cgaatcagtt catagaagct gtactccatt ccatagtttt tatcacattg acaaactccg 720  
aatcagttaa tagaagctgt actccattcg

(2) INFORMATION FOR SEQ ID NO:3818:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3818:

(2) INFORMATION FOR SEQ ID NO:3819:

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3819:

(2) INFORMATION FOR SEQ ID NO:3820:

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3820:

(x1) SEQUENCE DESCRIPTION: SEQ ID: 1

Met	Glu	Gly	Ala	Asp	Glu	Ile	Glu	Ile	Gly	Gln	Val	Asp	Cys	Gly	Val
1				5				10						15	
Ser	Lys	Pro	Val	Cys	Ser	Lys	Val	Asp	Ile	His	Ser	Tyr	Pro	Thr	Phe

20 25 30  
Lys Val Phe Tyr Glu Gly Glu Glu Val Val Lys Tyr Lys Gly Pro Arg  
35 40 45  
Asn Val Glu Ser Leu Lys Asn Phe Val Leu Asn Glu Ala Glu Lys Ala  
50 55 60  
Gly Glu Ala Lys Leu Gln Ala Asp  
65 70

(2) INFORMATION FOR SEQ ID NO:3821:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 689 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..689

(D) OTHER INFORMATION: / Ceres Seq. ID 1578416

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3821:

gagaagcgta cccggcagct ccgctccgct agtccgctccg cccccaagaa tgtcagacga 60  
ggccaggcgc gggcccgcgg ggcgcgcgca ggtgggtgctt cgggcctcct ccgaggaccg 120  
caagccggtg ggctcggggt ctccgcgcgc ggcagcgacc ggcactgcgG ttgcgcacaa 180  
gatccagctc aagagtgccg acatgaagga ggagatgcgg caggaggcct tcgaaattgc 240  
tcgcatcgca ttcgagaagc acagtatgga gaaggacatc gcggagtaca taaagaagga 300  
gttcgacaag aaccacggcc caacctggca ctgcatcgct gcccgcaact tcggttccta 360  
cgtgacgcac gagacaaact actttgtata tttctacatc gactctaaag ctgtcttgct 420  
attcaagtct gggtgattgt cgcagccaac agtcaacctt gcatgcctac atcttctttc 480  
tctcgtgtat gctccatccc ctcccctttc ccctcagagt cgtctgcagc caagcctgga 540  
agccggtaat cttatgagcc tgcattgttg tgcattgttg acggattatt cttcgcagtc 600  
catagtgtga gatcaggttg catcttattt atgtctgata tatcttggtg ttgtgagtac 660  
attatcttgt tgcattatga ttgccggac

(2) INFORMATION FOR SEQ ID NO:3822:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..135

(D) OTHER INFORMATION: / Ceres Seq. ID 1578417

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3822:

Glu Lys Arg Thr Arg Gln Leu Arg Ser Val Ser Pro Ser Ala Pro Lys  
1 5 10 15  
Asn Val Arg Arg Gly Gln Ala Arg Ala Arg Gly Arg Arg Ala Gly Gly  
20 25 30  
Ala Ser Gly Leu Leu Arg Gly Pro Gln Ala Gly Gly Leu Gly Val Ser  
35 40 45  
Ala Ala Gly Ser Asp Arg Asp Cys Gly Cys Ala Gln Asp Pro Ala Gln  
50 55 60  
Glu Cys Arg His Glu Gly Gly Asp Ala Ala Gly Gly Leu Arg Asn Cys  
65 70 75 80  
Ser His Arg Ile Arg Glu Ala Gln Tyr Gly Glu Gly His Arg Gly Val  
85 90 95  
His Lys Glu Gly Val Arg Gln Glu Pro Arg Pro Asn Leu Ala Leu His  
100 105 110  
Arg Arg Pro Gln Leu Arg Phe Leu Arg Asp Ala Arg Asp Lys Leu Leu  
115 120 125  
Cys Ile Phe Leu His Arg Leu  
130 135



(2) INFORMATION FOR SEQ ID NO:3823:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..144
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578418

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3823:

Arg	Ser	Val	Pro	Gly	Ser	Ser	Ala	Pro	Ser	Val	Arg	Pro	Pro	Pro	Arg
1				5					10					15	
Met	Ser	Asp	Glu	Ala	Arg	Arg	Gly	Pro	Ala	Gly	Ala	Ala	Gln	Val	Val
			20					25					30		
Leu	Arg	Ala	Ser	Ser	Glu	Asp	Arg	Lys	Pro	Val	Gly	Ser	Gly	Ser	Pro
			35				40					45			
Pro	Pro	Ala	Ala	Thr	Ala	Thr	Ala	Val	Ala	His	Lys	Ile	Gln	Leu	Lys
			50				55				60				
Ser	Ala	Asp	Met	Lys	Glu	Glu	Met	Arg	Gln	Glu	Ala	Phe	Glu	Ile	Ala
65				70					75					80	
Arg	Ile	Ala	Phe	Glu	Lys	His	Ser	Met	Glu	Lys	Asp	Ile	Ala	Glu	Tyr
				85					90					95	
Ile	Lys	Lys	Glu	Phe	Asp	Lys	Asn	His	Gly	Pro	Thr	Trp	His	Cys	Ile
			100					105					110		
Val	Gly	Arg	Asn	Phe	Gly	Ser	Tyr	Val	Thr	His	Glu	Thr	Asn	Tyr	Phe
			115				120					125			
Val	Tyr	Phe	Tyr	Ile	Asp	Ser	Lys	Ala	Val	Leu	Leu	Phe	Lys	Ser	Gly
			130				135					140			

(2) INFORMATION FOR SEQ ID NO:3824:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..128
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578419

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3824:

Met	Ser	Asp	Glu	Ala	Arg	Arg	Gly	Pro	Ala	Gly	Ala	Ala	Gln	Val	Val
1				5					10					15	
Leu	Arg	Ala	Ser	Ser	Glu	Asp	Arg	Lys	Pro	Val	Gly	Ser	Gly	Ser	Pro
			20					25					30		
Pro	Pro	Ala	Ala	Thr	Ala	Thr	Ala	Val	Ala	His	Lys	Ile	Gln	Leu	Lys
			35				40					45			
Ser	Ala	Asp	Met	Lys	Glu	Glu	Met	Arg	Gln	Glu	Ala	Phe	Glu	Ile	Ala
			50				55				60				
Arg	Ile	Ala	Phe	Glu	Lys	His	Ser	Met	Glu	Lys	Asp	Ile	Ala	Glu	Tyr
65				70					75					80	
Ile	Lys	Lys	Glu	Phe	Asp	Lys	Asn	His	Gly	Pro	Thr	Trp	His	Cys	Ile
			85						90					95	
Val	Gly	Arg	Asn	Phe	Gly	Ser	Tyr	Val	Thr	His	Glu	Thr	Asn	Tyr	Phe
			100				105						110		
Val	Tyr	Phe	Tyr	Ile	Asp	Ser	Lys	Ala	Val	Leu	Leu	Phe	Lys	Ser	Gly
			115				120					125			

(2) INFORMATION FOR SEQ ID NO:3825:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 855 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..855
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578422

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3825:

aactcactcg	tcccccttcca	gttccgcttc	cgatctgcgc	ttcgatctcc	ctcttcgcag	60
aggtgcttgt	gagcatgtat	ctgctaggca	acaaaagtgg	aaagaagaaa	gtgtatgtcg	120
attatatgaa	tgtccctcta	ccgatgccca	tcgaagagaa	ttacggtggg	cgcttctttg	180
acgacgacga	cgatcttgcc	caagttcttc	aagatcagga	aatattgtat	catttaattc	240
aaggaagtaa	tgggtgggga	ggtttctacc	tcaaagactg	gtaagcatgg	ccatgccaaa	300
tgccactttg	ttgccataga	catattcaac	gggaaaaagc	ttgaagatat	tgttccttca	360
tcacacaact	gtgatattcc	gcagtgaac	cgtactgagt	accagctgat	tgatatatca	420
gaggatggat	ttgtgagcct	tcttacttca	gatggcaaca	ctaaggatga	tcttagactc	480
ccaactgatg	agactcttgt	ggcccagatc	aaggaagggg	ttgaaagcgg	caaggatctt	540
Ggttgtgact	gtccagtcctg	ctatggggga	ggagcagatc	tgcgcgctga	aggatgtttg	600
ccccaaagtaa	cttacctgcc	ttggaatact	gtatctcaaa	acctaaatcg	aaaaaagaag	660
tgtatcaagg	attgctacag	agacatccat	ctggcttgag	ctggcttttg	ctatggcaaa	720
cacaagtgca	gggatcgctg	ggtgtgtcac	cgtgtctgca	ttatctgtgg	ttacattctg	780
gacctgtat	tttctatggg	tttatgcccc	ctactgttta	gtattaatta	tcaataaatt	840
tgtttgggac	ggttg					

(2) INFORMATION FOR SEQ ID NO:3826:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..93
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578423

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3826:

Leu	Thr	Arg	Pro	Leu	Pro	Val	Pro	Leu	Pro	Ile	Cys	Ala	Ser	Ile	Ser	
1				5				10						15		
Leu	Phe	Ala	Glu	Val	Leu	Val	Ser	Met	Tyr	Leu	Leu	Gly	Asn	Lys	Ser	
			20					25						30		
Gly	Lys	Lys	Lys	Val	Tyr	Val	Asp	Tyr	Met	Asn	Val	Pro	Leu	Pro	Tyr	
			35				40						45			
Ala	Ile	Glu	Glu	Asn	Tyr	Gly	Gly	Arg	Phe	Phe	Asp	Asp	Asp	Asp	Asp	
			50				55				60					
Leu	Ala	Gln	Val	Leu	Gln	Asp	Gln	Glu	Ile	Leu	Tyr	His	Leu	Ile	Gln	
			65				70				75				80	
Gly	Ser	Asn	Gly	Gly	Gly	Gly	Phe	Tyr	Leu	Lys	Asp	Trp				
			85							90						

(2) INFORMATION FOR SEQ ID NO:3827:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..149

(D) OTHER INFORMATION: / Ceres Seq. ID 1578424

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3827:

Met Val Val Glu Val Ser Thr Ser Lys Thr Gly Lys His Gly His Ala  
1 5 10 15  
Lys Cys His Phe Val Ala Ile Asp Ile Phe Asn Gly Lys Lys Leu Glu  
20 25 30  
Asp Ile Val Pro Ser Ser His Asn Cys Asp Ile Pro His Val Asn Arg  
35 40 45  
Thr Glu Tyr Gln Leu Ile Asp Ile Ser Glu Asp Gly Phe Val Ser Leu  
50 55 60  
Leu Thr Ser Asp Gly Asn Thr Lys Asp Asp Leu Arg Leu Pro Thr Asp  
65 70 75 80  
Glu Thr Leu Val Ala Gln Ile Lys Glu Gly Phe Glu Ser Gly Lys Asp  
85 90 95  
Leu Gly Cys Asp Cys Pro Val Cys Tyr Gly Gly Gly Ala Asp Leu Arg  
100 105 110  
Ala Glu Gly Cys Trp Pro Gln Val Thr Tyr Leu Pro Trp Asn Thr Val  
115 120 125  
Ser Gln Asn Leu Asn Arg Lys Lys Lys Cys Ile Lys Asp Cys Tyr Arg  
130 135 140  
Asp Ile His Leu Ala  
145

(2) INFORMATION FOR SEQ ID NO:3828:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..75

(D) OTHER INFORMATION: / Ceres Seq. ID 1578425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3828:

Met Leu Ala Pro Ser Asn Leu Pro Ala Leu Glu Tyr Cys Ile Ser Lys  
1 5 10 15  
Pro Lys Ser Lys Lys Glu Val Tyr Gln Gly Leu Leu Gln Arg His Pro  
20 25 30  
Ser Gly Leu Ser Trp Leu Leu Leu Trp Gln Thr Gln Val Gln Gly Ser  
35 40 45  
Leu Gly Val Ala Pro Cys Leu His Tyr Leu Trp Leu His Ser Gly Pro  
50 55 60  
Cys Ile Phe Tyr Gly Phe Met Pro Pro Thr Val  
65 70 75

(2) INFORMATION FOR SEQ ID NO:3829:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 670 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..670

(D) OTHER INFORMATION: / Ceres Seq. ID 1578443

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3829:

aaccggagaa caacgcactt gtgttgcgta cgtcggtcac atgcattgca tctgcatccg	60
gagtagcgag ttctagacac agcaggcaac agactgargt agcccagcga gcgagcgagc	120
aatggcaacc ctacgcgccg cccccctcgt cgGcgcgggc gccgtcgcca ggccgtgtca	180
ggctcaaggt ttgccgcagc tgagggtgag agccgagaag gcgaggtgcg gcgccgccca	240

(2) INFORMATION FOR SEQ ID NO:3830:

(A) LENGTH: 66 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..66

(D) OTHER INFORMATION: / Ceres Seq. ID 1578444

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3830:

[illegible]

(2) INFORMATION FOR SEQ ID NO:3831:

(A) LENGTH: 127 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..127

(D) OTHER INFORMATION: / Ceres Seq. ID 1578445

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3831:

(X1) SEQUENCE DESCRIPTION: 151																
Met	Ala	Thr	Leu	Ser	Ala	Ala	Pro	Leu	Val	Gly	Ala	Ala	Ala	Val	Ala	
1			5						10					15		
Arg	Pro	Cys	Gln	Ala	Gln	Gly	Leu	Pro	Gln	Leu	Arg	Val	Arg	Ala	Glu	
			20					25					30			
Lys	Ala	Arg	Cys	Gly	Ala	Ala	His	Ser	Arg	Arg	Pro	Ser	Gln	Arg	Arg	
			35				40					45				
Asp	Gly	Asn	Asn	Gly	Ala	Ser	Ser	Ser	Leu	Leu	Ala	Xaa	Ala	Thr	Ser	
	50					55					60					
Ala	Val	Thr	Thr	Ser	Pro	Xaa	Leu	Ala	Leu	Val	Asp	Glu	Arg	Met	Ser	
65					70					75				80		
Thr	Glu	Gly	Thr	Gly	Leu	Ser	Leu	Gly	Leu	Ser	Asn	Asn	Leu	Leu	Gly	
				85				90						95		
Trp	Ile	Leu	Leu	Gly	Val	Phe	Gly	Leu	Ile	Trp	Ser	Leu	Tyr	Thr	Val	
			100				105						110			
Tyr	Thr	Ser	Thr	Leu	Asp	Glu	Asp	Asp	Asp	Ser	Gly	Leu	Ser	Leu		
		115					120					125				

(2) INFORMATION FOR SEQ ID NO:3832:

(A) LENGTH: 1027 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..1027
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1578448

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3832:

ctcaataaaaa	tatgtactcg	gaatcggaag	aagctgcctt	ccttttccat	ccgcggaacg	60
acgcacgcgg	acgcctcctt	gttcgggtc	ctactccgc	cgcctagagg	cctcgccctc	120
ccccctccgg	cgaaaaccga	ttctctccgg	cgtttctctg	tcccttagtg	caagcaagga	180
caccgctcct	ctagcgagct	ccgttctgaa	gcggcaagaa	agatgattaa	tcttttcaaa	240
ataaagggtc	aaaagaaaga	ggaggcagca	agtctgctgg	aaaggccct	gttaagaaac	300
agtctgctgg	ggagctccgt	cttcataaag	atattagtga	gctcaacctg	ccgaagacca	360
cgtcaatttc	ttttcccaat	ggcaaggatg	atctgatgaa	ttttgagacc	accatccgac	420
ctgatgaagg	atattacatg	ggaggcactt	tcgttttcac	ctttcaagt	tccccatctt	480
atcctcatga	tcctccgaag	Gtcaaagca	agaccaagGt	gtaccatcca	aattattgatc	540
tggaaggcaa	tgtatgtctg	aacattctgc	gcgaagattg	gaagcctgtt	ctcaacatca	600
acactgttat	ttatggcctg	aatcttcttt	ttacgcaacc	aaacgacgag	gatoctctga	660
accacgaagc	tgcagttgtc	cttcgtgaca	atccaaagat	gtttgaggca	aatgtgagaa	720
gagccatggc	tggaggctac	gtcggccaac	actattttcca	aagatgtgct	tgacttgatg	780
tgggtggtggc	ttgaaaacga	tcaacagagc	ccctccccct	gtatcagcac	cagcgcgccc	840
agctttgtgt	gcggaaagta	cttctggaag	caaaatccaa	accgttcatg	gtgtgatact	900
gtgatgcata	tgtttgcccg	cctttgtgat	gtgtggtata	gtggtggtgc	ataatgacat	960
ggaaatgctt	ctctaactgt	atcattcatt	ccataaatcc	taaacgagga	atgggaagtg	1020

gattgtt

(2) INFORMATION FOR SEQ ID NO:3833:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 74 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..74
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1578449

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3833:

Ser	Ile	Lys	Tyr	Val	Leu	Gly	Ile	Gly	Arg	Ser	Cys	Leu	Pro	Phe	Pro
1				5				10					15		
Ser	Ala	Glu	Arg	Arg	Thr	Arg	Thr	Pro	Pro	Cys	Ser	Gly	Ser	Tyr	Ser
			20					25					30		
Arg	Arg	Leu	Glu	Ala	Ser	Pro	Ser	Pro	Leu	Arg	Arg	Lys	Pro	Ile	Leu
		35					40					45			
Ser	Gly	Val	Ser	Trp	Ser	Leu	Ser	Ala	Ser	Lys	Asp	Thr	Ala	Pro	Leu
		50				55					60				
Ala	Ser	Ser	Val	Leu	Lys	Arg	Gln	Glu	Arg						
65						70									

(2) INFORMATION FOR SEQ ID NO:3834:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 125 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..125
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1578450

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3834:

Met Asn Phe Glu Thr Thr Ile Arg Pro Asp Glu Gly Tyr Tyr Met Gly  
1 5 10 15  
Gly Thr Phe Val Phe Thr Phe Gln Val Ser Pro Ser Tyr Pro His Asp  
20 25 30  
Pro Pro Lys Val Lys Cys Lys Thr Lys Val Tyr His Pro Asn Ile Asp  
35 40 45  
Leu Glu Gly Asn Val Cys Leu Asn Ile Leu Arg Glu Asp Trp Lys Pro  
50 55 60  
Val Leu Asn Ile Asn Thr Val Ile Tyr Gly Leu Asn Leu Leu Phe Thr  
65 70 75 80  
Gln Pro Asn Asp Glu Asp Pro Leu Asn His Glu Ala Ala Val Val Leu  
85 90 95  
Arg Asp Asn Pro Lys Met Phe Glu Ala Asn Val Arg Arg Ala Met Ala  
100 105 110  
Gly Gly Tyr Val Gly Gln His Tyr Phe Gln Arg Cys Ala  
115 120 125

(2) INFORMATION FOR SEQ ID NO:3835:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..111

(D) OTHER INFORMATION: / Ceres Seq. ID 1578451

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3835:

Met Gly Gly Thr Phe Val Phe Thr Phe Gln Val Ser Pro Ser Tyr Pro  
1 5 10 15  
His Asp Pro Pro Lys Val Lys Cys Lys Thr Lys Val Tyr His Pro Asn  
20 25 30  
Ile Asp Leu Glu Gly Asn Val Cys Leu Asn Ile Leu Arg Glu Asp Trp  
35 40 45  
Lys Pro Val Leu Asn Ile Asn Thr Val Ile Tyr Gly Leu Asn Leu Leu  
50 55 60  
Phe Thr Gln Pro Asn Asp Glu Asp Pro Leu Asn His Glu Ala Ala Val  
65 70 75 80  
Val Leu Arg Asp Asn Pro Lys Met Phe Glu Ala Asn Val Arg Arg Ala  
85 90 95  
Met Ala Gly Gly Tyr Val Gly Gln His Tyr Phe Gln Arg Cys Ala  
100 105 110

(2) INFORMATION FOR SEQ ID NO:3836:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 847 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..847

(D) OTHER INFORMATION: / Ceres Seq. ID 1578452

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3836:

argccatggc tgcagccgc ccttgagtc tgccccaag atgacgatga tccccctcgc	60
cggttcacc gccctatctg ccgccgcct cctgtctatc ttctctctct tctgtctgca	120
aactcaagga ggagccagaa gcagcgagga ggagcggtag gtgccggtgc gcagggtggt	180
gtaccggtcc atgacaccgg crgcggcgag tgcrgcgacg acggcagagg cagcggcagc	240
gncggcatcg tacgagccgt tcgaggtgtg cgaggggtgc cgggtgCtgcg cgccgtcgtc	300
gtcgtcgtcc aacggcagca gcagctgcgt ggacacgagc tgctgCtacg ccatcgactg	360
cgacctcccc ggcaagccCt tcggcacctg cgccttcacc ccgcaaacct gcggctgcgcg	420

cgggcgccagc agcaactgca cccccctcgt cctgatgatg actcctcttt cctgcaactt 480  
ggctacttct tctggatcat ccacgtcttt acgttacgtt acgattagat cgcagattag 540  
atgactcacg tcacgtactc catcatgatg gatagattat ccagttaatt cccagctagc 600  
gttctgogtg aagttaataa tacaatgaat aataatgtgt gttcgtttca gagattgtga 660  
ctgcagttgg ttccatgcat ttccagagtc ggcggttctt gttggcttga caacttgtac 720  
tgtcagggtc ggcggcctaa cctgttgtcg tcgtatacct actgtatgtt aggtatagat 780  
tgaacacatta ttttatactg tatgactatt acaaaactat aaagcaatac actcatttat 840  
tattgcc

(2) INFORMATION FOR SEQ ID NO:3837:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 175 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..175

(D) OTHER INFORMATION: / Ceres Seq. ID 1578453

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3837:

Xaa Pro Trp Leu Asp Ala Ala Leu Glu Ser Cys Pro Gln Asp Asp Asp  
1 5 10 15  
Asp Pro Pro Arg Arg Leu His Arg Pro Ile Cys Arg Arg Pro Pro Ala  
20 25 30  
His Leu Leu Leu Leu Pro Ala Ala Asn Ser Arg Arg Ser Gln Lys Gln  
35 40 45  
Arg Gly Gly Ala Val Arg Ala Gly Ala Gln Gly Gly Val Pro Val His  
50 55 60  
Asp Thr Gly Xaa Gly Glu Cys Xaa Asp Asp Gly Arg Gly Ser Gly Ser  
65 70 75 80  
Xaa Gly Ile Val Arg Ala Val Arg Gly Val Arg Gly Val Pro Val Leu  
85 90 95  
Arg Ala Val Val Val Val Val Gln Arg Gln Gln Gln Leu Arg Gly His  
100 105 110  
Glu Leu Leu Leu Arg His Arg Leu Arg Pro Pro Arg Gln Ala Leu Arg  
115 120 125  
His Leu Arg Leu His Pro Ala Asn Leu Arg Leu Arg Arg Gln Gln  
130 135 140  
Gln Leu His Pro Pro Arg Pro Asp Asp Asp Ser Ser Phe Leu Gln Leu  
145 150 155 160  
Gly Tyr Phe Phe Trp Ile Ile His Arg Leu Thr Leu Arg Tyr Asp  
165 170 175

(2) INFORMATION FOR SEQ ID NO:3838:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 180 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..180

(D) OTHER INFORMATION: / Ceres Seq. ID 1578454

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3838:

Xaa His Gly Ser Thr Pro Pro Leu Ser Pro Ala Pro Lys Met Thr Met  
1 5 10 15  
Ile Pro Leu Ala Gly Phe Thr Ala Leu Ser Ala Ala Gly Leu Leu Leu  
20 25 30  
Ile Phe Ser Ser Phe Leu Leu Gln Thr Gln Gly Gly Ala Arg Ser Ser  
35 40 45  
Glu Glu Glu Arg Tyr Val Pro Val Arg Arg Val Val Tyr Arg Ser Met

50 55 60  
Thr Pro Xaa Ala Ala Ser Xaa Ala Thr Thr Ala Glu Ala Ala Ala Ala  
65 70 75 80  
Xaa Ala Ser Tyr Glu Pro Phe Glu Val Cys Glu Gly Cys Arg Cys Cys  
85 90 95  
Ala Pro Ser Ser Ser Ser Ser Asn Gly Ser Ser Ser Cys Val Asp Thr  
100 105 110  
Ser Cys Cys Tyr Ala Ile Asp Cys Asp Leu Pro Gly Lys Pro Phe Gly  
115 120 125  
Thr Cys Ala Phe Thr Pro Gln Thr Cys Gly Cys Gly Gly Ala Ser Ser  
130 135 140  
Asn Cys Thr Pro Leu Val Leu Met Met Thr Pro Leu Ser Cys Asn Leu  
145 150 155 160  
Ala Thr Ser Ser Gly Ser Ser Ile Val Leu Arg Tyr Val Thr Ile Arg  
165 170 175  
Ser Gln Ile Arg  
180

(2) INFORMATION FOR SEQ ID NO:3839:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 167 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..167

(D) OTHER INFORMATION: / Ceres Seq. ID 1578455

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3839:

Met Thr Met Ile Pro Leu Ala Gly Phe Thr Ala Leu Ser Ala Ala Gly  
1 5 10 15  
Leu Leu Leu Ile Phe Ser Ser Phe Leu Leu Gln Thr Gln Gly Gly Ala  
20 25 30  
Arg Ser Ser Glu Glu Glu Arg Tyr Val Pro Val Arg Arg Val Val Tyr  
35 40 45  
Arg Ser Met Thr Pro Xaa Ala Ala Ser Xaa Ala Thr Thr Ala Glu Ala  
50 55 60  
Ala Ala Ala Xaa Ala Ser Tyr Glu Pro Phe Glu Val Cys Glu Gly Cys  
65 70 75 80  
Arg Cys Cys Ala Pro Ser Ser Ser Ser Ser Asn Gly Ser Ser Ser Cys  
85 90 95  
Val Asp Thr Ser Cys Cys Tyr Ala Ile Asp Cys Asp Leu Pro Gly Lys  
100 105 110  
Pro Phe Gly Thr Cys Ala Phe Thr Pro Gln Thr Cys Gly Cys Gly Gly  
115 120 125  
Ala Ser Ser Asn Cys Thr Pro Leu Val Leu Met Met Thr Pro Leu Ser  
130 135 140  
Cys Asn Leu Ala Thr Ser Ser Gly Ser Ser Ile Val Leu Arg Tyr Val  
145 150 155 160  
Thr Ile Arg Ser Gln Ile Arg  
165

(2) INFORMATION FOR SEQ ID NO:3840:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 954 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..954



(D) OTHER INFORMATION: / Ceres Seq. ID 1578464

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3840:

aaacatactc	cgtttccgaa	tccgttccac	cattgcctat	tgccccatcc	tccccgctag	60
gtttttgccag	catggccgccc	gccgcgccc	ggaggctcct	ctccccgcgc	gcctcctcgt	120
cctccctctc	cgcgctcctc	cgtcgcggcg	ctgtcccgga	gcagtcgctg	gtgttgcgcc	180
cggctgttgt	cgcggcgggc	tcccgcctcg	gcttccagcg	cgggatggcg	cggcggcctg	240
gcggggacgg	ctacgtctcg	acgcggtctg	gcgcgggcgg	ggaccgcgcg	cmcatggcca	300
cggagatggc	gccgctgttc	cccgggtgcg	actacgagca	ttggctcatc	gtgatggaca	360
agccccggcg	ggagggcgcc	agCaagcagc	agatgattga	ctgctacatc	cagaccctcg	420
ccaaggtcct	tggaagcgag	gaggaggcga	agaagaagat	ctacaacgtc	tcgtgcgagc	480
gctacttcgg	gtttgggtgc	gagatcgatg	aggagacatc	taacaagctc	gaggggctcc	540
ctggGtggtc	tctttgtgct	cccggattcg	tatgttgatg	ctgaatacaa	ggactacgga	600
gctgaactct	tcgtcaacgg	tgagattggt	cagaggaccc	ccgagaggca	gaggagggtg	660
gagcccgtgc	cacagagggc	agcagacagg	ccgagggtaca	atgacagaac	ccgtacgcac	720
gcaggaggga	gaaccagcga	tgaactttgc	gataaaatca	taaaaaatac	cacagcaaca	780
agtcccaggt	ggtttcagct	ctggaattca	aggatcaccc	agtatcgctc	gtattaaatt	840
ggcaatctca	ctttacgtgc	agtctagagt	atcgtttcta	tgtgctcagc	ttggacgtat	900
tgtattctgt	aattacagct	acttggagat	ttggaaggac	ctggcttgca	acgt	

(2) INFORMATION FOR SEQ ID NO:3841:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..132

(D) OTHER INFORMATION: / Ceres Seq. ID 1578465

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3841:

Asn	Ile	Leu	Arg	Phe	Arg	Ile	Arg	Ser	Thr	Ile	Ala	Tyr	Cys	Pro	Ile
1			5						10					15	
Leu	Pro	Ala	Arg	Phe	Cys	Gln	His	Gly	Arg	Arg	Arg	Arg	Pro	Glu	Ala
		20						25					30		
Pro	Leu	Pro	Pro	Arg	Leu	Leu	Val	Leu	Pro	Leu	Arg	Ala	Pro	Pro	Ser
		35					40					45			
Arg	Arg	Cys	Pro	Gly	Ala	Val	Ala	Gly	Val	Ala	Pro	Gly	Cys	Cys	Arg
	50					55					60				
Gly	Gly	Leu	Pro	Pro	Arg	Leu	Pro	Ala	Arg	Asp	Gly	Ala	Ala	Ala	Trp
65					70				75						80
Arg	Gly	Arg	Leu	Arg	Leu	Asp	Ala	Val	Trp	Arg	Gly	Arg	Gly	Pro	Arg
				85				90						95	
Xaa	His	Gly	His	Gly	Asp	Gly	Ala	Ala	Val	Pro	Arg	Val	Arg	Leu	Arg
		100					105						110		
Ala	Leu	Ala	His	Arg	Asp	Gly	Gln	Ala	Arg	Arg	Gly	Gly	Arg	Gln	Gln
		115					120						125		
Ala	Ala	Asp	Asp												
		130													

(2) INFORMATION FOR SEQ ID NO:3842:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 191 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..191

(D) OTHER INFORMATION: / Ceres Seq. ID 1578466

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3842:

Thr Tyr Ser Val Ser Glu Ser Val Pro Pro Leu Pro Ile Ala Pro Ser

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(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..714
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1578468

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3844:

acatcccgat	ccttctctcg	gcggcccgtt	ggtcacgtga	ctcatcccc	tgtgctctcc	60
tctcgtaggc	ttgtttcctg	gcggcgacgg	ctggctgagc	ggcgccgccc	ttggctaggt	120
cttcgctggg	tccttccccg	gcgacgagcg	tccatctggg	gtcgactgaa	ctgagcaggc	180
agtaggaaga	gacactatgt	tgttcttctc	ctacttcCaa	ggagctggtg	gggaaggagg	240
tgacagtgga	gctcaagaat	gacttggcga	tccgcgggac	gctccactcg	gttgaccagt	300
acctcaacat	caagctcgag	aacacccgcg	tagtcgacca	ggacaagtat	ccccacatgc	360
tttcagtgcg	gaactgcttc	atcaggggct	cggtggtgcg	gtacgtgctg	ctcccgagG	420
acggcgtgga	catcgacatc	ctccacgacg	ccaccaggag	ggaggcgcg	ggaggctgat	480
cctgatgcgc	acccgctccc	tcacctgctg	gctgctgctt	catccccgat	tgtacgaagc	540
atgcatgtac	ggtgtgtggt	agacagatgc	cccagtttag	ttctttggtg	cttgccctgac	600
atagatatcc	caggttggtg	gatgacctga	atcacctgat	atattattgt	catatcatat	660
gcaatggtct	tgcatggggt	tgctatatta	ttaccatata	gtattatcac	atcg	

(2) INFORMATION FOR SEQ ID NO:3845:

- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 57 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..57
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1578469
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3845:

Thr	Ser	Arg	Ser	Phe	Ser	Arg	Arg	Pro	Val	Gly	His	Val	Thr	His	Pro
1				5					10					15	
Pro	Val	Leu	Ser	Ser	Arg	Gly	Leu	Val	Ser	Trp	Arg	Arg	Arg	Leu	Val
			20					25					30		
Glu	Arg	Arg	Arg	Pro	Trp	Leu	Gly	Leu	Arg	Trp	Val	Leu	Pro	Arg	Arg
			35				40					45			
Arg	Ala	Ser	Ile	Trp	Gly	Arg	Leu	Asn							
			50				55								

(2) INFORMATION FOR SEQ ID NO:3846:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 60 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..60
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1578470

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3846:

Ile	Pro	Ile	Leu	Ser	Ala	Ala	Arg	Trp	Ser	Arg	Asp	Ser	Ser	Pro
1				5				10					15	
Cys	Ala	Leu	Leu	Ser	Trp	Pro	Cys	Phe	Leu	Ala	Ala	Thr	Ala	Gly
			20					25					30	
Ala	Ala	Pro	Pro	Leu	Ala	Arg	Ser	Ser	Leu	Gly	Pro	Ser	Pro	Ala
			35				40					45		
Ser	Val	His	Leu	Gly	Ser	Thr	Glu	Leu	Ser	Arg	Gln			
			50				55				60			

(2) INFORMATION FOR SEQ ID NO:3847:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 40 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..40  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1578471  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3847:  
Met Leu Ser Val Arg Asn Cys Phe Ile Arg Gly Ser Val Val Arg Tyr  
1                  5                  10                  15  
Val Leu Leu Pro Gln Asp Gly Val Asp Ile Asp Ile Leu His Asp Ala  
                  20                  25                  30  
Thr Arg Arg Glu Ala Arg Gly Gly  
                  35                  40

(2) INFORMATION FOR SEQ ID NO:3848:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 905 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..905  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1578472  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3848:  
aaacagatac acacacactc gggtaaagct atctcgagct agctagctgc tgtaascggt 60  
gccatggcca aaatggtggt gctctgcgtg ctctgtctcct tcctcctgat gcccttggcc 120  
tccttagccc tgacgcagga cttctgcgtc gccgacctga cctgcagcga cacgccggcg 180  
gggtaccctg gcaagtccag cgtcaccgcc aacgacttct acttccacgg cctggccggc 240  
cagggcaaaa taaaccact catcaaggcc gccgtgacct cggccttctg gggccagttc 300  
ccggcggtca acgccttggc atctctgcgg ccaggctcga catcgagggtg ggcggcgctg 360  
tgccgctgca caccaccccg gcgggctcag agtccctctt cgtgacctcag ggcaccgNtc 420  
gccgcgggct tcatcagctc cggctccaac accgtctaca ccaagacgct gtacgccggc 480  
gacatcatgg tgttccccc gggcctgctc cactaccagt acaacgccgg canccggcgc 540  
tgccgtgggc ctctgcgcct tcagcagccc caaccgccg ctgcagatca ccgactttgc 600  
gctctttgcc aacaacctcc cgtccgccgt cgtggagaag gtcaccttct tggacgacgc 660  
gcagggtgaag aagctcaaga gtgtgctcgg cggcagcggg taacttggtt ttcgagacaa 720  
tacagtgcag gctgggtatg catcgctgcc gtcgtcgtct tgggccgtcg tcatogaatg 780  
gaacgcgtgt gcttgctgct gcatgcgtgc gtgcacctgt cgtcgcgtgt caaagtactc 840  
gtgggtctatt tcattctacc cttatttatt catctacttt tcattcaggg atgtattcag 900  
tttcc

(2) INFORMATION FOR SEQ ID NO:3849:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 113 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..113  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1578473  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3849:  
Met Ala Lys Met Val Leu Leu Cys Val Leu Val Ser Phe Leu Leu Met  
1                  5                  10                  15  
Pro Leu Ala Ser Leu Ala Leu Thr Gln Asp Phe Cys Val Ala Asp Leu  
                  20                  25                  30

Thr Cys Ser Asp Thr Pro Ala Gly Tyr Pro Cys Lys Ser Ser Val Thr  
35 40 45  
Ala Asn Asp Phe Tyr Phe His Gly Leu Ala Gly Gln Gly Lys Ile Asn  
50 55 60  
Pro Leu Ile Lys Ala Ala Val Thr Pro Ala Phe Val Gly Gln Phe Pro  
65 70 75 80  
Gly Val Asn Ala Leu Ala Ser Leu Arg Pro Gly Ser Thr Ser Arg Trp  
85 90 95  
Ala Ala Ser Cys Arg Cys Thr Pro Thr Arg Arg Ala Gln Ser Ser Ser  
100 105 110  
Ser

(2) INFORMATION FOR SEQ ID NO:3850:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 110 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..110

(D) OTHER INFORMATION: / Ceres Seq. ID 1578474

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3850:

Met Val Leu Leu Cys Val Leu Val Ser Phe Leu Leu Met Pro Leu Ala  
1 5 10 15  
Ser Leu Ala Leu Thr Gln Asp Phe Cys Val Ala Asp Leu Thr Cys Ser  
20 25 30  
Asp Thr Pro Ala Gly Tyr Pro Cys Lys Ser Ser Val Thr Ala Asn Asp  
35 40 45  
Phe Tyr Phe His Gly Leu Ala Gly Gln Gly Lys Ile Asn Pro Leu Ile  
50 55 60  
Lys Ala Ala Val Thr Pro Ala Phe Val Gly Gln Phe Pro Gly Val Asn  
65 70 75 80  
Ala Leu Ala Ser Leu Arg Pro Gly Ser Thr Ser Arg Trp Ala Ala Ser  
85 90 95  
Cys Arg Cys Thr Pro Thr Arg Arg Ala Gln Ser Ser Ser Ser  
100 105 110

(2) INFORMATION FOR SEQ ID NO:3851:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..139

(D) OTHER INFORMATION: / Ceres Seq. ID 1578475

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3851:

Met Val Phe Pro Gln Gly Leu Leu His Tyr Gln Tyr Asn Ala Gly Xaa  
1 5 10 15  
Arg Arg Cys Arg Gly Pro Arg Arg Leu Gln Gln Pro Gln Pro Arg Pro  
20 25 30  
Ala Asp His Arg Leu Cys Ala Leu Cys Gln Gln Pro Pro Val Arg Arg  
35 40 45  
Arg Gly Glu Gly His Leu Leu Gly Arg Arg Ala Gly Glu Glu Ala Gln  
50 55 60  
Glu Cys Ala Arg Arg Gln Arg Leu Thr Cys Phe Ser Arg Gln Tyr Ser  
65 70 75 80  
Ala Gly Trp Val Cys Ile Val Ala Val Val Val Leu Val Arg Arg His

85 90 95  
Arg Met Glu Arg Val Cys Leu Leu Leu His Ala Cys Val His Leu Ser  
100 105 110  
Ser Arg Val Lys Val Leu Val Val Tyr Phe Ile Leu Pro Leu Phe Ile  
115 120 125  
His Leu Leu Phe Ile Gln Gly Cys Ile Gln Phe  
130 135

(2) INFORMATION FOR SEQ ID NO:3852:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 590 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..590
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578479

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3852:

aaatcgaatc gagcccatcc atctccattt cmrcmgchgc mgccgccgag agaccccaac	60
cccacccatc caccaccatg tndmgcmgcc tccacaccct arcmcccgcc ttgcgcaggg	120
ctaccgcgcg cgccgccggg gccctgcGg cgctccgctc ctctgcagcc cgccgccgcc	180
cgctctcctc ggccggtacg gcggtggcgg cgccggctac ggtggcggcg gcggtacgg	240
tggtgggtggc ggccggtacg gcggtggcaa ccgtggcggc ggctacggca actccgacgg	300
gaactggagg aactgagcgg tggggcccgc gcggccaagt tatcctgttc gctaccgtgt	360
tgtttaccct agtcagagg gtttatcttc gttcgtctca tgttgtgtgt tgcccatctg	420
tgtttttgat tgcaaggctg ctttggtgca gttgttagtg ctgtgttcat cctcggtccc	480
agcagaccca tgcataacc agcatggact gcggatcgat ggatgctgtt acccccgtca	540
ggctttatcc taagttaatc ttcaaggaaa aaatggtgct tcttggtgct	

(2) INFORMATION FOR SEQ ID NO:3853:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..123
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578480

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3853:

Lys Ser Asn Arg Ala His Pro Ser Pro Phe Xaa Xaa Xaa Xaa Pro Pro  
1 5 10 15  
Arg Asp Pro Asn Pro Thr His Pro Pro Cys Xaa Xaa Ala Ser Thr  
20 25 30  
Pro Xaa Xaa Pro Pro Cys Ala Gly Leu Pro Pro Pro Pro Gly Pro  
35 40 45  
Leu Arg Arg Pro Pro Pro Leu Gln Pro Ala Pro Pro Arg Ser Pro Arg  
50 55 60  
Arg Leu Arg Arg Trp Arg Arg Arg Leu Arg Trp Arg Arg Arg Leu Arg  
65 70 75 80  
Trp Trp Trp Arg Arg Leu Arg Arg Trp Gln Pro Trp Arg Arg Leu Arg  
85 90 95  
Gln Leu Arg Arg Glu Leu Glu Glu Leu Ser Gly Gly Ala Arg Ala Ala  
100 105 110  
Lys Leu Ser Cys Ser Leu Pro Cys Cys Leu Pro  
115 120

(2) INFORMATION FOR SEQ ID NO:3854:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid

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- (C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..151  
(D) OTHER INFORMATION: / Ceres Seq. ID 1578481  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3854:

Ile Glu Ser Ser Pro Ser Ile Ser Ile Xaa Xaa Xaa Xaa Ala Ala Glu  
1 5 10 15  
Arg Pro Gln Pro His Pro Ser Thr Thr Met Xaa Xaa Xaa Leu His Thr  
20 25 30  
Leu Xaa Pro Ala Leu Arg Arg Ala Thr Ala Ala Ala Ala Gly Ala Pro  
35 40 45  
Ala Ala Ser Ala Ser Ser Ala Ala Arg Ala Ala Pro Leu Ser Ser Ala  
50 55 60  
Ala Thr Ala Val Ala Ala Ala Ala Thr Val Ala Ala Ala Ala Thr Val  
65 70 75 80  
Val Val Ala Ala Ala Thr Ala Val Ala Thr Val Ala Ala Ala Thr Ala  
85 90 95  
Thr Pro Thr Gly Thr Gly Gly Thr Glu Arg Trp Gly Pro Arg Gly Gln  
100 105 110  
Val Ile Leu Phe Ala Thr Val Leu Phe Thr Leu Val Gln Arg Val Tyr  
115 120 125  
Leu Arg Ser Ser His Val Cys Cys Cys Pro Ser Val Phe Leu Ile Ala  
130 135 140  
Arg Ser Leu Cys Val Ser Cys  
145 150

(2) INFORMATION FOR SEQ ID NO:3855:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 126 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..126  
(D) OTHER INFORMATION: / Ceres Seq. ID 1578482

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3855:

Met Xaa Xaa Xaa Leu His Thr Leu Xaa Pro Ala Leu Arg Arg Ala Thr  
1 5 10 15  
Ala Ala Ala Ala Gly Ala Pro Ala Ala Ser Ala Ser Ser Ala Ala Arg  
20 25 30  
Ala Ala Pro Leu Ser Ser Ala Ala Thr Ala Val Ala Ala Ala Thr  
35 40 45  
Val Ala Ala Ala Ala Thr Val Val Val Ala Ala Ala Thr Ala Val Ala  
50 55 60  
Thr Val Ala Ala Ala Thr Ala Thr Pro Thr Gly Thr Gly Gly Thr Glu  
65 70 75 80  
Arg Trp Gly Pro Arg Gly Gln Val Ile Leu Phe Ala Thr Val Leu Phe  
85 90 95  
Thr Leu Val Gln Arg Val Tyr Leu Arg Ser Ser His Val Cys Cys Cys  
100 105 110  
Pro Ser Val Phe Leu Ile Ala Arg Ser Leu Cys Val Ser Cys  
115 120 125

(2) INFORMATION FOR SEQ ID NO:3856:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 747 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

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- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..747  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1578486

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3856:

gacatatcgt	tcacgcatc	cagtcctctc	ccgggatctc	ctccggctat	aaatttccgg	60
cccccaattca	cccaatccag	atgcgcaaac	atcgaatcgt	ctcgctagtg	gctgccctac	120
tcgtgctgct	tgccctcgcc	gccgtttcct	ccacgcgcag	cGmacaaaag	gagtcgcggg	180
ctgacaacgc	cgggatgttg	gcaggcggca	tcaaggacgt	gccggcggaac	gagaacgacc	240
tccagctcca	ggagctcgcg	cgCttcgccg	tcaatgagca	caaccaaaag	gccaatgctc	300
ttctgggggt	cgagaagctt	gtgaaggcca	agacacaagt	ggttgctggc	acgatgtact	360
atctcactat	tgaagtgaag	gatggcggaag	tcaataagct	ctatgaagct	aaggtctggg	420
agaagccatg	ggagaacttc	aagcagctgc	aggaattcaa	gcctgttgaa	gaggggGcta	480
gcgcctaagg	atctgtcgtc	tccctgtgca	atttgctgcc	tgaagcgcaa	aactaagttg	540
cagaataagg	agctgcttcg	gaacatgcc	gagcatgcac	cctcgcgat	tttcataaaa	600
tcagtgcctc	taatgtaata	tcttgaattg	ccgtgccatg	tgtaataagt	aatatcatga	660
ataacagttg	ctattatggg	ttctaaatgt	gtattaacag	ccatccatgg	cagagttctc	720
atattacttt	gctgaagtct	ttgttg				

(2) INFORMATION FOR SEQ ID NO:3857:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..161  
(D) OTHER INFORMATION: / Ceres Seq. ID 1578487

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3857:

His	Ile	Val	His	Arg	Ile	Gln	Ser	Ser	Pro	Gly	Ile	Ser	Ser	Gly	Tyr	
1				5					10					15		
Lys	Phe	Pro	Ala	Pro	Ile	His	Pro	Ile	Gln	Met	Arg	Lys	His	Arg	Ile	
			20						25					30		
Val	Ser	Leu	Val	Ala	Ala	Leu	Leu	Val	Leu	Leu	Ala	Leu	Ala	Ala	Val	
			35						40					45		
Ser	Ser	Thr	Arg	Ser	Xaa	Gln	Lys	Glu	Ser	Ala	Ala	Asp	Asn	Ala	Gly	
			50											60		
Met	Leu	Ala	Gly	Gly	Ile	Lys	Asp	Val	Pro	Ala	Asn	Glu	Asn	Asp	Leu	
			65											80		
Gln	Leu	Gln	Glu	Leu	Ala	Arg	Phe	Ala	Val	Asn	Glu	His	Asn	Gln	Lys	
														95		
Ala	Asn	Ala	Leu	Leu	Gly	Phe	Glu	Lys	Leu	Val	Lys	Ala	Lys	Thr	Gln	
			100											110		
Val	Val	Ala	Gly	Thr	Met	Tyr	Tyr	Leu	Thr	Ile	Glu	Val	Lys	Asp	Gly	
			115											125		
Glu	Val	Asn	Lys	Leu	Tyr	Glu	Ala	Lys	Val	Trp	Glu	Lys	Pro	Trp	Glu	
			130											140		
Asn	Phe	Lys	Gln	Leu	Gln	Glu	Phe	Lys	Pro	Val	Glu	Glu	Gly	Ala	Ser	
145					150					155					160	
Ala																

(2) INFORMATION FOR SEQ ID NO:3858:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide



(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..135

(D) OTHER INFORMATION: / Ceres Seq. ID 1578488

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3858:

Met Arg Lys His Arg Ile Val Ser Leu Val Ala Ala Leu Leu Val Leu  
1 5 10 15  
Leu Ala Leu Ala Ala Val Ser Ser Thr Arg Ser Xaa Gln Lys Glu Ser  
20 25 30  
Ala Ala Asp Asn Ala Gly Met Leu Ala Gly Gly Ile Lys Asp Val Pro  
35 40 45  
Ala Asn Glu Asn Asp Leu Gln Leu Gln Glu Leu Ala Arg Phe Ala Val  
50 55 60  
Asn Glu His Asn Gln Lys Ala Asn Ala Leu Leu Gly Phe Glu Lys Leu  
65 70 75 80  
Val Lys Ala Lys Thr Gln Val Val Ala Gly Thr Met Tyr Tyr Leu Thr  
85 90 95  
Ile Glu Val Lys Asp Gly Glu Val Asn Lys Leu Tyr Glu Ala Lys Val  
100 105 110  
Trp Glu Lys Pro Trp Glu Asn Phe Lys Gln Leu Gln Glu Phe Lys Pro  
115 120 125  
Val Glu Glu Gly Ala Ser Ala  
130 135

(2) INFORMATION FOR SEQ ID NO:3859:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..97

(D) OTHER INFORMATION: / Ceres Seq. ID 1578489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3859:

Met Leu Ala Gly Gly Ile Lys Asp Val Pro Ala Asn Glu Asn Asp Leu  
1 5 10 15  
Gln Leu Gln Glu Leu Ala Arg Phe Ala Val Asn Glu His Asn Gln Lys  
20 25 30  
Ala Asn Ala Leu Leu Gly Phe Glu Lys Leu Val Lys Ala Lys Thr Gln  
35 40 45  
Val Val Ala Gly Thr Met Tyr Tyr Leu Thr Ile Glu Val Lys Asp Gly  
50 55 60  
Glu Val Asn Lys Leu Tyr Glu Ala Lys Val Trp Glu Lys Pro Trp Glu  
65 70 75 80  
Asn Phe Lys Gln Leu Glu Phe Lys Pro Val Glu Glu Gly Ala Ser  
85 90 95  
Ala

(2) INFORMATION FOR SEQ ID NO:3860:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 781 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..781

(D) OTHER INFORMATION: / Ceres Seq. ID 1578490

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3860:

agacagcctc cccattcatc agattcagat cagatcgtag cagccaagga ttccgcgctc 60  
cggggggtgcc atgaagctga agctcctctc tccctgcctt ctctcctcgc ccttctttgc 120  
caccgcggcg tacgcggcgt cggcgtcggc gtcgcgcgcg gcggccgctc tcaggggcgc 180  
gggcgccccg tcgcagtcgg agttggagtc ggaccgcgag aaccagtgcg tgtacacggt 240  
gtacgtgcgg acggggtcca tctggaaggg cggcacggac tcgaccatcg gcgtgacgct 300  
gctgggcgCc cgacggcacg ggcattccga tccgggacct ggcggggtgg ggcggcctca 360  
tgggcgccgg ccacgactac tacgagcgcg gcaacctgga catcttcagc ggccggggcc 420  
cctgcatgag ccaGGgcgcg ctgcGvcag aacctcacct ccgacggcac cggcgcgcac 480  
cacggctggt actgcaacta cctcgaggcc acggtcacgg ggccccacct cgggtgcgcg 540  
cagcagctct tcaccgtcga gcagtggctc gccaccgacg cgtcgcctta ccgcctgtac 600  
gcggtcgtcg acaagtgcaa gacgaagsgg caggagncgc gacgctcgcc ggccggcgag 660  
gccgaggcca ccgtgaccgc gctctaggta cgaccagtag taaatcatcg acagaggcta 720  
gctcctgcct ctgctgtgtg taattactgt atgtgagtga ccgatcccat cggattgcgt 780  
t

(2) INFORMATION FOR SEQ ID NO:3861:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..142
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3861:

Arg Gln Pro Pro His Ser Ser Asp Ser Asp Gln Ile Val Ala Ala Lys  
1 5 10 15  
Asp Ser Ala Leu Arg Gly Cys His Glu Ala Glu Ala Pro Leu Ser Leu  
20 25 30  
Pro Ser Pro Pro Arg Leu Leu Cys His Arg Gly Val Arg Gly Val Gly  
35 40 45  
Val Gly Val Ala Arg Gly Gly Arg Arg Gln Gly Arg Gly Arg Pro Val  
50 55 60  
Ala Val Gly Val Gly Val Gly Pro Gly Glu Pro Val Arg Val His Gly  
65 70 75 80  
Val Arg Ala Asp Gly Val His Leu Glu Gly Arg His Gly Leu Asp His  
85 90 95  
Arg Arg Asp Ala Ala Gly Arg Pro Thr Ala Arg Ala Ser Gly Ser Gly  
100 105 110  
Thr Trp Arg Gly Gly Ala Ala Ser Trp Ala Pro Ala Thr Thr Thr Thr  
115 120 125  
Ser Ala Ala Thr Trp Thr Ser Ser Ala Ala Gly Ala Pro Ala  
130 135 140

(2) INFORMATION FOR SEQ ID NO:3862:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..126
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578492

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3862:

Met Lys Leu Lys Leu Leu Ser Pro Cys Leu Leu Leu Leu Ala Phe Phe  
1 5 10 15  
Ala Thr Ala Ala Tyr Ala Ala Ser Ala Ser Ala Ser Arg Ala Ala Ala  
20 25 30  
Val Val Arg Gly Ala Gly Ala Pro Ser Gln Ser Glu Leu Glu Ser Asp

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35 40 45  
Pro Glu Asn Gln Cys Val Tyr Thr Val Tyr Val Arg Thr Gly Ser Ile  
50 55 60  
Trp Lys Gly Gly Thr Asp Ser Thr Ile Gly Val Thr Leu Leu Gly Ala  
65 70 75 80  
Arg Arg His Gly His Pro Asp Pro Gly Pro Gly Gly Val Gly Arg Pro  
85 90 95  
His Gly Arg Arg Pro Arg Leu Leu Arg Ala Arg Gln Pro Gly His Leu  
100 105 110  
Gln Arg Pro Gly Pro Leu His Glu Pro Gly Arg Pro Ala Xaa  
115 120 125

(2) INFORMATION FOR SEQ ID NO:3863:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: -  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..127  
(D) OTHER INFORMATION: / Ceres Seq. ID 1578493

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3863:

Met Gly Ala Gly His Asp Tyr Tyr Glu Arg Gly Asn Leu Asp Ile Phe  
1 5 10 15  
Ser Gly Arg Gly Pro Cys Met Ser Gln Gly Ala Leu Xaa His Glu Pro  
20 25 30  
His Leu Arg Arg His Arg Arg Ala Pro Arg Leu Val Leu Gln Leu Pro  
35 40 45  
Arg Gly His Gly His Gly Ala Pro Pro Arg Val Arg Ala Ala Ala Leu  
50 55 60  
His Arg Arg Ala Val Ala Arg His Arg Arg Val Ala Leu Pro Pro Val  
65 70 75 80  
Arg Gly Arg Arg Gln Val Gln Asp Glu Xaa Ala Gly Xaa Ala Thr Leu  
85 90 95  
Ala Gly Arg Arg Gly Arg Gly His Arg Asp Arg Ala Leu Gly Thr Thr  
100 105 110  
Ser Ser Lys Ser Ser Thr Glu Ala Ser Ser Cys Leu Cys Cys Val  
115 120 125

(2) INFORMATION FOR SEQ ID NO:3864:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 714 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..714  
(D) OTHER INFORMATION: / Ceres Seq. ID 1578510

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3864:

atcagcctcg attgattcgt cttccctttc cctcgatctc cattctccag tgtgggtcgtg 60  
cagtgtttctc tttcttgctt gagatacgat acgaagatca gcccctgarc cgatcccatg 120  
gctgcwgcctt cccctctccg tccagcaacg ccggcmgcgc tccGgcacgg ggcgtgccac 180  
gggctGgggc tggcgctacc gaggaNgttt kycGccgtcg gCGgcaaNcg cgatgcgccg 240  
cgCtaacgccg ggacgcgagc ggcgcccggg accagtagcg aggcgcgctg gtggacgagg 300  
gcatgcccgt gctgcggcgg cggtatccggg aggcgtggat ggtggagacc aactacgagg 360  
cgcccgcga gtgggcgcgg tgggagaagc ggtactacc cgcctaCgtc tccgacgtgt 420  
ctagcctcgt cggcgcgctg cagctgctgc tcatgggcac caggcccggc gtcgccatcg 480  
ccgtgcgccg cctgggtgctg gccagcgtcc ccgtgtccac cgtcgcccg ctagacatct 540  
ggcgatggtg gccgaggccg tctgcagtc cgtccatcac atttcttgat ccagtcggac 600

catcttttggg tctccttttt tcttttcatt tgtaaccttg aggcagtctg ccgcgtgaat 660  
agtattggag gcttgtagtt gcagctggat tgatctaaag attcttttagc cttg

(2) INFORMATION FOR SEQ ID NO:3865:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..210
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578511

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3865:

Gln Pro Arg Leu Ile Arg Leu Pro Phe Pro Ser Ile Ser Ile Leu Gln  
1 5 10 15  
Cys Gly Arg Ala Val Phe Ser Phe Leu Pro Glu Ile Arg Tyr Glu Asp  
20 25 30  
Gln Pro Leu Xaa Arg Ser His Gly Cys Xaa Phe Pro Leu Pro Ser Ser  
35 40 45  
Asn Ala Gly Xaa Ala Pro Ala Arg Gly Val Pro Arg Ala Gly Ala Gly  
50 55 60  
Ala Thr Glu Xaa Val Xaa Arg Arg Arg Arg Gln Xaa Arg Cys Ala Ala  
65 70 75 80  
Leu Arg Arg Asp Ala Ser Gly Gly Arg Asp Gln Tyr Gly Gly Ala Leu  
85 90 95  
Val Asp Glu Gly Met Pro Val Leu Arg Arg Arg Ile Arg Glu Ala Trp  
100 105 110  
Met Val Glu Thr Asn Tyr Glu Ala Pro Ala Glu Trp Ala Pro Trp Glu  
115 120 125  
Lys Arg Tyr Tyr Pro Ala Tyr Val Ser Asp Val Ser Ser Leu Val Gly  
130 135 140  
Ala Leu Gln Leu Leu Leu Met Gly Thr Arg Pro Gly Val Ala Ile Ala  
145 150 155 160  
Val Ala Ala Leu Val Leu Ala Ser Val Pro Val Ser Thr Val Ala Ala  
165 170 175  
Leu His Ile Trp Arg Trp Trp Pro Arg Pro Ser Cys Ser Pro Ser Ile  
180 185 190  
Thr Phe Leu Asp Pro Val Gly Pro Ser Phe Gly Leu Leu Phe Ser Phe  
195 200 205  
His Leu  
210

(2) INFORMATION FOR SEQ ID NO:3866:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..186
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578512

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3866:

Met Ala Xaa Ala Ser Leu Ser Arg Pro Ala Thr Pro Xaa Ala Leu Arg  
1 5 10 15  
His Gly Ala Cys His Gly Leu Gly Leu Ala Leu Pro Arg Xaa Phe Xaa  
20 25 30  
Ala Val Gly Gly Xaa Arg Asp Ala Pro Arg Tyr Ala Gly Thr Arg Ala  
35 40 45  
Ala Ala Gly Thr Ser Thr Glu Ala Arg Trp Trp Thr Arg Ala Cys Pro

50 55 60  
Cys Cys Gly Gly Gly Ser Gly Arg Arg Gly Trp Trp Arg Pro Thr Thr  
65 70 75 80  
Arg Arg Pro Pro Ser Gly Arg Arg Gly Arg Ser Gly Thr Thr Pro Pro  
85 90 95  
Thr Ser Pro Thr Cys Leu Ala Ser Ser Ala Arg Cys Ser Cys Cys Ser  
100 105 110  
Trp Ala Pro Gly Pro Ala Ser Pro Ser Pro Ser Pro Pro Trp Cys Trp  
115 120 125  
Pro Ala Ser Pro Cys Pro Pro Ser Pro Arg Tyr Thr Ser Gly Asp Gly  
130 135 140  
Gly Arg Gly Arg Pro Ala Val Arg Pro Ser His Phe Leu Ile Gln Ser  
145 150 155 160  
Asp His Leu Leu Val Ser Phe Phe Leu Phe Ile Cys Asn Leu Glu Ala  
165 170 175  
Val Cys Arg Val Asn Ser Ile Gly Gly Leu  
180 185

(2) INFORMATION FOR SEQ ID NO:3867:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 110 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..110

(D) OTHER INFORMATION: / Ceres Seq. ID 1578513

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3867:

Met Pro Val Leu Arg Arg Ile Arg Glu Ala Trp Met Val Glu Thr  
1 5 10 15  
Asn Tyr Glu Ala Pro Ala Glu Trp Ala Pro Trp Glu Lys Arg Tyr Tyr  
20 25 30  
Pro Ala Tyr Val Ser Asp Val Ser Ser Leu Val Gly Ala Leu Gln Leu  
35 40 45  
Leu Leu Met Gly Thr Arg Pro Gly Val Ala Ile Ala Val Ala Ala Leu  
50 55 60  
Val Leu Ala Ser Val Pro Val Ser Thr Val Ala Leu His Ile Trp  
65 70 75 80  
Arg Trp Trp Pro Arg Pro Ser Cys Ser Pro Ser Ile Thr Phe Leu Asp  
85 90 95  
Pro Val Gly Pro Ser Phe Gly Leu Leu Phe Ser Phe His Leu  
100 105 110

(2) INFORMATION FOR SEQ ID NO:3868:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 683 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..683

(D) OTHER INFORMATION: / Ceres Seq. ID 1578524

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3868:

aagcagacccc gggcgggccc tggcaattca cgcacctsgc gtgcacacag acacaggcag 60  
gcacacagcg caatcacctg ctgcctcgc agtcgtactc acggtcttgc acacaccctg 120  
ccccatcttc ttccggtgtc gccatcccct ccgtcgaccg ccgcgtccgg ccgcggcaac 180  
ccgacctgtg tcaatcgcca tgactacctc aaggcgttct gctgatagga agatatcacg 240  
atttgagaag aatatcaca agaggggtc tgttcctgag acagccaaga aggcaaacga 300  
ttatcctgtt gggcctattc ttcttgggtt ctttgtcttc gtggttggtg gatcatctct 360

```
ctttcagatc atcaagacag catcaaacgc tgggtctattc tgaggtgaat cggttgacac 420
atgcagtttg tcactagaaa ctatacaagt gtagggcgtg gcttaatgtc gcctttttaa 480
tggtgtaccg tggagagttt taagttatat atgtaatgga agtgctaatt taagtcacct 540
gtctgacagg aaagatggtg gagtagtCca taatacatat cgagtatagt tatagttcgt 600
gttaaattatt tctatgctca aattggtcgc atcattgggc tattgtactc ttcgatttat 660
cgagtaattt ggtaattctt cgc
```

(2) INFORMATION FOR SEQ ID NO:3869:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..74

(D) OTHER INFORMATION: / Ceres Seq. ID 1578525

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3869:

```
Lys Gln Thr Arg Ala Gly Pro Gly Asn Ser Arg Thr Xaa Arg Ala His
1      5      10      15
Arg His Arg Gln Ala His Ser Ala Ile Thr Val Ser Pro Arg Ser Arg
20     25     30
Thr His Gly Leu Ala His Thr Arg Pro His Pro Leu Pro Val Ser Pro
35     40     45
Ser Pro Pro Ser Thr Ala Ala Ser Gly Arg Gly Asn Pro Thr Cys Val
50     55     60
Asn Arg His Asp Tyr Leu Lys Ala Ser Cys
65     70
```

(2) INFORMATION FOR SEQ ID NO:3870:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..133

(D) OTHER INFORMATION: / Ceres Seq. ID 1578526

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3870:

```
Ser Arg Pro Gly Arg Ala Leu Ala Ile His Ala Pro Xaa Val His Thr
1      5      10      15
Asp Thr Gly Arg His Thr Ala Gln Ser Pro Ser Arg Leu Ala Val Val
20     25     30
Leu Thr Val Leu His Thr Pro Val Pro Ile Leu Phe Arg Cys Arg His
35     40     45
Pro Leu Arg Arg Pro Pro Arg Pro Ala Ala Ala Thr Arg Pro Val Ser
50     55     60
Ile Ala Met Thr Thr Ser Arg Arg Leu Ala Asp Arg Lys Ile Ser Arg
65     70     75     80
Phe Glu Lys Asn Ile Thr Lys Arg Gly Ser Val Pro Glu Thr Ala Lys
85     90     95
Lys Ala Asn Asp Tyr Pro Val Gly Pro Ile Leu Leu Gly Phe Phe Val
100    105    110
Phe Val Val Val Gly Ser Ser Leu Phe Gln Ile Ile Lys Thr Ala Ser
115    120    125
Asn Ala Gly Leu Phe
130
```

(2) INFORMATION FOR SEQ ID NO:3871:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..67  
(D) OTHER INFORMATION: / Ceres Seq. ID 1578527  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3871:  
Met Thr Thr Ser Arg Arg Leu Ala Asp Arg Lys Ile Ser Arg Phe Glu  
1 5 10 15  
Lys Asn Ile Thr Lys Arg Gly Ser Val Pro Glu Thr Ala Lys Lys Ala  
20 25 30  
Asn Asp Tyr Pro Val Gly Pro Ile Leu Leu Gly Phe Phe Val Phe Val  
35 40 45  
Val Val Gly Ser Ser Leu Phe Gln Ile Ile Lys Thr Ala Ser Asn Ala  
50 55 60  
Gly Leu Phe  
65

(2) INFORMATION FOR SEQ ID NO:3872:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 707 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..707  
(D) OTHER INFORMATION: / Ceres Seq. ID 1578540

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3872:

atccatatgc actagcagta tcacctcatt taatatgcgg ccggcatcgt cgccagagct 60  
ctcgataagg ctcgccagas tctcatctca tacgccggag gtgctccaga gagcagggct 120  
gaagaggtgc ggcaagagct gcaggctgag gtacaccaac tatcgcgcg tgatctgggc 180  
gacgaactgc gtgcgcgTtt tgcagggtgg cctgatcgcg gaaGcagctg ccggggcgga 240  
cgggcaacga cgtgaggaac cgttggaaca cgaaactgag agcaagcagc tgcggcagcg 300  
cgggatcgac cccaccgccc ccatcgccgg cctcatgcac atcttcgtcg gcgccctctc 360  
cttacggcga cgacggcacg ggaacgacga cggcacggga gagatcatcg acgccaccct 420  
ggactgRcga caagaagaca cgggtggacc agtcacgcg ctagtgtctg gccgaccggg 480  
cctactacgc tggctcctcc tccgagatgg gctggatcat gggcttgatg aatgctgatt 540  
aattagcggg tatacaatgg atccatgagg cttaaagcaaa ctgactgaaa tagtcacttt 600  
agaggctaaa gtttcaaaca taaagaacta aaagggacta aaatgtttta gtccttttag 660  
cttgtaagga cgagttaaac tcgactaaaa cagctgggtcc cacaccc

(2) INFORMATION FOR SEQ ID NO:3873:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 178 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..178  
(D) OTHER INFORMATION: / Ceres Seq. ID 1578541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3873:

Ser Ile Cys Thr Ser Ser Ile Thr Ser Phe Asn Met Arg Pro Ala Ser  
1 5 10 15  
Ser Pro Glu Leu Ser Ile Arg Leu Ala Arg Xaa Ser Ser His Thr Pro  
20 25 30  
Glu Val Leu Gln Arg Ala Gly Leu Lys Arg Cys Gly Lys Ser Cys Arg  
35 40 45

```
(2) INFORMATION FOR SEQ ID NO:3874:
  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 167 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS:
      (D) TOPOLOGY: linear
  (ii) MOLECULE TYPE: peptide
  (ix) FEATURE:
      (A) NAME/KEY: peptide
      (B) LOCATION: 1..167
      (D) OTHER INFORMATION: / Ceres Seq. ID 1578542
  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3874:
```

```
(2) INFORMATION FOR SEQ ID NO:3875:
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 697 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
      (ii) MOLECULE TYPE: DNA (genomic)
      (ix) FEATURE:
            (A) NAME/KEY: -
```



(B) LOCATION: 1..697

(D) OTHER INFORMATION: / Ceres Seq. ID 1578543

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3875:

aaacagtctc	ggcctctcct	cccggttcc	tcacacggca	ctccagccgc	tagccctcac	60
tcaaccagac	aaccagtaca	ccaccgccac	caagcccggg	ccgaataact	ctgccgggca	120
accgccgccc	ttcgccggca	aagaacgccc	accagatcca	ccccggcctg	ctatggagtc	180
cgcggtgaac	ccgaaGgcgt	acccgctggc	tgatgcgcaG	ctgacgatgg	gtatcctcga	240
tatcatccag	caggccgcca	actacaagca	gtcaagaag	ggagcgaacg	aagcgacgaa	300
aaccctgaat	agggggatat	cggagttcgt	tgtgatggcg	gcgacacg	agcctctcga	360
gatcctgctc	cacctccct	tgttagccga	ggataagaac	gtcccatatg	tatttgttcc	420
atcgaaacaa	gctcttgccc	gtgcttggtg	tgtgacaaga	cccgtcattg	cttgctcagt	480
gaccagcaat	gagggtagcc	agctgaaaca	acagatacag	ggtctcaagg	actcgattga	540
gaagcttctc	atctgattta	cctaagatct	ttcagtggtg	tgggcctcgg	cgacacattt	600
ttcagaggct	tggactgggtg	atgggtgtctt	gtttacatta	cgctttccaa	actatatttg	660
aacactgcta	agtcaatcat	atgtgaattg	tgcttcg			

(2) INFORMATION FOR SEQ ID NO:3876:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 184 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..184

(D) OTHER INFORMATION: / Ceres Seq. ID 1578544

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3876:

Asn	Ser	Leu	Gly	Leu	Ser	Ser	Arg	Leu	Pro	His	Thr	Ala	Leu	Gln	Pro	
1			5					10						15		
Leu	Ala	Leu	Thr	Gln	Pro	Asp	Asn	Gln	Tyr	Thr	Thr	Ala	Thr	Lys	Pro	
			20					25						30		
Gly	Pro	Asn	Asn	Ser	Ala	Gly	Gln	Pro	Pro	Pro	Phe	Ala	Gly	Lys	Glu	
			35				40						45			
Arg	Pro	Pro	Asp	Pro	Pro	Arg	Pro	Ala	Met	Glu	Ser	Ala	Val	Asn	Pro	
			50				55					60				
Lys	Ala	Tyr	Pro	Leu	Ala	Asp	Ala	Gln	Leu	Thr	Met	Gly	Ile	Leu	Asp	
							70				75				80	
Ile	Ile	Gln	Gln	Ala	Ala	Asn	Tyr	Lys	Gln	Leu	Lys	Lys	Gly	Ala	Asn	
							85				90				95	
Glu	Ala	Thr	Lys	Thr	Leu	Asn	Arg	Gly	Ile	Ser	Glu	Phe	Val	Val	Met	
			100					105						110		
Ala	Ala	Asp	Thr	Glu	Pro	Leu	Glu	Ile	Leu	Leu	His	Leu	Pro	Leu	Leu	
			115					120						125		
Ala	Glu	Asp	Lys	Asn	Val	Pro	Tyr	Val	Phe	Val	Pro	Ser	Lys	Gln	Ala	
			130					135						140		
Leu	Gly	Arg	Ala	Cys	Gly	Val	Thr	Arg	Pro	Val	Ile	Ala	Cys	Ser	Val	
							150							155		
Thr	Ser	Asn	Glu	Gly	Ser	Gln	Leu	Lys	Gln	Gln	Ile	Gln	Gly	Leu	Lys	
							165							170		
Asp	Ser	Ile	Glu	Lys	Leu	Leu	Ile									
							180									

(2) INFORMATION FOR SEQ ID NO:3877:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..127

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3877:

(2) INFORMATION FOR SEO ID NO:3878:

(A) LENGTH: 109 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..109

(D) OTHER INFORMATION: / Ceres Seq. ID 1578546

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3878:

(2) INFORMATION FOR SEQ ID NO:3879:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 472 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..472

(D) OTHER INFORMATION: / Ceres Seq. ID 1578582

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3879:

gatacgttag	tagttcacca	gagttcacac	aaaaatcaca	agcaagcagt	cgcgtgtgta	60
gctcgcaaca	atggcgacga	acccgggcct	cttcaccgag	tggcogtgga	agaagctcgg	120
caacttcaag	gtagctcccg	gcacggcgcc	cgtctcagta	ccctgcgtgc	gtacgtccat	180
ggcacagag	gggggagaag	gtgaaggaaa	attagcaact	cgtcttctgc	tcaccggcgg	240
cdtcccatgc	catggcaatc	ttgggcgcgt	ggtatatggc	catgtgcggc	acgCagtgtc	300

(2) INFORMATION FOR SEQ ID NO:3880:

(A) LENGTH: 67 amino aci

- (A) LENGTH: 67 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..67  
(D) OTHER INFORMATION: / Ceres Seq. ID 1578583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3880:

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..95  
(D) OTHER INFORMATION: / Ceres Seq. ID 1578584

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3881:

Met	Ala	Thr	Asn	Pro	Gly	Leu	Phe	Thr	Glu	Trp	Pro	Trp	Lys	Lys	Leu
1				5					10					15	
Gly	Asn	Phe	Lys	Val	Ala	Pro	Gly	Thr	Gly	Pro	Val	Ser	Val	Pro	Cys
			20					25					30		
Val	Arg	Thr	Ser	Met	Ala	Gln	Ser	Gly	Gly	Glu	Gly	Glu	Gly	Lys	Leu
		35					40					45			
Ala	Thr	Arg	Leu	Leu	Leu	Thr	Gly	Gly	Val	Pro	Cys	His	Gly	Asn	Leu
	50					55					60				
Gly	Arg	Met	Val	Tyr	Gly	His	Val	Arg	His	Ala	Val	Ser	Glu	His	Ala
65					70					75					80
Cys	Thr	His	Gly	Leu	Ala	Ile	His	Thr	Cys	Met	His	Arg	Gln	Pro	
				85					90					95	

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..66  
(D) OTHER INFORMATION: / Ceres Seq. ID 1578585

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3882:

Met Pro Trp Gln Ser Trp Ala His Gly Ile Trp Pro Cys Ala Ala Arg  
1 5 10 15  
Ser Val Gly Thr Cys Met His Ala Trp Thr Cys Tyr Thr Tyr Met His  
20 25 30  
Ala Pro Ala Ala Val Arg Pro Ser Val His Glu Ser Tyr Ala Pro Val  
35 40 45  
His Leu Met Phe Arg Pro Thr His Glu His Gly Arg Lys Pro Pro Lys  
50 55 60  
Val His  
65

(2) INFORMATION FOR SEQ ID NO:3883:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 780 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..780
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578586

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3883:

aattcacgac cttattgata ctccccactg cacaaagatg acatagagaa acatgtgaag 60  
gagctcttgg cctcgggtat gatcgtcccc agtaatagcc catttgctc cccggttttg 120  
tgtcaattac tggaagttaa actcactatc aaaaaccggt ttccattcc gatcatgat 180  
gaaattctgg acgagttggc aggcacaaaa cttttcacca agctggacat gagatcgggt 240  
taccatcaag tcgggatgca ttcagatgat gagtttaaaa cgacattcaa aatacatcat 300  
ggacattttc agtttcattg ttgacagact tcagttcgca agacctgttg ccggatcaac 360  
ttctggactg tcgcttggtg aagaaaggca gtaaggcggg tccacaagtg ttagtccaat 420  
ggcgcaatct tctagctgct tctgctacgt gggaggactg gtacgtgttg aagaatcact 480  
ttccacacat ggctgcttgg ggacaggcat caactgaagg ggaggagat gtagcgCccg 540  
acgtgtcGgg tgcggtacag gagtctgcag aagccgtgcc caagtgaagg cgtaatgtgt 600  
taggtccgt catttacttt gttaagagtc atttaaggta ccattggtgg gctcaatgta 660  
atgaccagca actatgctgt taaggtcctt gtggtcggaa cctgaggaac attatcatgc 720  
aaaaagaata tacacgaaag tgaactcggg gttgccttgc ctcgcaagtt catcatccct 780

(2) INFORMATION FOR SEQ ID NO:3884:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..81
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578587

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3884:

Met Ile Val Pro Ser Asn Ser Pro Phe Ala Ser Pro Val Leu Cys Gln  
1 5 10 15  
Leu Leu Glu Val Lys Leu Thr Ile Lys Asn Arg Phe Pro Ile Pro Ile  
20 25 30  
Ile Asp Glu Ile Leu Asp Glu Leu Ala Gly Thr Lys Leu Phe Thr Lys  
35 40 45  
Leu Asp Met Arg Ser Gly Tyr His Gln Val Gly Met His Ser Asp Asp  
50 55 60  
Glu Phe Lys Thr Thr Phe Lys Ile His His Gly His Phe Gln Phe His  
65 70 75 80  
Cys

(2) INFORMATION FOR SEQ ID NO:3885:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 42 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..42  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1578588  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3885:  
Met Met Ser Leu Lys Arg His Ser Lys Tyr Ile Met Asp Ile Phe Ser  
1                  5                  10                  15  
Phe Ile Val Asp Arg Leu Gln Phe Ala Arg Pro Val Ala Gly Ser Thr  
                  20                  25                  30  
Ser Gly Leu Ser Leu Gly Glu Glu Arg Gln  
                  35                  40

(2) INFORMATION FOR SEQ ID NO:3886:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 41 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..41  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1578589  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3886:  
Met Ser Leu Lys Arg His Ser Lys Tyr Ile Met Asp Ile Phe Ser Phe  
1                  5                  10                  15  
Ile Val Asp Arg Leu Gln Phe Ala Arg Pro Val Ala Gly Ser Thr Ser  
                  20                  25                  30  
Gly Leu Ser Leu Gly Glu Glu Arg Gln  
                  35                  40

(2) INFORMATION FOR SEQ ID NO:3887:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 514 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..514  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1578590  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3887:  
atcgcaactcg tagtcgtagc tcaagcatca rcvgcaggag ctctgggcag cgtgcgcacg          60  
trgggtacct agctcgctct gctagcctac catggtgat caccaccggg gcgcgcacggg          120  
argtgscggg ggctacggcg acctccagcg cgggggcggc atgcacggcg aggcgcagCa          180  
gcagcagaag cagggcgcca tgatgacggc gctcaaggcc gcgacggccg cgacctcctt          240  
gaaccactgc cggcgcgggc gcatatggcc cttaaaggcg gtggtctgtg ctacgtacgc          300  
tgccgtagag tctcggtcgc cgcatagCt ctagctagtc gtttatgtgt tgtgctttgt          360  
gtgtgcatgc ttgtgtctgg gggcatgcag tgcagtgcag tactatatgc tgtatgcgtc          420  
tctctttgat cggagaggcg gatgtacagc atgctcgata tgtctagttt ggatgtcatg          480  
tttatgatga ggaataaaat gcagtgttca ggtg

(2) INFORMATION FOR SEQ ID NO:3888:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 66 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..66  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1578591  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3888:  
Arg Thr Arg Ser Arg Ser Ser Ser Ile Xaa Xaa Arg Ser Ser Gly Gln  
1                  5                  10                  15  
Arg Ala His Xaa Gly Tyr Leu Ala Arg Ser Ala Ser Leu Pro Trp Leu  
          20                  25                  30  
Ile Thr Thr Gly Ala Arg Arg Xaa Val Xaa Gly Ala Thr Ala Thr Ser  
          35                  40                  45  
Ser Ala Gly Ala Ala Cys Thr Ala Arg Arg Ser Ser Ser Arg Ser Arg  
50                  55                  60  
Ala Pro  
65

(2) INFORMATION FOR SEQ ID NO:3889:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..78
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578592

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3889:

Met Ala Asp His His Arg Gly Ala Thr Gly Xaa Xaa Gly Gly Tyr Gly  
1                  5                  10                  15  
Asp Leu Gln Arg Gly Gly Gly Met His Gly Glu Ala Gln Gln Gln Gln  
          20                  25                  30  
Lys Gln Gly Ala Met Met Thr Ala Leu Lys Ala Ala Thr Ala Ala Thr  
          35                  40                  45  
Ser Leu Asn His Cys Arg Arg Gly Gly Ile Trp Pro Leu Lys Ala Val  
50                  55                  60  
Ala Ala Ala Thr Tyr Ala Ala Val Glu Ser Arg Ser Pro Arg  
65                  70                  75

(2) INFORMATION FOR SEQ ID NO:3890:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..55
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578593

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3890:

Met His Gly Glu Ala Gln Gln Gln Gln Lys Gln Gly Ala Met Met Thr  
1                  5                  10                  15  
Ala Leu Lys Ala Ala Thr Ala Ala Thr Ser Leu Asn His Cys Arg Arg  
          20                  25                  30  
Gly Gly Ile Trp Pro Leu Lys Ala Val Ala Ala Ala Thr Tyr Ala Ala  
35                  40                  45  
Val Glu Ser Arg Ser Pro Arg  
50                  55

(2) INFORMATION FOR SEQ ID NO:3891:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1077 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..1077  
(D) OTHER INFORMATION: / Ceres Seq. ID 1578630  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3891:

gtaccttggt tcatgctcag ttgatggaat aattgaagtc tgggattatc ttagtggaag 60  
gcttaaaaag gatcttcaat atcaagccga tgaaagcttt atgatgcacg aggaacctgt 120  
gctgtgtggt gatcttagta gggattctga aatgctggca totggatcac aggatggaaa 180  
gattaagggt tggcgtatac gaactgggtca gtgcttgcaa cgccttgagc gtgcacattc 240  
gaaagggtgtt acaagtgtta catttttcacg tgatggaacc caaatattga gtacatcctt 300  
tgacactacc gcgagggtac atggcctcaa gtctggaaag atgctgaaag aatttcgagg 360  
tcattcttca tatgtaaatt atgccatctt cactactgac ggtagccgtg tcattacagc 420  
ttccagtgat tgtactgtta aggtctggGa tactaaaaca acagattgct tgcatacttt 480  
caagccacca cctcctttga ggggaggaga tgcactgttt aattctgtcc atttatttcc 540  
aaaaaatact gatcacattg ttgtctgcaa taagacttca tcaatattca tcatKgactt 600  
tacaaggaca ggttgtgaag agtttctcat caggtaaagcg agaaggggga gattttgttg 660  
cagcttcagt ttcacaaaaa ggagaatgga tatattgtgt tgggtgaagac atgaacatgt 720  
attgcttttag ctaccaatct ggtaaactgg agcatctgat gaagggtgat gagaaggatg 780  
tcataggcat tacgcaccat cctcacagga acttagtagc caccattgct gaggattgta 840  
tgatgaagat atggaagcct tgactttttt tctttttaaa aaaaccttga accgatgatt 900  
aaataggatg tattttgttt tgtaatttag ataactggta ggcgctacag ctatggactc 960  
gttggtgctt atgttgcccc atgtcttact accattgtat cctgtactag atttagggac 1020  
ctttcaatgg tgtaaacaca gcttactacg actcctcgct acaagttcat tatggtc

(2) INFORMATION FOR SEQ ID NO:3892:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 211 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..211  
(D) OTHER INFORMATION: / Ceres Seq. ID 1578631  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3892:

Tyr Leu Val Ser Cys Ser Val Asp Gly Ile Ile Glu Val Trp Asp Tyr  
1 5 10 15  
Leu Ser Gly Lys Leu Lys Lys Asp Leu Gln Tyr Gln Ala Asp Glu Ser  
20 25 30  
Phe Met Met His Glu Glu Pro Val Leu Cys Val Asp Phe Ser Arg Asp  
35 40 45  
Ser Glu Met Leu Ala Ser Gly Ser Gln Asp Gly Lys Ile Lys Val Trp  
50 55 60  
Arg Ile Arg Thr Gly Gln Cys Leu Gln Arg Leu Glu Arg Ala His Ser  
65 70 75 80  
Lys Gly Val Thr Ser Val Thr Phe Ser Arg Asp Gly Thr Gln Ile Leu  
85 90 95  
Ser Thr Ser Phe Asp Thr Thr Ala Arg Val His Gly Leu Lys Ser Gly  
100 105 110  
Lys Met Leu Lys Glu Phe Arg Gly His Ser Ser Tyr Val Asn Tyr Ala  
115 120 125  
Ile Phe Thr Thr Asp Gly Ser Arg Val Ile Thr Ala Ser Ser Asp Cys  
130 135 140  
Thr Val Lys Val Trp Asp Thr Lys Thr Thr Asp Cys Leu His Thr Phe  
145 150 155 160  
Lys Pro Pro Pro Pro Leu Arg Gly Gly Asp Ala Ser Val Asn Ser Val

165 170 175  
His Leu Phe Pro Lys Asn Thr Asp His Ile Val Val Cys Asn Lys Thr  
180 185 190  
Ser Ser Ile Phe Ile Xaa Asp Phe Thr Arg Thr Gly Cys Glu Glu Phe  
195 200 205  
Leu Ile Arg  
210

(2) INFORMATION FOR SEQ ID NO:3893:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 178 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..178

(D) OTHER INFORMATION: / Ceres Seq. ID 1578632

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3893:

Met Met His Glu Glu Pro Val Leu Cys Val Asp Phe Ser Arg Asp Ser  
1 5 10 15  
Glu Met Leu Ala Ser Gly Ser Gln Asp Gly Lys Ile Lys Val Trp Arg  
20 25 30  
Ile Arg Thr Gly Gln Cys Leu Gln Arg Leu Glu Arg Ala His Ser Lys  
35 40 45  
Gly Val Thr Ser Val Thr Phe Ser Arg Asp Gly Thr Gln Ile Leu Ser  
50 55 60  
Thr Ser Phe Asp Thr Thr Ala Arg Val His Gly Leu Lys Ser Gly Lys  
65 70 75 80  
Met Leu Lys Glu Phe Arg Gly His Ser Ser Tyr Val Asn Tyr Ala Ile  
85 90 95  
Phe Thr Thr Asp Gly Ser Arg Val Ile Thr Ala Ser Ser Asp Cys Thr  
100 105 110  
Val Lys Val Trp Asp Thr Lys Thr Thr Asp Cys Leu His Thr Phe Lys  
115 120 125  
Pro Pro Pro Pro Leu Arg Gly Asp Ala Ser Val Asn Ser Val His  
130 135 140  
Leu Phe Pro Lys Asn Thr Asp His Ile Val Val Cys Asn Lys Thr Ser  
145 150 155 160  
Ser Ile Phe Ile Xaa Asp Phe Thr Arg Thr Gly Cys Glu Glu Phe Leu  
165 170 175  
Ile Arg

(2) INFORMATION FOR SEQ ID NO:3894:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..177

(D) OTHER INFORMATION: / Ceres Seq. ID 1578633

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3894:

Met His Glu Glu Pro Val Leu Cys Val Asp Phe Ser Arg Asp Ser Glu  
1 5 10 15  
Met Leu Ala Ser Gly Ser Gln Asp Gly Lys Ile Lys Val Trp Arg Ile  
20 25 30  
Arg Thr Gly Gln Cys Leu Gln Arg Leu Glu Arg Ala His Ser Lys Gly  
35 40 45



Val Thr Ser Val Thr Phe Ser Arg Asp Gly Thr Gln Ile Leu Ser Thr  
50 55 60  
Ser Phe Asp Thr Thr Ala Arg Val His Gly Leu Lys Ser Gly Lys Met  
65 70 75 80  
Leu Lys Glu Phe Arg Gly His Ser Ser Tyr Val Asn Tyr Ala Ile Phe  
85 90 95  
Thr Thr Asp Gly Ser Arg Val Ile Thr Ala Ser Ser Asp Cys Thr Val  
100 105 110  
Lys Val Trp Asp Thr Lys Thr Thr Asp Cys Leu His Thr Phe Lys Pro  
115 120 125  
Pro Pro Pro Leu Arg Gly Gly Asp Ala Ser Val Asn Ser Val His Leu  
130 135 140  
Phe Pro Lys Asn Thr Asp His Ile Val Val Cys Asn Lys Thr Ser Ser  
145 150 155 160  
Ile Phe Ile Xaa Asp Phe Thr Arg Thr Gly Cys Glu Glu Phe Leu Ile  
165 170 175  
Arg

(2) INFORMATION FOR SEQ ID NO:3895:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 906 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..906
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578674

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3895:

aatgatattc agcttagtat tcgtatgccc agtggaata gactggagat caaactaaca	60
aaacaagatg ttttaaggaa agtgaagaat ttcgtggatg aaaaccaagg caatgggctt	120
ggctcatatg acctttctct ggtttatcct aaaagagttt tctctgaaca agatatggaa	180
gcaacactat ccgagctggg tattcaaaac cgtcatgcaa tgattgttgt tccacatcgg	240
cagtctggtc aggtatcaag gcgtcactcc tcggcatctt atgatatggg tgtcaattca	300
ggtgcggatg atgttggtg caattcagggt gcggggggat actttgggta cctgagaacc	360
gtcctgtctt atgtgaatcc actctcctac ctgaggggaa ataccaactc atcaaataca	420
gagctacagt caaatgaagG Cctgcggcag cttagacatg gatctgggtcc atggagtga	480
ccacggcctc ttggcaatag gggccatgaa gtgactgatg cagactctgc aaacacgctg	540
cgaaggcggc ctagaccatt tgggtgccaat atccacactc tggggagcga ggatcatggt	600
ccgtctgatg aaagaaatgt tttctggaac gggaactcga cagagtttgg aggcgacgac	660
agaaaatagg ttgtggcgtg gctggcaggg cctgggacga cactatcaga cagaatcaaa	720
gttggaata gacagctgaa acaaatgcct cgacaggctt attgaggaat aagtattgag	780
attatagtgc tgaaataatc gctgaattgt gatgtttaca tttgtggaaa catacggtcg	840
ctggatccgt atactcgttg tatagtacat agccacagat atattaaatc cgaactgctt	900

ggttcc

(2) INFORMATION FOR SEQ ID NO:3896:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..222
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578675

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3896:

Asn Asp Ile Gln Leu Ser Ile Arg Met Pro Ser Gly Asn Arg Leu Glu	
1 5 10 15	
Ile Lys Leu Thr Lys Gln Asp Val Leu Arg Lys Val Lys Asn Phe Val	

20 25 30  
Asp Glu Asn Gln Gly Asn Gly Leu Gly Ser Tyr Asp Leu Ser Leu Val  
35 40 45  
Tyr Pro Lys Arg Val Phe Ser Glu Gln Asp Met Glu Ala Thr Leu Ser  
50 55 60  
Glu Leu Gly Ile Gln Asn Arg His Ala Met Ile Val Val Pro His Arg  
65 70 75 80  
Gln Ser Gly Gln Val Ser Arg Arg His Ser Ser Ala Ser Tyr Asp Met  
85 90 95  
Gly Val Asn Ser Gly Ala Asp Asp Val Gly Gly Asn Ser Gly Ala Gly  
100 105 110  
Gly Tyr Phe Gly Tyr Leu Arg Thr Val Leu Ser Tyr Val Asn Pro Leu  
115 120 125  
Ser Tyr Leu Arg Gly Asn Thr Asn Ser Ser Asn Thr Glu Leu Gln Ser  
130 135 140  
Asn Glu Gly Leu Arg Gln Leu Arg His Gly Ser Gly Pro Trp Ser Glu  
145 150 155 160  
Pro Arg Pro Leu Gly Asn Arg Gly His Glu Val Thr Asp Ala Asp Ser  
165 170 175  
Ala Asn Thr Leu Arg Arg Arg Pro Arg Pro Phe Gly Ala Asn Ile His  
180 185 190  
Thr Leu Gly Ser Glu Asp His Gly Pro Ser Asp Glu Arg Asn Val Phe  
195 200 205  
Trp Asn Gly Asn Ser Thr Glu Phe Gly Gly Asp Asp Arg Lys  
210 215 220

(2) INFORMATION FOR SEQ ID NO:3897:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 214 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..214

(D) OTHER INFORMATION: / Ceres Seq. ID 1578676

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3897:

Met Pro Ser Gly Asn Arg Leu Glu Ile Lys Leu Thr Lys Gln Asp Val  
1 5 10 15  
Leu Arg Lys Val Lys Asn Phe Val Asp Glu Asn Gln Gly Asn Gly Leu  
20 25 30  
Gly Ser Tyr Asp Leu Ser Leu Val Tyr Pro Lys Arg Val Phe Ser Glu  
35 40 45  
Gln Asp Met Glu Ala Thr Leu Ser Glu Leu Gly Ile Gln Asn Arg His  
50 55 60  
Ala Met Ile Val Val Pro His Arg Gln Ser Gly Gln Val Ser Arg Arg  
65 70 75 80  
His Ser Ser Ala Ser Tyr Asp Met Gly Val Asn Ser Gly Ala Asp Asp  
85 90 95  
Val Gly Gly Asn Ser Gly Ala Gly Gly Tyr Phe Gly Tyr Leu Arg Thr  
100 105 110  
Val Leu Ser Tyr Val Asn Pro Leu Ser Tyr Leu Arg Gly Asn Thr Asn  
115 120 125  
Ser Ser Asn Thr Glu Leu Gln Ser Asn Glu Gly Leu Arg Gln Leu Arg  
130 135 140  
His Gly Ser Gly Pro Trp Ser Glu Pro Arg Pro Leu Gly Asn Arg Gly  
145 150 155 160  
His Glu Val Thr Asp Ala Asp Ser Ala Asn Thr Leu Arg Arg Arg Pro  
165 170 175  
Arg Pro Phe Gly Ala Asn Ile His Thr Leu Gly Ser Glu Asp His Gly  
180 185 190

Pro Ser Asp Glu Arg Asn Val Phe Trp Asn Gly Asn Ser Thr Glu Phe  
195 200 205  
Gly Gly Asp Asp Arg Lys  
210

(2) INFORMATION FOR SEQ ID NO:3898:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..164
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578677

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3898:

Met Glu Ala Thr Leu Ser Glu Leu Gly Ile Gln Asn Arg His Ala Met  
1 5 10 15  
Ile Val Val Pro His Arg Gln Ser Gly Gln Val Ser Arg Arg His Ser  
20 25 30  
Ser Ala Ser Tyr Asp Met Gly Val Asn Ser Gly Ala Asp Asp Val Gly  
35 40 45  
Gly Asn Ser Gly Ala Gly Gly Tyr Phe Gly Tyr Leu Arg Thr Val Leu  
50 55 60  
Ser Tyr Val Asn Pro Leu Ser Tyr Leu Arg Gly Asn Thr Asn Ser Ser  
65 70 75 80  
Asn Thr Glu Leu Gln Ser Asn Glu Gly Leu Arg Gln Leu Arg His Gly  
85 90 95  
Ser Gly Pro Trp Ser Glu Pro Arg Pro Leu Gly Asn Arg Gly His Glu  
100 105 110  
Val Thr Asp Ala Asp Ser Ala Asn Thr Leu Arg Arg Arg Pro Arg Pro  
115 120 125  
Phe Gly Ala Asn Ile His Thr Leu Gly Ser Glu Asp His Gly Pro Ser  
130 135 140  
Asp Glu Arg Asn Val Phe Trp Asn Gly Asn Ser Thr Glu Phe Gly Gly  
145 150 155 160  
Asp Asp Arg Lys

(2) INFORMATION FOR SEQ ID NO:3899:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 745 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..745
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578682

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3899:

cagacaataa tatacaatgc tgtgtttaag gtcataatg ctgttatatc agacatgcgg 60  
cctggagtta attggatgga tatgcacaaa ttagcagaac gggcaatact tgaatctctc 120  
aggaaggaac aaattgtaca aggggatggt gatgatatga tggctcaaag gttaggggct 180  
gttttcatgc ctcatggtct tggccactta cttggtattg acacccatga tccaggaggc 240  
taccctgagg gattggagag gccaaggat coaggactga actccttgcg gaccacaaga 300  
gaactgaaag aaggaatggt tatcacagt gagccaggct gctatttcat tgatgctttg 360  
ctaactaaaa caagggatga tccaatttcc tcaaagttct tcaactggca agaggttgaa 420  
aagtataaaa gctttggtgg cgttcgcatt gaaagtgatg tgtatgtgac ggctcaagga 480  
tgccggaacc tcacaaactg cccgagagag acctgggaga tcgaggctgt aatGgctggc 540  
gcaccatggc ctctgccggc ttcaaGttct atggtggtag cagcagagAa tagcaatgac 600  
atatctaaag cgtcgtaatt ttctctatgc tcaatccata tcccgagttg aaacaaattc 660

gacctggatt cttatattca ataaatagtg aggcctgaggc gcaaaacatt gttggattga 720  
tggttggaac acatttcata cgccc

(2) INFORMATION FOR SEQ ID NO:3900:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..205
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578683

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3900:

Gln Thr Ile Ile Tyr Asn Ala Val Phe Lys Ala His Asn Ala Val Ile  
1 5 10 15  
Ser Asp Met Arg Pro Gly Val Asn Trp Met Asp Met His Lys Leu Ala  
20 25 30  
Glu Arg Ala Ile Leu Glu Ser Leu Arg Lys Glu Gln Ile Val Gln Gly  
35 40 45  
Asp Val Asp Asp Met Met Ala Gln Arg Leu Gly Ala Val Phe Met Pro  
50 55 60  
His Gly Leu Gly His Leu Leu Gly Ile Asp Thr His Asp Pro Gly Gly  
65 70 75 80  
Tyr Pro Glu Gly Leu Glu Arg Pro Lys Asp Pro Gly Leu Asn Ser Leu  
85 90 95  
Arg Thr Thr Arg Glu Leu Lys Glu Gly Met Val Ile Thr Val Glu Pro  
100 105 110  
Gly Cys Tyr Phe Ile Asp Ala Leu Thr Lys Thr Arg Asp Asp Pro  
115 120 125  
Ile Ser Ser Lys Phe Phe Asn Trp Gln Glu Val Glu Lys Tyr Lys Ser  
130 135 140  
Phe Gly Gly Val Arg Ile Glu Ser Asp Val Tyr Val Thr Ala Gln Gly  
145 150 155 160  
Cys Arg Asn Leu Thr Asn Cys Pro Arg Glu Thr Trp Glu Ile Glu Ala  
165 170 175  
Val Met Ala Gly Ala Pro Trp Pro Leu Pro Ala Ser Ser Ser Met Val  
180 185 190  
Val Ala Ala Glu Asn Ser Asn Asp Ile Ser Lys Ala Ser  
195 200 205

(2) INFORMATION FOR SEQ ID NO:3901:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..187
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578684

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3901:

Met Arg Pro Gly Val Asn Trp Met Asp Met His Lys Leu Ala Glu Arg  
1 5 10 15  
Ala Ile Leu Glu Ser Leu Arg Lys Glu Gln Ile Val Gln Gly Asp Val  
20 25 30  
Asp Asp Met Met Ala Gln Arg Leu Gly Ala Val Phe Met Pro His Gly  
35 40 45  
Leu Gly His Leu Leu Gly Ile Asp Thr His Asp Pro Gly Gly Tyr Pro  
50 55 60  
Glu Gly Leu Glu Arg Pro Lys Asp Pro Gly Leu Asn Ser Leu Arg Thr

(B) LOCATION: 1..789

(D) OTHER INFORMATION: / Ceres Seq. ID 1578692

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3903:

aagagccaac	agagcaacgc	ccaggcacac	acgacacgaa	ccargcagcc	agccgcggag	60
ggaggaacct	tagcggaaca	ggtgacggcg	gcgcgctacc	ggtgacgggg	gatacggcgg	120
catcgtcccc	tcctccatcc	ccggcgcgcc	ggcgagcag	ccggcctgca	ggctgtttga	180
agagctcgcc	atttaatctc	aatggaagcc	aagtttttcc	gtttcctgaa	gctcgttggg	240
gtcggcttca	aagcgaggtc	agagagccaa	ggcgtgagt	tgttccttaa	actgggcttc	300
agccatgagg	tgcagttcac	cgctcctcca	gctgtccgtg	tcttctgctt	caaaccacaac	360
ataatctgct	gcaccggcat	cgataaggac	agggtgcacc	agttcgcccg	cgccatccgg	420
agctctaagg	ctccagaggt	gtacaagggg	aaggggatcc	tgtacattga	cgagggttatc	480
aagctgaagc	ccggaaagaa	gcgaaaaaat	aagtgcagat	ccgaaGgcgt	tacaactttt	540
tctgtctttt	Aaccccatcc	ttcgcatttg	tagtgatctg	gatctggggg	ctgctgtgtt	600
gtgttggtga	cttgcggttg	gctacacaga	tcaccattat	cttaccttta	cctcagctgc	660
atgtaggacc	atgagtggga	ataagttacc	agtttggtga	tatgagctgg	aacgttgctt	720
tgcaatttgg	attggattac	cgagtgggat	gttttggttc	aaacttgaag	tctttcaata	780
gattgttgc						

(2) INFORMATION FOR SEQ ID NO:3904:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 91 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..91

(D) OTHER INFORMATION: / Ceres Seq. ID 1578693

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3904:

Glu	Pro	Thr	Glu	Gln	Arg	Pro	Gly	Thr	His	Asp	Thr	Asn	Xaa	Ala	Ala	
1				5				10					15			
Ser	Arg	Gly	Gly	Arg	Asn	Pro	Ser	Gly	Thr	Gly	Asp	Gly	Gly	Ala	Leu	
			20					25					30			
Pro	Val	Thr	Gly	Asp	Thr	Ala	Ala	Ser	Ser	Pro	Pro	Pro	Ser	Pro	Ala	
			35				40					45				
Arg	Arg	Arg	Ser	Ser	Arg	Pro	Ala	Gly	Cys	Leu	Lys	Ser	Ser	Pro	Phe	
			50			55				60						
Asn	Leu	Asn	Gly	Ser	Gln	Val	Phe	Pro	Phe	Pro	Glu	Ala	Arg	Trp	Gly	
65				70				75						80		
Arg	Leu	Gln	Ser	Glu	Val	Arg	Glu	Pro	Arg	Pro						
			85					90								

(2) INFORMATION FOR SEQ ID NO:3905:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 104 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..104

(D) OTHER INFORMATION: / Ceres Seq. ID 1578694

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3905:

Met	Glu	Ala	Lys	Phe	Phe	Arg	Phe	Leu	Lys	Leu	Val	Gly	Val	Gly	Phe	
1			5					10					15			
Lys	Ala	Arg	Ser	Glu	Ser	Gln	Gly	Arg	Glu	Leu	Phe	Leu	Lys	Leu	Gly	
			20				25					30				
Phe	Ser	His	Glu	Val	Gln	Phe	Thr	Ala	Pro	Pro	Ala	Val	Arg	Val	Phe	
			35			40					45					
Cys	Phe	Lys	Pro	Asn	Ile	Ile	Cys	Cys	Thr	Gly	Ile	Asp	Lys	Asp	Arg	
			50			55			60							
Val	His	Gln	Phe	Ala	Gly	Ala	Ile	Arg	Ser	Ser	Lys	Ala	Pro	Glu	Val	

Ser	Gly	Cys	Leu	Gly	Arg	Phe	Leu	Ile	Leu	Leu	Ala	Ser	Pro	Asn	Pro
1				5					10					15	
Lys	Pro	Lys	Pro	Phe	Thr	Arg	Xaa	Arg	Arg	Arg	Arg	Arg	Arg	Arg	His
			20					25					30		
His	Ile	Arg	Ser	Ala	Gln	Pro	Pro	Glu	Lys	Arg	Arg	Glu	Pro	Ala	Pro
		35					40					45			
Ala	Thr	Met	Gly	Arg	Val	Arg	Thr	Lys	Thr	Val	Lys	Lys	Thr	Ser	Arg
	50					55					60				
Gln	Val	Ile	Glu	Lys	Tyr	Tyr	Ser	Arg	Met	Thr	Leu	Asp	Phe	His	Thr
65					70					75					80
Asn	Lys	Lys	Val	Leu	Glu	Glu	Val	Ser	Ile	Leu	Pro	Ser	Lys	Arg	Leu
			85						90					95	
Arg	Asn	Lys	Val	Ala	Gly	Phe	Thr	Thr	His	Leu	Met	Arg	Arg	Ile	Gln
			100					105					110		
Arg	Gly	Pro	Arg	Pro	Leu	Leu	Arg	Arg	Leu	Gly	Ala	Thr	Glu	Val	Val
		115					120					125			
Ala	Ala	Thr	Ala	Ala	Ala	Ala	Xaa	Ala	Gly	Gly	Thr	Asp	Val	Trp	Ala
	130					135					140				
His	Pro	Gly	Phe	Gly	Arg	Val	Ile	Leu	Ser	Ile	Tyr	Ser	Ile	Val	Leu
145					150					155					160
Pro	Phe	Ala	Ser	Val	Thr	Val	Leu	Val	Ser	Val	Leu	Pro	Leu	Asp	

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(2) INFORMATION FOR SEQ ID NO:3909:
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 102 amino acids
            (B) TYPE: amino acid
            (C) STRANDEDNESS:
            (D) TOPOLOGY: linear
      (ii) MOLECULE TYPE: peptide
      (ix) FEATURE:
            (A) NAME/KEY: peptide
            (B) LOCATION: 1..102
            (D) OTHER INFORMATION: / Ceres Seq. ID 1578698
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3909:
Met Thr Leu Asp Phe His Thr Asn Lys Lys Val Leu Glu Glu Val Ser
1          5          10          15
Ile Leu Pro Ser Lys Arg Leu Arg Asn Lys Val Ala Gly Phe Thr Thr
          20          25          30
His Leu Met Arg Arg Ile Gln Arg Gly Pro Arg Pro Leu Leu Arg Arg
          35          40          45
Leu Gly Ala Thr Glu Val Val Ala Ala Thr Ala Ala Ala Ala Xaa Ala
          50          55          60
Gly Gly Thr Asp Val Trp Ala His Pro Gly Phe Gly Arg Val Ile Leu
65          70          75          80
Ser Ile Tyr Ser Ile Val Leu Pro Phe Ala Ser Val Thr Val Leu Val
          85          90          95
Ser Val Leu Pro Leu Asp
          100

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[illegible]



(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..592

(D) OTHER INFORMATION: / Ceres Seq. ID 1578699

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3910:

acacacacca	tcgtcctctc	ctttgccagc	gccgccgaac	ccgccaccag	ccttctccca	60
tcctcgaagc	acggaaggct	cccagaagga	gctctcacct	cgcagccatc	tctggcacgt	120
ccgtccttct	tctccctcgg	tccctcccct	tctccacagc	tatcggattg	gcgttggagt	180
ggagatcgac	ccgggctcgg	aattcccttc	gttggttaag	aaccctaatt	tggtcagatg	240
ggatttccaa	cttcgacaaa	gcccgcgagg	tcgatcgatc	tcagttgacg	cgagggattg	300
gaaaactaag	ttgcgggtgt	agttaatttt	ctaggaagat	tggggtttca	gctcaaactc	360
ccatgctcga	cgctgaggac	gaccCtggcg	ggagatgacg	aggatottcg	tgcagcgcg	420
gaccgcccgc	tcctcgtcca	gctccggccg	ctcggacacg	cagccagtgc	agccggcagc	480
agctgcccgg	gaggaggagt	tgccgctgca	acotcaacca	cagctgccgg	agctattggc	540
catagatgat	acaactgata	atttaaata	gggcagcgag	aatatcagca	at	

(2) INFORMATION FOR SEQ ID NO:3911:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..75

(D) OTHER INFORMATION: / Ceres Seq. ID 1578700

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3911:

Thr	His	Thr	Ile	Val	Leu	Ser	Phe	Ala	Ser	Ala	Ala	Glu	Pro	Ala	Thr	
1				5					10					15		
Ser	Leu	Leu	Pro	Ser	Ser	Lys	His	Gly	Arg	Leu	Pro	Glu	Gly	Ala	Leu	
			20					25						30		
Thr	Ser	Gln	Pro	Ser	Leu	Ala	Arg	Pro	Ser	Phe	Phe	Ser	Leu	Gly	Pro	
			35				40						45			
Ser	Pro	Ser	Pro	Gln	Leu	Ser	Asp	Trp	Arg	Trp	Ser	Gly	Asp	Arg	Pro	
			50			55						60				
Gly	Leu	Gly	Ile	Pro	Phe	Val	Gly	Lys	Glu	Pro						
65				70					75							

(2) INFORMATION FOR SEQ ID NO:3912:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 106 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..106

(D) OTHER INFORMATION: / Ceres Seq. ID 1578701

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3912:

His	Thr	Pro	Ser	Ser	Ser	Pro	Leu	Pro	Ala	Pro	Pro	Asn	Pro	Pro	Pro	
1				5					10					15		
Ala	Phe	Ser	His	Pro	Arg	Ser	Thr	Glu	Ser	Gln	Lys	Glu	Leu	Ser		
			20					25					30			
Pro	Arg	Ser	His	Leu	Trp	His	Val	Arg	Pro	Ser	Ser	Pro	Ser	Val	Pro	
			35			40						45				
Pro	Leu	Leu	His	Ser	Tyr	Arg	Ile	Gly	Val	Gly	Val	Glu	Ile	Asp	Pro	
			50			55					60					
Gly	Ser	Glu	Phe	Pro	Ser	Leu	Val	Arg	Asn	Pro	Asn	Leu	Val	Arg	Trp	
65				70					75					80		
Asp	Phe	Gln	Leu	Arg	Gln	Ser	Pro	Arg	Gly	Arg	Ser	Ile	Ser	Val	Asp	

85 90 95  
Ala Arg Asp Trp Lys Thr Lys Leu Arg Val  
100 105

(2) INFORMATION FOR SEQ ID NO:3913:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..71

(D) OTHER INFORMATION: / Ceres Seq. ID 1578702

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3913:

Thr His His Arg Pro Leu Leu Cys Gln Arg Arg Arg Thr Arg His Gln  
1 5 10 15  
Pro Ser Pro Ile Leu Glu Ala Arg Lys Ala Pro Arg Arg Ser Ser His  
20 25 30  
Leu Ala Ala Ile Ser Gly Thr Ser Val Leu Leu Leu Pro Arg Ser Leu  
35 40 45  
Pro Phe Ser Thr Ala Ile Gly Leu Ala Leu Glu Trp Arg Ser Thr Arg  
50 55 60  
Ala Arg Asn Ser Leu Arg Trp  
65 70

(2) INFORMATION FOR SEQ ID NO:3914:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1051 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1051

(D) OTHER INFORMATION: / Ceres Seq. ID 1578703

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3914:

gagccaccaa gagatccacg aatataccca tccattccc cacaaggctc cgtcccttcg 60  
gcggcgcgca tgtctctccc cctrgccc gcggacagt gcgcccgcac cggagacgac 120  
tggttccctcg actgcrat cctcgacgac ctgcccgcgc cggcctgcgc ggccttccc 180  
tgggacgcgt ccccgctcgt ttccaacccc agtgtggaag tgggcagcta tgtaaacgcc 240  
aatgatgcat tcaaggagcc caatgatgtc ttcaaggagc ctggcagcag taaacgttta 300  
cggtcaggat ccagtatat gccaacatct aaagcttgca gggaaagaat gaggaggaac 360  
aagctgaatg acagggttct tgaactgggg tctgcattag aacctgggaa gccagtgaac 420  
gctgacaaaag ctgccatccc taagcgatgc tactgcgatg gttattcagc tccgttcaga 480  
atcacagcaa ctgaaggaga ctaatggcag cctcgaagaa aagattaaag aactaaaggc 540  
cgagaaggac gagttcgcga cgagaagcag aaactgaaac tggagaagga gagtctagag 600  
caccagatga agctgatggc atcggctcca gcctacatgc cccatccgac cctgatgccg 660  
gcgcctttcg cccaggcgcc cctaactcca ttccatgccc agggccaagc tgcagggcag 720  
aagctgatga tgcccttcgt cggctaccca gggtaaccaa tgtggcagtt catgcgcct 780  
tcagaggtcg acacctcgaa ggacagcgag gcgtgccctc ctgtcgcatg atcaacctga 840  
tggggctggc cctgctcaca ccatgtggat tagccgcaac tagttgtcgt tgcgatcca 900  
ttgatggggt ataactgatg ttcttaggct atctccagca gcctctctat cctattctct 960  
atcttactcc ctattttaaa ttttactctg taaacagtac agtctatagt gtaagacaat 1020  
gttttgcatg tttatatcca cgccttgctg g

(2) INFORMATION FOR SEQ ID NO:3915:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..167

(D) OTHER INFORMATION: / Ceres Seq. ID 1578704

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3915:

Glu Pro Pro Arg Asp Pro Arg Ile Tyr Pro Ser His Ser Pro Gln Gly  
1 5 10 15  
Ser Val Pro Ser Ala Ala Ala Met Ser Leu Pro Pro Xaa Pro Ala Asp  
20 25 30  
Ser Gly Ala Gly Thr Gly Asp Asp Trp Phe Leu Asp Cys Xaa Ile Leu  
35 40 45  
Asp Asp Leu Pro Ala Ala Ala Cys Gly Ala Phe Pro Trp Asp Ala Ser  
50 55 60  
Pro Ser Ser Ser Asn Pro Ser Val Glu Val Gly Ser Tyr Val Asn Ala  
65 70 75 80  
Asn Asp Ala Phe Lys Glu Pro Asn Asp Val Phe Lys Glu Pro Gly Ser  
85 90 95  
Ser Lys Arg Leu Arg Ser Gly Ser Ser Asp Met Pro Thr Ser Lys Ala  
100 105 110  
Cys Arg Glu Arg Met Arg Arg Asn Lys Leu Asn Asp Arg Phe Leu Glu  
115 120 125  
Leu Gly Ser Ala Leu Glu Pro Gly Lys Pro Val Lys Ala Asp Lys Ala  
130 135 140  
Ala Ile Pro Lys Arg Cys Tyr Ser His Gly Tyr Ser Ala Pro Phe Arg  
145 150 155 160  
Ile Thr Ala Thr Glu Gly Asp  
165

(2) INFORMATION FOR SEQ ID NO:3916:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 144 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..144

(D) OTHER INFORMATION: / Ceres Seq. ID 1578705

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3916:

Met Ser Leu Pro Pro Xaa Pro Ala Asp Ser Gly Ala Gly Thr Gly Asp  
1 5 10 15  
Asp Trp Phe Leu Asp Cys Xaa Ile Leu Asp Asp Leu Pro Ala Ala Ala  
20 25 30  
Cys Gly Ala Phe Pro Trp Asp Ala Ser Pro Ser Ser Ser Asn Pro Ser  
35 40 45  
Val Glu Val Gly Ser Tyr Val Asn Ala Asn Asp Ala Phe Lys Glu Pro  
50 55 60  
Asn Asp Val Phe Lys Glu Pro Gly Ser Ser Lys Arg Leu Arg Ser Gly  
65 70 75 80  
Ser Ser Asp Met Pro Thr Ser Lys Ala Cys Arg Glu Arg Met Arg Arg  
85 90 95  
Asn Lys Leu Asn Asp Arg Phe Leu Glu Leu Gly Ser Ala Leu Glu Pro  
100 105 110  
Gly Lys Pro Val Lys Ala Asp Lys Ala Ala Ile Pro Lys Arg Cys Tyr  
115 120 125  
Ser His Gly Tyr Ser Ala Pro Phe Arg Ile Thr Ala Thr Glu Gly Asp  
130 135 140

(2) INFORMATION FOR SEQ ID NO:3917:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 991 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..991  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1578737  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3917:

aaaaatcgaa tcgagcccat ccattccat ttccgcccgc gccgcccgc agagacccca 60  
accccaacca tccaccacca tgtggcgccg cctccacacc ctagcccccg ccttgccgag 120  
ggctacccgc gccgcccgcg gggccctgc ggcgccgc tcctctgcag cccgcgccgc 180  
cccgtctccc tggcgccgcg ccgctttccg ccgcaccagc ccgctcctct caggggacaa 240  
gccggcgagt gtggaggacg tcatgcccac cgccacgggg ctcgagcggg aggagctgga 300  
ggccgagctc aagggggaaga agcgggtttga catggatccc ctggtcggcc ccttcgggtac 360  
caaggaggaa ccattctgtag ttgagtccta ctataacaag cggatagtcg gctgccctgg 420  
tggtgaggga gaggatgaac acgatgttgt atggttcttg ttgaaaaaag atgagccgca 480  
tgagtgtcca gtctgctcgc aatactttgt gcttaaggtc attggtgatg ggtggtgatc 540  
cagatggtca tgacgatgaa gatgatggac atcactaagg atgccttgtg gttctgaaaa 600  
taagaatttg gtgaggcaga tgaatccaat acacttcttt ttctagaacc agactgctcc 660  
acggcatcct tgtttatgaa aagacagttg gccatcaagc aggtggtagt ttccacctag 720  
gtattttgtc caaacaaaag ctgtttgaga ttgaccctt gcgtttcttt aagagcatcg 780  
tcgaataaaa gatgactgca gtcagattgc ttctttttga tacctcatat tggcccatcg 840  
ggtgtgatgg acatgtaata ttcagtaatg gaacagcccc atttctatgc ttagcgtgct 900  
gggaattttg caaaaggcct cctatatcat tgacgagttt taagccagag tttgatgatc 960  
caacatgttt atgaccattg ttttaatagc c

(2) INFORMATION FOR SEQ ID NO:3918:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 109 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..109  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1578738  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3918:

Lys Asn Arg Ile Glu Pro Ile His Leu His Phe Arg Arg Arg Arg Arg  
1 5 10 15  
Arg Glu Thr Pro Thr Pro Pro Ile His His His Val Ala Pro Pro Pro  
20 25 30  
His Pro Ser Pro Arg Leu Ala Gln Gly Tyr Arg Arg Arg Arg Arg Gly  
35 40 45  
Pro Cys Gly Val Arg Leu Leu Cys Ser Pro Arg Arg Pro Ala Leu Leu  
50 55 60  
Gly Gly Arg Arg Phe Pro Pro His Gln Pro Ala Pro Leu Arg Gly Gln  
65 70 75 80  
Ala Gly Glu Cys Gly Gly Arg His Ala His Arg His Gly Ala Arg Ala  
85 90 95  
Gly Gly Ala Gly Gly Arg Ala Gln Gly Glu Glu Ala Val  
100 105

(2) INFORMATION FOR SEQ ID NO:3919:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 178 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..178

(D) OTHER INFORMATION: / Ceres Seq. ID 1578739

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3919:

Lys Ile Glu Ser Ser Pro Ser Ile Ser Ile Ser Ala Ala Ala Ala Ala  
1 5 10 15  
Glu Arg Pro Gln Pro His Pro Ser Thr Thr Met Trp Arg Arg Leu His  
20 25 30  
Thr Leu Ala Pro Ala Leu Arg Arg Ala Thr Ala Ala Ala Ala Gly Ala  
35 40 45  
Pro Ala Ala Ser Ala Ser Ser Ala Ala Arg Ala Ala Pro Leu Ser Ser  
50 55 60  
Ala Ala Ala Ala Phe Arg Arg Thr Ser Pro Leu Leu Ser Gly Asp Lys  
65 70 75 80  
Pro Ala Ser Val Glu Asp Val Met Pro Ile Ala Thr Gly Leu Glu Arg  
85 90 95  
Glu Glu Leu Glu Ala Glu Leu Lys Gly Lys Lys Arg Phe Asp Met Asp  
100 105 110  
Pro Leu Val Gly Pro Phe Gly Thr Lys Glu Glu Pro Ser Val Val Glu  
115 120 125  
Ser Tyr Tyr Asn Lys Arg Ile Val Gly Cys Pro Gly Gly Glu Gly Glu  
130 135 140  
Asp Glu His Asp Val Val Trp Phe Trp Leu Lys Lys Asp Glu Pro His  
145 150 155 160  
Glu Cys Pro Val Cys Ser Gln Tyr Phe Val Leu Lys Val Ile Gly Asp  
165 170 175  
Gly Trp

(2) INFORMATION FOR SEQ ID NO:3920:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 152 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..152

(D) OTHER INFORMATION: / Ceres Seq. ID 1578740

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3920:

Met Trp Arg Arg Leu His Thr Leu Ala Pro Ala Leu Arg Arg Ala Thr  
1 5 10 15  
Ala Ala Ala Ala Gly Ala Pro Ala Ala Ser Ala Ser Ser Ala Ala Arg  
20 25 30  
Ala Ala Pro Leu Ser Ser Ala Ala Ala Phe Arg Arg Thr Ser Pro  
35 40 45  
Leu Leu Ser Gly Asp Lys Pro Ala Ser Val Glu Asp Val Met Pro Ile  
50 55 60  
Ala Thr Gly Leu Glu Arg Glu Glu Leu Glu Ala Glu Leu Lys Gly Lys  
65 70 75 80  
Lys Arg Phe Asp Met Asp Pro Leu Val Gly Pro Phe Gly Thr Lys Glu  
85 90 95  
Glu Pro Ser Val Val Glu Ser Tyr Tyr Asn Lys Arg Ile Val Gly Cys  
100 105 110  
Pro Gly Gly Glu Gly Glu Asp Glu His Asp Val Val Trp Phe Trp Leu  
115 120 125  
Lys Lys Asp Glu Pro His Glu Cys Pro Val Cys Ser Gln Tyr Phe Val  
130 135 140  
Leu Lys Val Ile Gly Asp Gly Trp  
145 150

(2) INFORMATION FOR SEQ ID NO:3921:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 865 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..865

(D) OTHER INFORMATION: / Ceres Seq. ID 1578744

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3921:

gttgacatc	gcgccctcac	gcgttcgacg	tgcgcgcgtg	cgttactcgt	cgtcgtcggg	60
ccgcggcgct	tggtgcatca	cactgtagta	tatagaacga	gccatccacg	cacataaagc	120
tacagcatct	gctcgatcgt	ctagcttgga	cggtggaccg	agagaccagc	cagctagatg	180
gcgcgcaggg	cggtcggcgt	tctactggcc	gtggccgcgc	tcctcgcggc	ggcgacggcg	240
agggcgggcg	acgacgacga	caagacgcag	ccctggcagt	gcttcaagtc	atgctccaga	300
rgctgccacc	accaccacga	ccacgaccac	gacaacggcg	ctgctgccgt	ggcggacttc	360
ctctccgggg	ccgccgccaa	ggtctccgcc	gccgtcaccc	gcgagtgcaa	gaacaacagc	420
tgccatgaca	acgcgtgctt	caaggacctg	ccggccatca	cctaccgcga	gtgcgccatc	480
gccacctgcc	Ctcagccatc	cgcaccatag	cagaaagaaa	acggcgtgct	tgaaggactg	540
ctgcgagaag	tgcttcatca	atggcccacc	tgcgcctggc	ccacctgcgc	ctggcccgcg	600
tgtgcctggc	ccacctgcgc	ctggcccgcg	tgtccttggt	cccagcccga	cgccaccatc	660
tccgccaat	taagcccatg	ttgcatggat	gctcttggtg	cacatgcatg	aagtagtaga	720
gagcaacggt	caacttactc	cttatattcc	cataataata	aaatacttag	gagtacttac	780
ttcaaaaaaa	gaaggatctc	atgactgtaa	ccgaagtgac	attttctctt	gagttggggg	840
gtaacataaa	cccagcacca	aagcc				

(2) INFORMATION FOR SEQ ID NO:3922:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..110

(D) OTHER INFORMATION: / Ceres Seq. ID 1578745

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3922:

Met	Ala	Arg	Arg	Ala	Val	Gly	Val	Leu	Leu	Ala	Val	Ala	Ala	Leu	Leu
1				5					10					15	
Ala	Ala	Ala	Thr	Ala	Arg	Ala	Ala	Asp	Asp	Asp	Asp	Lys	Thr	Gln	Pro
			20					25					30		
Trp	Gln	Cys	Phe	Lys	Ser	Cys	Ser	Arg	Xaa	Cys	His	His	His	His	Asp
		35					40				45				
His	Asp	His	Asp	Asn	Gly	Ala	Ala	Val	Ala	Asp	Phe	Leu	Ser	Gly	
	50				55				60						
Ala	Ala	Ala	Lys	Val	Ser	Ala	Ala	Val	Thr	Arg	Glu	Cys	Lys	Asn	Asn
65					70				75					80	
Ser	Cys	His	Asp	Asn	Ala	Cys	Phe	Lys	Asp	Leu	Pro	Ala	Ile	Thr	Tyr
			85					90					95		
Pro	Gln	Cys	Ala	Ile	Ala	Thr	Cys	Pro	Gln	Pro	Ser	Ala	Pro		
	100						105						110		

(2) INFORMATION FOR SEQ ID NO:3923:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..82  
(D) OTHER INFORMATION: / Ceres Seq. ID 1578746

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3923:

```
Met Thr Thr Arg Ala Ser Arg Thr Cys Arg Pro Ser Pro Thr Arg Ser
1          5          10          15
Ala Pro Ser Pro Pro Ala Leu Ser His Pro His His Ser Arg Lys Lys
          20          25          30
Thr Ala Cys Leu Lys Asp Cys Cys Glu Lys Cys Phe Ile Asn Gly Pro
          35          40          45
Pro Ala Pro Gly Pro Pro Ala Pro Gly Pro Pro Val Pro Gly Pro Pro
          50          55          60
Ala Pro Gly Pro Pro Ala Pro Gly Pro Ser Pro Thr Pro Pro Ser Pro
65          70          75          80
Pro Asn
```

(2) INFORMATION FOR SEQ ID NO:3924:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 857 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..857  
(D) OTHER INFORMATION: / Ceres Seq. ID 1578754

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3924:

```
acagccgcac agccgcgcgc gctccatcca cctctccaca ccatctgacg ctgcttccac      60
cgaggtctcc aaggctcact cctcaccagc ttctgctctc tccctcctca tctctgctct      120
gctctggacc gttaactctc cagctcccc tcgctccgtt cccttccgcc caaatcaccg      180
ggaccaccac gccttcttcc aagatcggcg ggccgggcacc ggccggcgat gacatccacc      240
gtcaccacaa ccgttgggtg cggggggctc cccgtccgcc cgttgtcgac agcgaccaga      300
ggacgcccac gcagatgcCg ccgtccgagc ccaggccgcg ggagcgratg cctccaatga      360
taagtcagtg gaggtcatgc gcaagttctc cgagcagtac gcccgccgct ccaacacttt      420
cttctgcgcc gacaagacag tcaactgccg cgatcatcaag ggacttgctg atcacaggga      480
tactcttgga gctcctctat gccctttagt gcattatgat gacaaagctg cggaggtagc      540
acaaggattt tggaaattgcc catgtgtccc catgcgtgag aggaaggaaat gccactgtat      600
gctttttctt actcccgata atgactttgc tgggaaggat caggttatct ccttcgagga      660
gatcaaagag gcgacatcga agttctaagc ccttgatatt gtcacggagt gtttacttga      720
cagctaattt tttatatgta tatgtactta agtagcatct ataagatatg ccatcaggaa      780
aattttcata aaatgtgcag taaacagcac ttcgcaaggc tgccgatcat ataagnncg      840
ttcggccttt ttattgc
```

(2) INFORMATION FOR SEQ ID NO:3925:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..178  
(D) OTHER INFORMATION: / Ceres Seq. ID 1578755

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3925:

```
Ser Arg Thr Ala Ala Ala Pro Ser Thr Ser Pro His His Leu Thr
1          5          10          15
Leu Leu Pro Pro Arg Ser Pro Arg Leu Thr Pro His Gln Leu Leu Leu
          20          25          30
Ser Pro Ser Ser Ser Leu Leu Cys Ser Gly Pro Leu Thr Leu Gln Leu
          35          40          45
```

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Pro Leu Ala Pro Phe Pro Ser Ala Gln Ile Thr Gly Thr Thr Thr Ala  
50 55 60  
Phe Phe Lys Ile Gly Gly Arg Ala Pro Ala Gly Asp Asp Ile His Arg  
65 70 75 80  
His His Asn Arg Trp Val Arg Gly Ala Pro Arg Pro Pro Val Val Asp  
85 90 95  
Ser Asp Gln Arg Thr Pro Thr Gln Met Pro Pro Ser Glu Pro Arg Pro  
100 105 110  
Arg Glu Xaa Met Pro Pro Met Ile Ser Gln Trp Arg Ser Cys Ala Ser  
115 120 125  
Ser Pro Ser Ser Thr Pro Ala Ala Pro Thr Leu Ser Ser Ala Pro Thr  
130 135 140  
Arg Gln Ser Leu Pro Ser Ser Arg Asp Leu Leu Ile Thr Gly Ile  
145 150 155 160  
Leu Leu Glu Leu Leu Tyr Ala Leu Val Gly Ile Met Met Thr Lys Leu  
165 170 175  
Arg Arg

(2) INFORMATION FOR SEQ ID NO:3926:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 103 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..103

(D) OTHER INFORMATION: / Ceres Seq. ID 1578756

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3926:

Met Arg Lys Phe Ser Glu Gln Tyr Ala Arg Arg Ser Asn Thr Phe Phe  
1 5 10 15  
Cys Ala Asp Lys Thr Val Thr Ala Val Val Ile Lys Gly Leu Ala Asp  
20 25 30  
His Arg Asp Thr Leu Gly Ala Pro Leu Cys Pro Cys Arg His Tyr Asp  
35 40 45  
Asp Lys Ala Ala Glu Val Ala Gln Gly Phe Trp Asn Cys Pro Cys Val  
50 55 60  
Pro Met Arg Glu Arg Lys Glu Cys His Cys Met Leu Phe Leu Thr Pro  
65 70 75 80  
Asp Asn Asp Phe Ala Gly Lys Asp Gln Val Ile Ser Phe Glu Glu Ile  
85 90 95  
Lys Glu Ala Thr Ser Lys Phe  
100

(2) INFORMATION FOR SEQ ID NO:3927:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 713 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..713

(D) OTHER INFORMATION: / Ceres Seq. ID 1578759

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3927:

acacatatata accttctctc ttccgctgtgc tccgatttga cacacctccc aaaccctaca 60  
ctcccggcgg cgccggcggc ggcgcasagc ggcagcagca tccgaagatg gtgaagttcc 120  
tcaagcccgga caaggccgtt atcctcctcc agggccgCtt cgccggcagg aaggcagtta 180  
tcgtgcgcgt gttcgaggag ggcacccgcg accgccccta tggccactgc ctcgtcgagc 240  
gcctcgccaa gtacccaaag aagtgatcc gcaaggactc cgccaagaag actgcgaaga 300



agtcgcgcgt caagtgttcc atcaagctcg tcaacttcac tcacctcatg cccacccgct 360  
acaccctcga cgtcgatttc aaggatgtcg ccaccggtgg gcccgacgca ctctctaccc 420  
acgacaagaa ggtcgccgcc tgcaagacgg ccaaagcgcg ccttgaggag aggttcaaga 480  
ccggcaagaa caggtgggttc ttaccaaGc tccgcttcta gatgctcggc ctcccgaata 540  
gtcctgtcttt agctgtcgat ttgttgtatc ggacacactc catctctgtt ttcgtattac 600  
catgaatatt tcgtgTttta gtccctggggc tctcagagat aaatttgcta agatatgccg 660  
ttgttgtgtt acatgttttc gtgataggtc tggttaaaat tttgttctgt ttc

(2) INFORMATION FOR SEQ ID NO:3928:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..137
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578760

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3928:

Met Val Lys Phe Leu Lys Pro Gly Lys Ala Val Ile Leu Leu Gln Gly  
1 5 10 15  
Arg Phe Ala Gly Arg Lys Ala Val Ile Val Arg Val Phe Glu Glu Gly  
20 25 30  
Thr Arg Asp Arg Pro Tyr Gly His Cys Leu Val Ala Gly Leu Ala Lys  
35 40 45  
Tyr Pro Lys Lys Val Ile Arg Lys Asp Ser Ala Lys Lys Thr Ala Lys  
50 55 60  
Lys Ser Arg Val Lys Cys Phe Ile Lys Leu Val Asn Phe Thr His Leu  
65 70 75 80  
Met Pro Thr Arg Tyr Thr Leu Asp Val Asp Phe Lys Asp Val Ala Thr  
85 90 95  
Gly Gly Pro Asp Ala Leu Ser Thr His Asp Lys Lys Val Ala Ala Cys  
100 105 110  
Lys Thr Ala Lys Ala Arg Leu Glu Glu Arg Phe Lys Thr Gly Lys Asn  
115 120 125  
Arg Trp Phe Phe Thr Lys Leu Arg Phe  
130 135

(2) INFORMATION FOR SEQ ID NO:3929:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 889 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..889
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578777

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3929:

catgaggatg gaaactttta ccctggaact ggagctgctc atgaggtggg agttcttgat 60  
ggtcaaggat tctcagttaa tataccttgg agccgtgggtg gtgttgagaga tgatgactac 120  
atcttttgctt ttcagactgt ggtgcttcca atagcttcag agtttgccgc agacatcact 180  
ataatatctg caggattcga tgcagctaga ggtgaccctc tgggttggtg tgacgtcact 240  
ccaactggat actcttggat gacatccctg ctgactgggtt cctcaaattg aagattgttg 300  
gtgatacttg agggaggata caatctccgg tccgatccct catcagctac tgaagtgtt 360  
aaggtcctac ttggggaggg tcccaatcgt gcttcatttg tagtttcacc atcaaaagag 420  
gccttgcgta ctgtttctca agtccctgaag attcaacaac aatttttgcc agtttttaggt 480  
ccaacatacg catcactaca ggcgcaGcag gggtcggttt cttccaatca tagcaatgag 540  
ctgaagaaaa ggaagcggtt aggaggagga ccagggccct tctggtggaa gatgggaagc 600  
aaaaggcttc tatacgaagc gcttattgag cctcgcagcc gtccgaggaa actcaagggg 660  
tcaactgggtt cagcagcgcc ttagatgtgg gcagtttgct ggccgttgat cttctagaca 720

tgaacagggt agctcgctga ccgcgtttcc tcaagcagag taggctgcgt ttacgtagaa 780  
aacctacttt tggctgggta cttgcatgat ggtcgaccgt ttcagatgga gtttgacagc 840  
aaaccggttg tgtaaccat gcgtggcgta tcagccgatg tttcatgcc

(2) INFORMATION FOR SEQ ID NO:3930:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..227
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578778

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3930:

His Glu Asp Gly Asn Phe Tyr Pro Gly Thr Gly Ala Ala His Glu Val  
1 5 10 15  
Gly Val Leu Asp Gly Gln Gly Phe Ser Val Asn Ile Pro Trp Ser Arg  
20 25 30  
Gly Gly Val Gly Asp Asp Asp Tyr Ile Phe Ala Phe Gln Thr Val Val  
35 40 45  
Leu Pro Ile Ala Ser Glu Phe Ala Ala Asp Ile Thr Ile Ile Ser Ala  
50 55 60  
Gly Phe Asp Ala Ala Arg Gly Asp Pro Leu Gly Cys Cys Asp Val Thr  
65 70 75 80  
Pro Thr Gly Tyr Ser Trp Met Thr Ser Leu Leu Ala Gly Ser Ser Asn  
85 90 95  
Gly Arg Leu Leu Val Ile Leu Glu Gly Gly Tyr Asn Leu Arg Ser Ile  
100 105 110  
Ser Ser Ser Ala Thr Glu Val Val Lys Val Leu Leu Gly Glu Gly Pro  
115 120 125  
Asn Arg Ala Ser Phe Val Val Ser Pro Ser Lys Glu Ala Leu Arg Thr  
130 135 140  
Val Ser Gln Val Leu Lys Ile Gln Gln Gln Phe Trp Pro Val Leu Gly  
145 150 155 160  
Pro Thr Tyr Ala Ser Leu Gln Ala Gln Gln Gly Ser Val Ser Ser Asn  
165 170 175  
His Ser Asn Glu Leu Lys Lys Arg Lys Arg Ser Gly Gly Gly Pro Gly  
180 185 190  
Pro Phe Trp Trp Lys Met Gly Ser Lys Arg Leu Leu Tyr Glu Ala Leu  
195 200 205  
Ile Glu Pro Arg Ser Arg Pro Arg Lys Leu Lys Gly Ser Thr Gly Ser  
210 215 220  
Ala Ala Pro  
225

(2) INFORMATION FOR SEQ ID NO:3931:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..141
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578779

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3931:

Met Thr Ser Leu Leu Ala Gly Ser Ser Asn Gly Arg Leu Leu Val Ile  
1 5 10 15  
Leu Glu Gly Gly Tyr Asn Leu Arg Ser Ile Ser Ser Ser Ala Thr Glu  
20 25 30

Val Val Lys Val Leu Leu Gly Glu Gly Pro Asn Arg Ala Ser Phe Val  
35 40 45  
Val Ser Pro Ser Lys Glu Ala Leu Arg Thr Val Ser Gln Val Leu Lys  
50 55 60  
Ile Gln Gln Gln Phe Trp Pro Val Leu Gly Pro Thr Tyr Ala Ser Leu  
65 70 75 80  
Gln Ala Gln Gln Gly Ser Val Ser Ser Asn His Ser Asn Glu Leu Lys  
85 90 95  
Lys Arg Lys Arg Ser Gly Gly Gly Pro Gly Pro Phe Trp Trp Lys Met  
100 105 110  
Gly Ser Lys Arg Leu Leu Tyr Glu Ala Leu Ile Glu Pro Arg Ser Arg  
115 120 125  
Pro Arg Lys Leu Lys Gly Ser Thr Gly Ser Ala Ala Pro  
130 135 140

(2) INFORMATION FOR SEQ ID NO:3932:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 810 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..810
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578782

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3932:

gatggatatt tgcagattag tctacacgag tcacgatagg aggaagactg gaagaggagg	60
cgagcacggt tgcggtgccc accctcaccg tccactccaa aaccccaa at ccagttccgt	120
tccaatcgcc gagaagggca gcaaagggga gaaaaaaaag gaaaacgatr gmngrgccc	180
gcggcgagaa cagcggcgcg gngcgagggc gagggcgagt tttacctgcg ctactacgtg	240
ggtcacaaag gcaagttcgg gcacgagttc ctcgagttcg agttccgccc cgacggcaag	300
ctccgCtacc ccaacaactc caactacaag aacgacacca tgatccgcaa ggaggtcttc	360
gtctcgccct ccgtcctccg cgaggccagg aggatcatcc aggagtccga catcatgaag	420
gaggacgaca gcaactggcc cgagcccgcg cgcacgcggc gccaggagct cgagatcgtc	480
atgggcaacg agcacatttc attcaccact tccaagatcg gtcctcctcg cgatgtccag	540
tccagcaagg acccgaggagg cctccggatc ttctactacc ttgtccagga tctgaagtgt	600
ttcgtgttct cgtcctatcaa ccttcacttc aagatcaagc caatccagtc ttgagctcca	660
tccaagcct tcatgtagct ggtttgtgag actgcgagtg ttttgagaga gaacctttta	720
accatgtaag atgatgttga tattgtggac gatgcgcgag atcgaccctg tgtggtgcac	780
ttagtggaag tggaaccccc ctttgcattt	

(2) INFORMATION FOR SEQ ID NO:3933:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..113
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578783

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3933:

Met Asp Ile Cys Arg Leu Val Tyr Thr Ser His Asp Arg Arg Lys Thr  
1 5 10 15  
Gly Arg Gly Gly Glu His Val Cys Gly Ala His Pro His Arg Pro Leu  
20 25 30  
Gln Asn Pro Lys Ser Ser Ser Val Pro Ile Ala Glu Lys Gly Ser Lys  
35 40 45  
Gly Glu Lys Lys Lys Glu Asn Asp Xaa Xaa Xaa Arg Arg Arg Glu Gln  
50 55 60  
Arg Arg Xaa Ala Arg Ala Arg Ala Ser Phe Thr Cys Ala Thr Thr Trp

```
(2) INFORMATION FOR SEQ ID NO:3934:
  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 104 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS:
      (D) TOPOLOGY: linear
  (ii) MOLECULE TYPE: peptide
  (ix) FEATURE:
      (A) NAME/KEY: peptide
      (B) LOCATION: 1..104
      (D) OTHER INFORMATION: / Ceres Seq. ID 1578785
  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3934:
```

```
(2) INFORMATION FOR SEQ ID NO:3935:
  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 653 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear
  (ii) MOLECULE TYPE: DNA (genomic)
  (ix) FEATURE:
      (A) NAME/KEY: -
      (B) LOCATION: 1..653
      (D) OTHER INFORMATION: / Ceres Seq. ID 1578786
  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3935:
```

(2) INFORMATION FOR SEQ ID NO:3936:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 53 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:

(2) INFORMATION FOR SEQ ID NO:3937:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3937:

(2) INFORMATION FOR SEQ ID NO:3938:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3938:

(2) INFORMATION FOR SEQ ID NO:3939:

(B) TYPE: nucleic acid

[illegible]

- (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..713  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1578793

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3939:

```
gctagcggctc cgcaccact caccggttgc ctccaaactc atttctccc agcgccgccg      60
cgagcctctg ttccagcttc gttcatggct tccctcaccg gatccgctct ctcttttgcg      120
aggcccgctca aggcaatcag cattaagtct gtctctttCc tctgggtctaa ggaaggataa      180
tgtagccttc cgcttgccagc cagtggccaca aagattcgct gtctgctgtc ctgctaaaaa      240
ggagactgtg gatcggggtt gtgatattgt caagaagcag cttgcacttc ctgagggcac      300
tgaggtctgt ggctcctcta agtttcaaga cctcggtgtg gattcggttg acactgttga      360
gattgttatg ggccttgagg aggctttcaa gatcactgta gaggagtcga gcgcgcagtc      420
aatcgcaact gtggaagatg ctgctaactc catcgacgaa cttgttgagc gagcagcaaa      480
atcgtgttaa actcgtggtc gtattgcggt ggggtgctgta ccagggcatc acttgttgtt      540
ctatgcccc ttccctacta gattttcttt tctaccctgg gcctggagag atgtttctgt      600
catgactgtc attgtggatc tcgcgatatt gttatattga agcttttgtg cttgttcaag      660
aaaagaaaat gttgttgcca tatatatgtt attatattga attttttttt gtc
```

(2) INFORMATION FOR SEQ ID NO:3940:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..162  
(D) OTHER INFORMATION: / Ceres Seq. ID 1578794

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3940:

```
Leu Ala Val Arg Thr His Ser Pro Val Ala Ser Lys Leu Ile Ser Pro
1           5           10           15
Glu Arg Arg Arg Glu Pro Leu Phe Gln Leu Arg Ser Trp Leu Pro Ser
20           25           30
Pro Asp Pro Leu Ser Pro Leu Arg Gly Pro Ser Arg Gln Ser Ala Leu
35           40           45
Ser Leu Ser Leu Ser Ser Gly Leu Arg Lys Asp Asn Val Ala Phe Arg
50           55           60
Leu Gln Pro Val Pro Gln Arg Phe Ala Val Cys Cys Pro Ala Lys Lys
65           70           75           80
Glu Thr Val Asp Arg Val Cys Asp Ile Val Lys Lys Gln Leu Ala Leu
85           90           95
Pro Glu Gly Thr Glu Val Cys Gly Ser Lys Phe Gln Asp Leu Gly
100          105          110
Ala Asp Ser Leu Asp Thr Val Glu Ile Val Met Gly Leu Glu Glu Ala
115          120          125
Phe Lys Ile Thr Val Glu Glu Ser Ser Ala Gln Ser Ile Ala Thr Val
130          135          140
Glu Asp Ala Ala Asn Leu Ile Asp Glu Leu Val Ala Gly Ala Ala Lys
145          150          155          160
Ser Cys
```

(2) INFORMATION FOR SEQ ID NO:3941:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 674 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

000001-166666

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..674

(D) OTHER INFORMATION: / Ceres Seq. ID 1578799

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3941:

attagtcagc	agattgtgaa	gaaacagctg	tctccaaagc	gagaagacga	agaaagggga	60
aatcgagaga	tgagctacca	gagagtcctt	cccagggaac	cctaccctcc	tccaggacat	120
cctcgatctc	aGgcgcaccc	ttaccacccg	ccaccagatg	tgtacccgcc	ttcccctcgg	180
ggccatggac	atccaccacc	accccatggc	gtgtaccgcg	cgcgcgcgca	gggtccttac	240
ccccaccac	agcagcctcc	accgggggtac	caggggtact	tcaacgacca	gcagcgtcct	300
tactaccgcg	cgccgcatgg	agagcatcaa	cacaaccacc	accagggaaa	ccagggtagc	360
tcctctgggt	tcctcaaagg	atgtttggct	gctctctctg	ctgctgcgtg	ctggaggaat	420
gctgcggctg	cttctgagac	gtgagatgtc	cggaatccg	atcgcaagtt	atcgctcgta	480
gcattcggga	gcaccccgat	tattatcata	taatagtaac	tgtgcttgta	aataatctgg	540
agcagcagtg	ttcatgagct	cccagccccg	catttatatt	ctcataattt	gtagtacgtt	600
ctatgattta	tcgaaaata	aaggactcta	tatatgggat	tctaaataag	gtatttgcac	660
atttcattgg	attc					

(2) INFORMATION FOR SEQ ID NO:3942:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 147 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..147

(D) OTHER INFORMATION: / Ceres Seq. ID 1578800

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3942:

Ile	Ser	Gln	Gln	Ile	Val	Lys	Lys	Gln	Leu	Ser	Pro	Lys	Arg	Glu	Asp	
1			5					10						15		
Glu	Glu	Arg	Gly	Asn	Arg	Glu	Met	Ser	Tyr	Gln	Arg	Val	Pro	Pro	Glu	
			20					25					30			
Glu	Pro	Tyr	Pro	Pro	Pro	Gly	His	Pro	Arg	Ser	Gln	Ala	His	Pro	Tyr	
			35				40					45				
Pro	Pro	Pro	Pro	Asp	Val	Tyr	Pro	Pro	Pro	Pro	Arg	Gly	His	Gly	His	
	50					55					60					
Pro	Pro	Pro	Pro	His	Gly	Val	Tyr	Pro	Pro	Pro	Pro	Gln	Gly	Pro	Tyr	
65				70				75						80		
Pro	Pro	Pro	Gln	Gln	Pro	Pro	Pro	Gly	Tyr	Gln	Gly	Tyr	Phe	Asn	Asp	
			85					90						95		
Gln	Gln	Arg	Pro	Tyr	Tyr	Pro	Pro	Pro	His	Gly	Glu	His	Gln	His	Asn	
			100					105					110			
His	His	Gln	Gly	Asn	Gln	Gly	Ser	Ser	Gly	Phe	Leu	Lys	Gly	Cys		
	115					120					125					
Leu	Ala	Ala	Leu	Ser	Ala	Ala	Cys	Trp	Arg	Asn	Ala	Ala	Ala	Ala		
	130					135					140					
Ser	Glu	Thr														
145																

(2) INFORMATION FOR SEQ ID NO:3943:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 124 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..124

(D) OTHER INFORMATION: / Ceres Seq. ID 1578801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3943:

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Met Ser Tyr Gln Arg Val Pro Pro Glu Glu Pro Tyr Pro Pro Pro Gly  
1 5 10 15  
His Pro Arg Ser Gln Ala His Pro Tyr Pro Pro Pro Asp Val Tyr  
20 25 30  
Pro Pro Pro Pro Arg Gly His Gly His Pro Pro Pro Pro His Gly Val  
35 40 45  
Tyr Pro Pro Pro Pro Gln Gly Pro Tyr Pro Pro Pro Gln Gln Pro Pro  
50 55 60  
Pro Gly Tyr Gln Gly Tyr Phe Asn Asp Gln Gln Arg Pro Tyr Tyr Pro  
65 70 75 80  
Pro Pro His Gly Glu His Gln His Asn His His Gln Gly Asn Gln Gly  
85 90 95  
Ser Ser Ser Gly Phe Leu Lys Gly Cys Leu Ala Ala Leu Ser Ala Ala  
100 105 110  
Ala Cys Trp Arg Asn Ala Ala Ala Ala Ser Glu Thr  
115 120

(2) INFORMATION FOR SEQ ID NO:3944:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..107
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578802

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3944:

Met Cys Thr Arg Leu Pro Leu Gly Ala Met Asp Ile His His His Pro  
1 5 10 15  
Met Ala Cys Thr Arg Arg Arg Arg Arg Val Leu Thr Pro His His Ser  
20 25 30  
Ser Leu His Arg Gly Thr Arg Ala Thr Ser Thr Thr Ser Ser Val Leu  
35 40 45  
Thr Thr Arg Arg Arg Met Glu Ser Ile Asn Thr Thr Thr Thr Arg Glu  
50 55 60  
Thr Arg Val Ala Pro Leu Gly Ser Ser Lys Asp Val Trp Leu Leu Ser  
65 70 75 80  
Leu Leu Leu Arg Ala Gly Gly Met Leu Arg Leu Leu Leu Arg Arg Glu  
85 90 95  
Met Ser Gly Asn Pro Ile Ala Ser Tyr Arg Arg  
100 105

(2) INFORMATION FOR SEQ ID NO:3945:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 923 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..923
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578817

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3945:

agaagctcct ccggtcctcc cttctctccg tagaaacatt tcccgaacggg tgtttccac	60
gccggaatgg accagccggc accataagcc caagattcgt ttgatgagtt tgtacgatac	120
tggtctaca gttaggagaa cacatttaac ctaccttcac tagcattcag taatgccttt	180
gcctaaatca gacctggggt cataactctt tagtagagaa ccaagaagat gcaggcatct	240
agggaaggc ttttcaagga gtacaaggag gtacagcgag agaagtcagc tgaccctgat	300
atccaattaa tatgtgatga ttctaacata ttcaagtga ctgctcttat caaGggccct	360
tctgaaacac cttatgaagg tgggtgtgtt caacttgcac tcgcaattcc agagcagtat	420



```
cctctgctgc ctcctcaagt tcgatttttg accaaaactt tccacccaaa tgtgcatttc 480
aagacaggtg agatttgtct ggatatattg Aaagaatgca tggagCocta tatggacct 540
tcagtctggt tgtagagcca taattgctct gatggccac cctgaaccag acagcccact 600
taactgtgat tcaggcaatc tctgcggtcc ggtgatatca gaggctatca atcaatggcc 660
cgcatgtata caaggctggc ggccatgcc aagaaagggt agccgtaaaa catgtgccag 720
gccaaagacc tattgtccat gcatggctac atgtgtcag gtctgccttg tgctgtctgt 780
atgaactttg tggttcttga ttcatgaaat actaaccgtt cgtgtgttgc gtgtgtgtct 840
gggtaatga gaggacactc gggttctcga tgggtgttgg ctgtgatgta tttagtaata 900
agaaaataaa aatgatttc tcg
```

(2) INFORMATION FOR SEQ ID NO:3946:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..108
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578818

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3946:

```
Met Gln Ala Ser Arg Leu Phe Lys Glu Tyr Lys Glu Val Gln
1      5      10      15
Arg Glu Lys Ser Ala Asp Pro Asp Ile Gln Leu Ile Cys Asp Asp Ser
      20      25      30
Asn Ile Phe Lys Trp Thr Ala Leu Ile Lys Gly Pro Ser Glu Thr Pro
      35      40      45
Tyr Glu Gly Gly Val Phe Gln Leu Ala Phe Ala Ile Pro Glu Gln Tyr
      50      55      60
Pro Leu Leu Pro Pro Gln Val Arg Phe Leu Thr Lys Thr Phe His Pro
      65      70      75      80
Asn Val His Phe Lys Thr Gly Glu Ile Cys Leu Asp Ile Leu Lys Glu
      85      90      95
Cys Met Glu Pro Tyr Met Asp Pro Ser Val Cys Leu
      100     105
```

(2) INFORMATION FOR SEQ ID NO:3947:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..70
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578819

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3947:

```
Met Ala His Pro Glu Pro Asp Ser Pro Leu Asn Cys Asp Ser Gly Asn
1      5      10      15
Leu Cys Gly Pro Val Ile Ser Glu Ala Ile Asn Gln Trp Pro Ala Cys
      20      25      30
Ile Gln Gly Trp Arg Pro Cys Gln Arg Lys Val Ser Arg Lys Thr Cys
      35      40      45
Ala Arg Pro Arg Ala Tyr Cys Pro Cys Met Ala Thr Cys Cys Gln Val
      50      55      60
Cys Leu Val Leu Ser Val
      65      70
```

(2) INFORMATION FOR SEQ ID NO:3948:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 626 base pairs
- (B) TYPE: nucleic acid

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- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..626
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1578834

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3948:

gatgcaacca	gaacccatag	ctgacgacac	caccgtgtgg	tgcacaaaat	aaaaaggaga	60
gagagagaga	tggctctgtc	gtctcgccgt	atggccgccg	caccattctt	cgtcgtcgtc	120
cttctcgctc	tcgtggcggc	agagaggacg	atgggcaggg	tgggtggtgga	agagacgctc	180
tgcttgctgc	agagccatgc	cttcaaaggc	gtgtgcctca	gcaacaccaa	ctgcgacaac	240
gtatgcaaga	cggagaagtt	cacaggcggc	gagtgcaaga	tggacggcgt	catgcgcaag	300
tgctactgca	agaaggtctg	ctagggcatg	accggcagca	agNCCCCcag	ccgtacggct	360
gggGtgatcc	ggttgcacac	cgtttgggca	cgcggtcatg	ttccggcttc	tcggctttat	420
ttatttcttc	tttgttataa	taaatagact	ctgttagtca	gggtgcgtttt	agtctgggtc	480
gtacgttatt	aattctctag	tgtattgtat	ttRcgcaaCG	cgcgctgtac	ttaacgtagc	540
caggcatgta	ttcgcgttgc	gtggtcgaga	ggccaacgat	ttatcttgat	tgtacaaaaa	600
aattatatat	atttgtgatg	gtggtc				

(2) INFORMATION FOR SEQ ID NO:3949:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 84 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..84
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1578835

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3949:

Met	Ala	Leu	Ser	Ser	Arg	Arg	Met	Ala	Ala	Ala	Pro	Phe	Phe	Val	Val
1				5					10					15	
Val	Leu	Leu	Val	Leu	Val	Ala	Ala	Glu	Arg	Thr	Met	Gly	Arg	Val	Val
			20						25				30		
Val	Glu	Glu	Thr	Leu	Cys	Leu	Ser	Gln	Ser	His	Ala	Phe	Lys	Gly	Val
			35				40					45			
Cys	Leu	Ser	Asn	Thr	Asn	Cys	Asp	Asn	Val	Cys	Lys	Thr	Glu	Lys	Phe
	50					55					60				
Thr	Gly	Gly	Glu	Cys	Lys	Met	Asp	Gly	Val	Met	Arg	Lys	Cys	Tyr	Cys
65					70				75					80	
Lys	Lys	Val	Cys												

(2) INFORMATION FOR SEQ ID NO:3950:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 77 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..77
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1578836

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3950:

Met	Ala	Ala	Ala	Pro	Phe	Phe	Val	Val	Val	Leu	Leu	Val	Leu	Val	Ala
1				5					10					15	
Ala	Glu	Arg	Thr	Met	Gly	Arg	Val	Val	Val	Glu	Glu	Thr	Leu	Cys	Leu
			20					25					30		
Ser	Gln	Ser	His	Ala	Phe	Lys	Gly	Val	Cys	Leu	Ser	Asn	Thr	Asn	Cys
			35				40					45			

Asp Asn Val Cys Lys Thr Glu Lys Phe Thr Gly Gly Glu Cys Lys Met  
50 55 60  
Asp Gly Val Met Arg Lys Cys Tyr Cys Lys Lys Val Cys  
65 70 75

(2) INFORMATION FOR SEQ ID NO:3951:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..65
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578837

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3951:

Met Gln Asp Gly Glu Val His Arg Arg Arg Val Gln Asp Gly Arg Arg  
1 5 10 15  
His Ala Gln Val Leu Leu Gln Glu Gly Leu Leu Gly His Asp Arg Gln  
20 25 30  
Gln Xaa Pro Gln Pro Tyr Gly Trp Cys Asp Pro Val Ala His Arg Leu  
35 40 45  
Gly Thr Arg Ser Cys Ser Gly Phe Ser Ala Leu Phe Ile Ser Ser Leu  
50 55 60  
Leu  
65

(2) INFORMATION FOR SEQ ID NO:3952:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 950 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..950
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578845

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3952:

gtcaggcacc caagcaccac acgcgacgsg cacttccaca aggtggatag cgaaccacaca	60
gcacgtctcc atctctggtt tgaccgcgcg cgcgcgcgcc ctacgcggct acgccaggcg	120
ccgaggcctt cgtcggcatt ttcgtcggca agcactcacc aggtattcag ccatggtttt	180
tcttgaggca gagatgtcat ggaatgtgtt gatctcacct agccagctgg accgcaagg	240
cctcctgctc cgcaaggcta tcattgtgcg tcttctggag gatgtcacia acaggagggc	300
ttcgaaagag catggctact acattgctgt taatcagctg aaggcaatat ctgaaggaa	360
agtgcgtgaG ctaactggag atgttctgtt cccagtttca ttacttgca ttacacagaa	420
gcctatgaag ggagagggtca tgggtgggca cgtggacagg atcctcaagc atggcgtgtt	480
cctcaaattcc ggacccgtgg agagcatctt cctggctgag aagtcgatga gtaattacaa	540
gtacataggt ggggagaatg cgatgttcat gaacgaccac tcgaagctgg agaaggacac	600
cgccgtgcmc ttcaagggtcc tagggttccg ctggatggag gctgaccgcc aattccagct	660
ccttgctacg atcgctgggtg acttctcttg gccgctgtga actgcttcca cagggtcaa	720
aggtttctaat gtacattgct cgtaggatgg tggatggatg gttggatctg atgtgtagaa	780
ttaaactttg ctaccagtgg tttggtcttg tagaacctga gacatggtag gttttctaga	840
tgctgttgcc agtgatatct agctctgggt tgaacgtatc agtgtacctg tatgatgaac	900
aagcgttgct atggatgtac cttttctatg cttgcttgga agttaacgtt	

(2) INFORMATION FOR SEQ ID NO:3953:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..232

(D) OTHER INFORMATION: / Ceres Seq. ID 1578846

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3953:

Ser Gly Thr Gln Ala Pro His Ala Thr Xaa Thr Ser Thr Arg Trp Ile  
1 5 10 15  
Ala Asn Pro Gln His Val Ser Ile Ser Gly Leu Thr Ala Ala Ala Ala  
20 25 30  
Ala Leu Arg Gly Tyr Ala Arg Arg Gly Leu Arg Arg His Phe Arg  
35 40 45  
Arg Gln Ala Leu Thr Arg Tyr Ser Ala Met Val Phe Leu Glu Ala Glu  
50 55 60  
Met Ser Trp Asn Val Leu Ile Ser Pro Ser Gln Leu Asp Arg Lys Xaa  
65 70 75 80  
Leu Leu Leu Arg Lys Ala Ile Ile Val Arg Leu Leu Glu Asp Val Thr  
85 90 95  
Asn Arg Arg Ala Ser Lys Glu His Gly Tyr Tyr Ile Ala Val Asn Gln  
100 105 110  
Leu Lys Ala Ile Ser Glu Gly Lys Val Arg Glu Leu Thr Gly Asp Val  
115 120 125  
Leu Phe Pro Val Ser Phe Thr Cys Ile Thr Gln Lys Pro Met Lys Gly  
130 135 140  
Glu Val Met Val Gly His Val Asp Arg Ile Leu Lys His Gly Val Phe  
145 150 155 160  
Leu Lys Ser Gly Pro Val Glu Ser Ile Phe Leu Ala Glu Lys Ser Met  
165 170 175  
Ser Asn Tyr Lys Tyr Ile Gly Gly Glu Asn Ala Met Phe Met Asn Asp  
180 185 190  
His Ser Lys Leu Glu Lys Asp Thr Ala Val Arg Phe Lys Val Leu Gly  
195 200 205  
Phe Arg Trp Met Glu Ala Asp Arg Gln Phe Gln Leu Leu Ala Thr Ile  
210 215 220  
Ala Gly Asp Phe Leu Gly Pro Leu  
225 230

(2) INFORMATION FOR SEQ ID NO:3954:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 175 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..175

(D) OTHER INFORMATION: / Ceres Seq. ID 1578847

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3954:

Met Val Phe Leu Glu Ala Glu Met Ser Trp Asn Val Leu Ile Ser Pro  
1 5 10 15  
Ser Gln Leu Asp Arg Lys Xaa Leu Leu Leu Arg Lys Ala Ile Ile Val  
20 25 30  
Arg Leu Leu Glu Asp Val Thr Asn Arg Arg Ala Ser Lys Glu His Gly  
35 40 45  
Tyr Tyr Ile Ala Val Asn Gln Leu Lys Ala Ile Ser Glu Gly Lys Val  
50 55 60  
Arg Glu Leu Thr Gly Asp Val Leu Phe Pro Val Ser Phe Thr Cys Ile  
65 70 75 80  
Thr Gln Lys Pro Met Lys Gly Glu Val Met Val Gly His Val Asp Arg  
85 90 95  
Ile Leu Lys His Gly Val Phe Leu Lys Ser Gly Pro Val Glu Ser Ile  
100 105 110

Phe Leu Ala Glu Lys Ser Met Ser Asn Tyr Lys Tyr Ile Gly Gly Glu  
115 120 125  
Asn Ala Met Phe Met Asn Asp His Ser Lys Leu Glu Lys Asp Thr Ala  
130 135 140  
Val Arg Phe Lys Val Leu Gly Phe Arg Trp Met Glu Ala Asp Arg Gln  
145 150 155 160  
Phe Gln Leu Leu Ala Thr Ile Ala Gly Asp Phe Leu Gly Pro Leu  
165 170 175

(2) INFORMATION FOR SEQ ID NO:3955:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 168 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..168

(D) OTHER INFORMATION: / Ceres Seq. ID 1578848

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3955:

Met Ser Trp Asn Val Leu Ile Ser Pro Ser Gln Leu Asp Arg Lys Xaa  
1 5 10 15  
Leu Leu Leu Arg Lys Ala Ile Ile Val Arg Leu Leu Glu Asp Val Thr  
20 25 30  
Asn Arg Arg Ala Ser Lys Glu His Gly Tyr Tyr Ile Ala Val Asn Gln  
35 40 45  
Leu Lys Ala Ile Ser Glu Gly Lys Val Arg Glu Leu Thr Gly Asp Val  
50 55 60  
Leu Phe Pro Val Ser Phe Thr Cys Ile Thr Gln Lys Pro Met Lys Gly  
65 70 75 80  
Glu Val Met Val Gly His Val Asp Arg Ile Leu Lys His Gly Val Phe  
85 90 95  
Leu Lys Ser Gly Pro Val Glu Ser Ile Phe Leu Ala Glu Lys Ser Met  
100 105 110  
Ser Asn Tyr Lys Tyr Ile Gly Gly Glu Asn Ala Met Phe Met Asn Asp  
115 120 125  
His Ser Lys Leu Glu Lys Asp Thr Ala Val Arg Phe Lys Val Leu Gly  
130 135 140  
Phe Arg Trp Met Glu Ala Asp Arg Gln Phe Gln Leu Leu Ala Thr Ile  
145 150 155 160  
Ala Gly Asp Phe Leu Gly Pro Leu  
165

(2) INFORMATION FOR SEQ ID NO:3956:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 686 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..686

(D) OTHER INFORMATION: / Ceres Seq. ID 1578852

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3956:

gctccggcct gtagccgtga cggtgacggc gtcaggctca gctcgctcgc cccccccacg 60  
aaaaccctaa tggcgtcccg cctccttcac ctccgcgcgc tcattactcc tccccccacc 120  
gtccccgcgc cttcctttctc caccgccgctc agcgcgaccc cgs gcgtctc cgcgctcgtc 180  
gacgagatct gcgggctcac cctcctcgag gcctcttccc tggccgatgc cctgcgcggc 240  
cgcctcggcg tcgaccagtt gccgccacta gctatcctca cgggcggcgg cgcaccgctc 300  
gtcggcggcg gagtaggtcc cggcgcggcc ggccgaggagg cgaaggccaa ggaggagaag 360  
atggcgttcg acgtgaagct ggaggggttc gacgccgcgc cgaaGctcaa gatcatcaag 420

gagctgaggg cgttcacgaa tctgggtctg aaggaggcca aggatctcgt ggagaaggcg 480  
cccgccgtgc tgaaggctgg agttcccaag gaggaggcgg agagtatcgc cgagaagatg 540  
cggcgctcgg cgccaagatt gttctcgagt gaacgacgag agctgtgtat gccctcgttt 600  
cttgatttgt ttctgttttc ttgtatgaaa aaaagagaga attttggaac aaggagataa 660  
taattagtaa atttgactag agatcc

(2) INFORMATION FOR SEQ ID NO:3957:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..219
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578853

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3957:

Ala Pro Ala Cys Ser Arg Asp Gly Asp Gly Val Arg Leu Ser Ser Leu  
1 5 10 15  
Ala Pro Pro Thr Lys Thr Leu Met Ala Ser Arg Leu Leu His Leu Arg  
20 25 30  
Arg Leu Ile Thr Pro Pro Pro Thr Val Pro Ala Ala Ser Phe Ser Thr  
35 40 45  
Ala Val Ser Ala Thr Pro Xaa Val Ser Ala Leu Val Asp Glu Ile Cys  
50 55 60  
Gly Leu Thr Leu Leu Glu Ala Ser Ser Leu Ala Asp Ala Leu Arg Gly  
65 70 75 80  
Arg Leu Gly Val Asp Gln Leu Pro Pro Leu Ala Ile Leu Thr Gly Gly  
85 90 95  
Gly Ala Pro Leu Val Gly Gly Gly Val Gly Pro Gly Ala Ala Gly Glu  
100 105 110  
Glu Ala Lys Ala Lys Glu Glu Lys Met Ala Phe Asp Val Lys Leu Glu  
115 120 125  
Gly Phe Asp Ala Ala Ala Lys Leu Lys Ile Ile Lys Glu Leu Arg Ala  
130 135 140  
Phe Thr Asn Leu Gly Leu Lys Glu Ala Lys Asp Leu Val Glu Lys Ala  
145 150 155 160  
Pro Ala Val Leu Lys Ala Gly Val Pro Lys Glu Glu Ala Glu Ser Ile  
165 170 175  
Ala Glu Lys Met Arg Arg Ser Ala Pro Arg Leu Phe Ser Ser Glu Arg  
180 185 190  
Arg Glu Leu Cys Met Pro Ser Phe Leu Asp Leu Phe Arg Val Ser Cys  
195 200 205  
Met Lys Lys Arg Glu Asn Phe Gly Thr Arg Arg  
210 215

(2) INFORMATION FOR SEQ ID NO:3958:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..196
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578854

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3958:

Met Ala Ser Arg Leu Leu His Leu Arg Arg Leu Ile Thr Pro Pro Pro  
1 5 10 15  
Thr Val Pro Ala Ala Ser Phe Ser Thr Ala Val Ser Ala Thr Pro Xaa  
20 25 30

Val Ser Ala Leu Val Asp Glu Ile Cys Gly Leu Thr Leu Leu Glu Ala  
35 40 45  
Ser Ser Leu Ala Asp Ala Leu Arg Gly Arg Leu Gly Val Asp Gln Leu  
50 55 60  
Pro Pro Leu Ala Ile Leu Thr Gly Gly Gly Ala Pro Leu Val Gly Gly  
65 70 75 80  
Gly Val Gly Pro Gly Ala Ala Gly Glu Glu Ala Lys Ala Lys Glu Glu  
85 90 95  
Lys Met Ala Phe Asp Val Lys Leu Glu Gly Phe Asp Ala Ala Lys  
100 105 110  
Leu Lys Ile Ile Lys Glu Leu Arg Ala Phe Thr Asn Leu Gly Leu Lys  
115 120 125  
Glu Ala Lys Asp Leu Val Glu Lys Ala Pro Ala Val Leu Lys Ala Gly  
130 135 140  
Val Pro Lys Glu Glu Ala Glu Ser Ile Ala Glu Lys Met Arg Arg Ser  
145 150 155 160  
Ala Pro Arg Leu Phe Ser Ser Glu Arg Arg Glu Leu Cys Met Pro Ser  
165 170 175  
Phe Leu Asp Leu Phe Arg Val Ser Cys Met Lys Lys Arg Glu Asn Phe  
180 185 190  
Gly Thr Arg Arg  
195

(2) INFORMATION FOR SEQ ID NO:3959:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 772 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..772
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578861

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3959:

aatcaaaccc	tcacagcgaa	ggacacaaaa	acacaggtag	ggttaggcga	cgcggcggcg	60
agagcrcgag	agtaggagga	ggcgctcgcc	atgacgggga	aggcgaacrn	angaagcaca	120
cggcgaagga	gatcgccgcg	aagatcgacg	cggcgacgac	gaaccgnrgc	ggcggaagg	180
tcgggcaggc	ggatcggtca	gggcaggaca	aggrcgggca	cgcgaaactg	cgtgcccgt	240
ctgcccgcacc	cgggcgccc	acatcaagtc	catgcagatc	caccacgagg	cgcgccatcc	300
caagctccct	ttcgagccg	agaagctcgt	caacctgcac	tcctccaccc	ccgcccgcgc	360
cgaggccacc	acctccaagc	ccaagcccgg	ggtccgcggc	aGcctcaaga	agtagctggc	420
tggcttgcc	gcctgactgc	ctggggtaat	tcccttcgat	ttcaatccca	tccaccgacc	480
cgatctacaa	tcaatcaaag	taccgcccgc	cctccggctg	cggtgtactg	ttagtctgct	540
gctgcttctt	attgttggtt	tattgtctgat	acatgtctcg	cgtgatagat	gtgcaactat	600
atatcagtct	cgtcgccggc	aacactggca	tgcttaaaca	tgtgtcgctg	ctgctccgtg	660
atgccggcka	ckgctgctat	tagcggtta	gttagtgtcg	atcggtctc	cttgaacaat	720
ggcaggaatc	tggtgcttgt	ttactttctt	ctaattggcaa	gtaaagttcc	ct	

(2) INFORMATION FOR SEQ ID NO:3960:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..148
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578862

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3960:

Ser	Asn	Pro	His	Ser	Glu	Gly	His	Lys	Asn	Thr	Gly	Arg	Val	Arg	Arg
1				5				10					15		

Arg Gly Gly Glu Ser Xaa Arg Val Gly Gly Gly Val Gly His Asp Gly  
20 25 30  
Glu Gly Glu Xaa Xaa Lys His Thr Ala Lys Glu Ile Ala Ala Lys Ile  
35 40 45  
Asp Ala Ala Thr Thr Asn Xaa Xaa Gly Gly Lys Val Gly Gln Ala Asp  
50 55 60  
Arg Leu Gly Gln Asp Lys Xaa Gly His Ala Asn Trp Arg Ala Arg Ser  
65 70 75 80  
Ala Ala Pro Arg Arg Pro Thr Ser Ser Pro Cys Arg Ser Thr Thr Arg  
85 90 95  
Arg Ala Ile Pro Ser Ser Leu Ser Ser Arg Arg Ser Ser Ser Thr Cys  
100 105 110  
Thr Pro Pro Pro Pro Pro Pro Pro Pro Pro Pro Ser Pro Ser  
115 120 125  
Pro Gly Ser Ala Ala Ala Ser Arg Ser Ser Trp Leu Ala Cys Leu Pro  
130 135 140  
Asp Cys Leu Gly  
145

(2) INFORMATION FOR SEQ ID NO:3961:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..825
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578909

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3961:

actcccaagc	cccaatacac	agcacagcag	catcaacaca	acctcagagg	agcactactg	60
cgagtcaatc	agcgaccagc	acagcaaccg	aactcaaaaag	caagagccca	agatccgagc	120
ggtaggagaa	tccggacatg	gcggcggcag	cgagggcgtc	gtggatggtg	gcgatgagcg	180
tcggcgcggt	ggaggcgctc	aaggaccagg	caggcctctg	ccgctggaac	tacgccggcg	240
tggtcggttg	aggagtggac	gtggaacasa	acagctcctg	cgcgaagagc	gctgccagga	300
ggagcatgga	gagcgtcgtc	ggcgccggcg	ccgctgtggc	ggtcgtcgtc	gtcgtccagg	360
tatatgttgg	agctggtgta	gacgaggagc	gaggcgtaga	tgatggcgtg	ctcgtggttc	420
ggcaGccgct	caggcgggat	ggagccgctg	gcgcggaacg	gcacggcgca	gtaggcgagc	480
atctgggttg	ccagcccgtg	scctccgcgg	ccagcatggc	gatgggctcg	aggcgacgca	540
ccccgtggcg	ccgggaacca	tgctgccggc	gcgaggacga	cgacgcgcga	cgatgaggac	600
gacggggtcg	gggcgaggga	gaccaagagc	ctcatgtggt	tgaagaggtg	ccataggccg	660
aggcctgaga	gcacgcgcgc	tgccagggtg	tggctgatga	ttttatccgc	ggcgccgcgg	720
ggcagcatcg	tcacgcgcat	cgatgtcagt	cgtctaaact	gttgatgctg	gcttgctgat	780
ttctttgttt	gcaatgcatg	ctcgatcggg	aaggatttat	tctct		

(2) INFORMATION FOR SEQ ID NO:3962:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..152
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578910

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3962:

Met Ala Ala Ala Arg Ala Ser Trp Met Val Ala Met Ser Val Gly  
1 5 10 15  
Ala Val Glu Ala Leu Lys Asp Gln Ala Gly Leu Cys Arg Trp Asn Tyr  
20 25 30  
Ala Gly Val Val Gly Gly Gly Val Asp Val Glu Xaa Asn Ser Ser Cys

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35 40 45  
Ala Lys Ser Ala Ala Arg Arg Ser Met Glu Ser Val Val Gly Ala Gly  
50 55 60  
Ala Ala Trp Ala Val Val Val Val Val Gln Val Tyr Val Gly Ala Gly  
65 70 75 80  
Val Asp Glu Glu Arg Gly Val Asp Asp Gly Val Leu Val Val Arg Gln  
85 90 95  
Pro Leu Arg Arg Asp Gly Ala Val Gly Ala Glu Arg His Arg Arg Val  
100 105 110  
Gly Glu His Leu Gly Gly Gln Pro Val Xaa Pro Ala Ala Ser Met Ala  
115 120 125  
Met Gly Ser Arg Arg Arg Thr Pro Trp Arg Arg Glu Pro Cys Cys Arg  
130 135 140  
Arg Glu Asp Asp Asp Ala Arg Arg  
145 150

(2) INFORMATION FOR SEQ ID NO:3963:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..143

(D) OTHER INFORMATION: / Ceres Seq. ID 1578911

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3963:

Met Val Ala Met Ser Val Gly Ala Val Glu Ala Leu Lys Asp Gln Ala  
1 5 10 15  
Gly Leu Cys Arg Trp Asn Tyr Ala Gly Val Val Gly Gly Gly Val Asp  
20 25 30  
Val Glu Xaa Asn Ser Ser Cys Ala Lys Ser Ala Ala Arg Arg Ser Met  
35 40 45  
Glu Ser Val Val Gly Ala Gly Ala Ala Trp Ala Val Val Val Val Val  
50 55 60  
Gln Val Tyr Val Gly Ala Gly Val Asp Glu Glu Arg Gly Val Asp Asp  
65 70 75 80  
Gly Val Leu Val Val Arg Gln Pro Leu Arg Arg Asp Gly Ala Val Gly  
85 90 95  
Ala Glu Arg His Arg Arg Val Gly Glu His Leu Gly Gly Gln Pro Val  
100 105 110  
Xaa Pro Ala Ala Ser Met Ala Met Gly Ser Arg Arg Arg Thr Pro Trp  
115 120 125  
Arg Arg Glu Pro Cys Cys Arg Arg Glu Asp Asp Asp Ala Arg Arg  
130 135 140

(2) INFORMATION FOR SEQ ID NO:3964:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..140

(D) OTHER INFORMATION: / Ceres Seq. ID 1578912

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3964:

Met Ser Val Gly Ala Val Glu Ala Leu Lys Asp Gln Ala Gly Leu Cys  
1 5 10 15  
Arg Trp Asn Tyr Ala Gly Val Val Gly Gly Gly Val Asp Val Glu Xaa  
20 25 30

Asn Ser Ser Cys Ala Lys Ser Ala Ala Arg Arg Ser Met Glu Ser Val  
35 40 45  
Val Gly Ala Gly Ala Ala Trp Ala Val Val Val Val Val Gln Val Tyr  
50 55 60  
Val Gly Ala Gly Val Asp Glu Glu Arg Gly Val Asp Asp Gly Val Leu  
65 70 75 80  
Val Val Arg Gln Pro Leu Arg Arg Asp Gly Ala Val Gly Ala Glu Arg  
85 90 95  
His Arg Arg Val Gly Glu His Leu Gly Gly Gln Pro Val Xaa Pro Ala  
100 105 110  
Ala Ser Met Ala Met Gly Ser Arg Arg Arg Thr Pro Trp Arg Arg Glu  
115 120 125  
Pro Cys Arg Arg Glu Asp Asp Asp Ala Arg Arg  
130 135 140

(2) INFORMATION FOR SEQ ID NO:3965:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 869 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..869
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578945

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3965:

ctagcatttta	cgcggnvgag	ctcgagccgg	cggcgctcgac	gggcggcggt	ggcgacgacc	60
acaacctgga	cctgtcgctg	gggagctcgg	cggggaacaa	aaggggcagc	cttgacgacg	120
gctccccac	tcagaaaacc	cagccgccc	cgcacgcggc	tcccaggtaa	gcagtgcgt	180
ccacccagc	cgccgccatg	aagcgcaacc	cccggtcac	gagctccgc	cggaagtgcc	240
gcaagggcan	cttcacggcc	ccgtcctccg	tccgcgcgt	gctcatgtcc	gcggcgctat	300
cgacggagCt	ccgccacaag	tacaatgtgc	gttccatccc	gatccgcaag	gacgacgagg	360
tgcaggtcgt	gcgcggcacc	tacaagggcc	gtgagggcaa	agtgggtgag	gtgtaccgcc	420
gtcgctgggt	catccaagtt	gagcggatca	cccgcgagaa	ggtgaacggc	tccaccgtga	480
acgtgggcat	ccacccttcc	aagggtcatg	ttacaaagct	gaagcttgac	aaggaccgca	540
aggcgctcct	cgaccgcaag	gcccggggcc	gcgcgcgccg	caaggctaag	ggcaagttta	600
ctgcccagca	cgtcgccgcc	gctgctgggt	gcgcgcgcgc	cactggcgcg	tctctccagg	660
agatcgacta	ggcttcgcgg	ggatctgatg	gtggtcctac	cgcctattac	tccttatcgc	720
tctagttttt	gctatcaatg	attatgtgct	aggagtttta	tgttacttat	aaactgcttt	780
gagcctcgat	gggagttgaa	cttaatgtgg	agtgtatctg	agatatgaag	aactcattat	840
atggctaata	tctctgtgtg	tggtctgct				

(2) INFORMATION FOR SEQ ID NO:3966:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..157
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578946

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3966:

Met Lys Arg Asn Pro Arg Val Thr Ser Ser Arg Arg Lys Cys Arg Lys  
1 5 10 15  
Gly Xaa Phe Thr Ala Pro Ser Ser Val Arg Arg Val Leu Met Ser Ala  
20 25 30  
Ala Leu Ser Thr Glu Leu Arg His Lys Tyr Asn Val Arg Ser Ile Pro  
35 40 45  
Ile Arg Lys Asp Asp Glu Val Gln Val Val Arg Gly Thr Tyr Lys Gly  
50 55 60

Arg Glu Gly Lys Val Val Gln Val Tyr Arg Arg Arg Trp Val Ile His  
65 70 75 80  
Val Glu Arg Ile Thr Arg Glu Lys Val Asn Gly Ser Thr Val Asn Val  
85 90 95  
Gly Ile His Pro Ser Lys Val Met Val Thr Lys Leu Lys Leu Asp Lys  
100 105 110  
Asp Arg Lys Ala Leu Leu Asp Arg Lys Ala Arg Gly Arg Ala Ala Asp  
115 120 125  
Lys Ala Lys Gly Lys Phe Thr Ala Asp Asp Val Ala Ala Ala Gly  
130 135 140  
Gly Ala Ala Ala Thr Gly Ala Ser Leu Gln Glu Ile Asp  
145 150 155

(2) INFORMATION FOR SEQ ID NO:3967:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..128
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578947

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3967:

Met Ser Ala Ala Leu Ser Thr Glu Leu Arg His Lys Tyr Asn Val Arg  
1 5 10 15  
Ser Ile Pro Ile Arg Lys Asp Asp Glu Val Gln Val Val Arg Gly Thr  
20 25 30  
Tyr Lys Gly Arg Glu Gly Lys Val Val Gln Val Tyr Arg Arg Arg Trp  
35 40 45  
Val Ile His Val Glu Arg Ile Thr Arg Glu Lys Val Asn Gly Ser Thr  
50 55 60  
Val Asn Val Gly Ile His Pro Ser Lys Val Met Val Thr Lys Leu Lys  
65 70 75 80  
Leu Asp Lys Asp Arg Lys Ala Leu Leu Asp Arg Lys Ala Arg Gly Arg  
85 90 95  
Ala Ala Asp Lys Ala Lys Gly Lys Phe Thr Ala Asp Asp Val Ala Ala  
100 105 110  
Ala Ala Gly Gly Ala Ala Ala Thr Gly Ala Ser Leu Gln Glu Ile Asp  
115 120 125

(2) INFORMATION FOR SEQ ID NO:3968:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 557 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..557
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578951

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3968:

agtctaataca ctattgcagt cggcttctct aatactgggc cactggtttc gctccgcact 60  
tccgccgcta tggccgcgc aaccttctcc gccgcggcc gccggtctct ctccaccgcc 120  
gcggcaggca ngnagaaaac cgagctcccc gtccctatcg cccgtmttcg ccagctcgcc 180  
cgcgctggcc gctcgcacga catcgacgcg actctcgcgc cctgttccc tccccacccc 240  
gtcgcgcgcg tctcgccct ctccacggtg ggctccccg ancCgcgcct ccgcgctgct 300  
cggcaccatg acgtcgcca ataccgcgc cctgaacgcg gtccctcggtc cactcctccg 360  
ccgcgcgcgc ctgAgccggg ctcggtgcct caatcctcgc cgcgcgatgcc tctgtcccg 420

gggacgccgt cacggacagc atcctcgcca agtcgctctg cctcacctcg ggcgccgact 480  
ccgcgctcca cctcctccgg aagccttcgt cgggagcgcc gccgnygctc cagctcttca 540  
caaccatcat cgactcc

(2) INFORMATION FOR SEQ ID NO:3969:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..185
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578952

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3969:

Ser Leu Ile Thr Ile Ala Val Gly Phe Ser Asn Thr Gly Pro Leu Val  
1 5 10 15  
Ser Leu Arg Thr Ser Ala Ala Met Ala Ala Ala Thr Phe Ser Ala Ala  
20 25 30  
Gly Arg Arg Leu Leu Ser Thr Ala Ala Gly Xaa Xaa Lys Thr Glu  
35 40 45  
Leu Pro Val Pro Ile Ala Arg Xaa Arg Gln Leu Ala Arg Ala Gly Arg  
50 55 60  
Leu Asp Asp Ile Asp Ala Thr Leu Ala Pro Leu Phe Pro Ser His Pro  
65 70 75 80  
Val Ala Ala Leu Ser Ala Leu Ser Thr Val Gly Leu Pro Xaa Pro Arg  
85 90 95  
Leu Arg Ala Ala Arg His His Asp Val Ala Gln Tyr Arg Ala Pro Glu  
100 105 110  
Arg Gly Pro Arg Ser Thr Pro Pro Pro Pro Pro Glu Pro Gly Ser  
115 120 125  
Cys Pro Gln Ser Ser Pro Arg Met Pro Leu Ser Arg Gly Thr Pro Ser  
130 135 140  
Arg Thr Ala Ser Ser Pro Ser Arg Ser Ala Ser Pro Arg Ala Pro Thr  
145 150 155 160  
Pro Arg Ser Thr Ser Ser Gly Ser Leu Arg Arg Glu Arg Arg Xaa Xaa  
165 170 175  
Ser Ser Ser Ser Gln Pro Ser Ser Thr  
180 185

(2) INFORMATION FOR SEQ ID NO:3970:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..162
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578953

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3970:

Met Ala Ala Ala Thr Phe Ser Ala Ala Gly Arg Arg Leu Leu Ser Thr  
1 5 10 15  
Ala Ala Ala Gly Xaa Xaa Lys Thr Glu Leu Pro Val Pro Ile Ala Arg  
20 25 30  
Xaa Arg Gln Leu Ala Arg Ala Gly Arg Leu Asp Asp Ile Asp Ala Thr  
35 40 45  
Leu Ala Pro Leu Phe Pro Ser His Pro Val Ala Ala Leu Ser Ala Leu  
50 55 60  
Ser Thr Val Gly Leu Pro Xaa Pro Arg Leu Arg Ala Ala Arg His His  
65 70 75 80

Asp Val Ala Gln Tyr Arg Ala Pro Glu Arg Gly Pro Arg Ser Thr Pro  
85 90 95  
Pro Pro Pro Pro Pro Glu Pro Gly Ser Cys Pro Gln Ser Ser Pro Arg  
100 105 110  
Met Pro Leu Ser Arg Gly Thr Pro Ser Arg Thr Ala Ser Ser Pro Ser  
115 120 125  
Arg Ser Ala Ser Pro Arg Ala Pro Thr Pro Arg Ser Thr Ser Ser Gly  
130 135 140  
Ser Leu Arg Arg Glu Arg Arg Xaa Xaa Ser Ser Ser Ser Gln Pro Ser  
145 150 155 160  
Ser Thr

(2) INFORMATION FOR SEQ ID NO:3971:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 752 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..752
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578993

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3971:

gactagggtt	ctgtccacct	tccaggtcct	tcgaacttcc	acgcattcct	actactcctg	60
gtccccgcga	cctaacgccg	ccactcctga	cttcgccatc	cggcgatcac	cagagcccta	120
gtccggcggt	ctctagcgat	ccccaaaaAc	ccactccgcc	gcattttctgc	cgacttggcc	180
ggatttggtcg	cttattgaaN	atgGCTacgc	cacttatagc	aggacttgca	gttgcagcaa	240
ctgctcttgc	tggtcgatat	ggtgtccaag	catggcaagc	ttataaggca	aggcctatag	300
ttccaaggat	gcgcaaattc	tatgaagggtg	gctttcaacc	tacaatgaac	cgaaggraag	360
ctgcattaat	ccttggtgtc	agggaaactg	ccaacgcaga	gaaggtaaaa	gaggcgcaca	420
agaggggttat	ggtcgccaac	catccagatg	ctggtggaag	tcattacctt	gcgtcaaaga	480
ttaatgaggc	gaaggatgtg	ttgtcaggga	aaacaaaagg	aggtgggtcg	gccttctgat	540
tgtagaatta	agaatgcact	ctctgctaga	aggataattt	tgtgcctcta	aatttagcat	600
taKTTgaaga	tactgtagac	cgcagtttag	tcttggtatt	gcggaaattt	ctggacaaag	660
catattgggc	cttctgtgaa	gtagttatcc	agtgcctatt	aatactcagc	tgtgcctgct	720
tctataaaga	tatacatgat	gaaggttaca	tc			

(2) INFORMATION FOR SEQ ID NO:3972:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..178
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578994

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3972:

Leu Gly Phe Cys Pro Pro Ser Arg Ser Phe Glu Leu Pro Arg Ile Pro	
1 5 10 15	
Thr Thr Pro Gly Ser Arg Asp Leu Thr Pro Pro Leu Leu Thr Ser Pro	
20 25 30	
Ser Gly Asp His Gln Ser Pro Ser Ser Gly Val Ser Ser Asp Pro Gln	
35 40 45	
Lys Pro Thr Pro Pro His Phe Cys Arg Leu Gly Arg Ile Gly Arg Leu	
50 55 60	
Leu Xaa Met Ala Thr Pro Leu Ile Ala Gly Leu Ala Val Ala Ala Thr	
65 70 75 80	
Ala Leu Ala Gly Arg Tyr Gly Val Gln Ala Trp Gln Ala Tyr Lys Ala	
85 90 95	

Arg Pro Ile Val Pro Arg Met Arg Lys Phe Tyr Glu Gly Gly Phe Gln  
100 105 110  
Pro Thr Met Asn Arg Arg Xaa Ala Ala Leu Ile Leu Gly Val Arg Glu  
115 120 125  
Thr Ala Asn Ala Glu Lys Val Lys Glu Ala His Lys Arg Val Met Val  
130 135 140  
Ala Asn His Pro Asp Ala Gly Gly Ser His Tyr Leu Ala Ser Lys Ile  
145 150 155 160  
Asn Glu Ala Lys Asp Val Leu Ser Gly Lys Thr Lys Gly Gly Gly Ser  
165 170 175  
Ala Phe

(2) INFORMATION FOR SEQ ID NO:3973:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..112
- (D) OTHER INFORMATION: / Ceres Seq. ID 1578995

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3973:

Met Ala Thr Pro Leu Ile Ala Gly Leu Ala Val Ala Ala Thr Ala Leu  
1 5 10 15  
Ala Gly Arg Tyr Gly Val Gln Ala Trp Gln Ala Tyr Lys Ala Arg Pro  
20 25 30  
Ile Val Pro Arg Met Arg Lys Phe Tyr Glu Gly Gly Phe Gln Pro Thr  
35 40 45  
Met Asn Arg Arg Xaa Ala Ala Leu Ile Leu Gly Val Arg Glu Thr Ala  
50 55 60  
Asn Ala Glu Lys Val Lys Glu Ala His Lys Arg Val Met Val Ala Asn  
65 70 75 80  
His Pro Asp Ala Gly Gly Ser His Tyr Leu Ala Ser Lys Ile Asn Glu  
85 90 95  
Ala Lys Asp Val Leu Ser Gly Lys Thr Lys Gly Gly Gly Ser Ala Phe  
100 105 110

(2) INFORMATION FOR SEQ ID NO:3974:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 848 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..848
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579004

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3974:

aaaaagataa agttaggctc ggcaccgggg gctcatccgc aagcctgtgg acgcgagtga 60  
gtgaacacca gccgtattgt cccgaccccg accgatcctc gcctgctgca gccatggcga 120  
cctccgcggc gctctctacc gccgccaatc ccacccagct ctgccgggcc cgcgcttcgc 180  
tgggcaagcc ggtgaagggg cttggcctga gcatggggcc cgagcgcgcc cagcggagca 240  
ttgtgtgccg ggcggcgagc agcatctccg ccgaccgcgt ccccgacatg gagaagcgga 300  
agctgatgaa cctcctctct ctcggcgcca tctcgttgcc caccgtcggc atggtcgtcc 360  
cctacggcgc cttcttcgtc cctgccggct ccgggaacgc cggcggCggg acctacgcga 420  
aggacaagct gggcaacgac atcacggtgg aggcgtggct caacacgcac ggtcccaacg 480  
accgcacgct cgcgcagggg ctcaagggtg accccacgta cctggtggtg gagcaggaca 540

(2) INFORMATION FOR SEQ ID NO:3975:

(A) LENGTH: 246 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptid

(A) NAM

(B) LOCATION: 1..246

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:3975:

Asp Lys Val Arg Leu Gly Thr Gly Gly Ser Se

(2) INFORMATION FOR SEQ ID NO:3976:

(A) LENGTH: 209 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..209

(D) OTHER INFORMATION: / Ceres Seq. ID 1579006

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3976:

Met Ala Thr Ser Ala Ala Leu Ser Thr Ala Ala Asn Pro Thr Gln Leu  
1 5 10 15  
Cys Arg Ser Arg Ala Ser Leu Gly Lys Pro Val Lys Gly Leu Gly Leu  
20 25 30  
Ser Met Gly Arg Glu Arg Ala Gln Arg Ser Ile Val Cys Gln Ala Ala  
35 40 45  
Ser Ser Ile Ser Ala Asp Arg Val Pro Asp Met Glu Lys Arg Lys Leu  
50 55 60  
Met Asn Leu Leu Leu Leu Gly Ala Ile Ser Leu Pro Thr Val Gly Met  
65 70 75 80  
Val Val Pro Tyr Gly Ala Phe Phe Val Pro Ala Gly Ser Gly Asn Ala  
85 90 95  
Gly Gly Gly Thr Tyr Ala Lys Asp Lys Leu Gly Asn Asp Ile Thr Val  
100 105 110  
Glu Ala Trp Leu Asn Thr His Gly Pro Asn Asp Arg Thr Leu Ala Gln  
115 120 125  
Gly Leu Lys Gly Asp Pro Thr Tyr Leu Val Val Glu Gln Asp Lys Thr  
130 135 140  
Leu Ala Thr Tyr Gly Ile Asn Ala Val Cys Thr His Leu Gly Cys Val  
145 150 155 160  
Val Pro Trp Asn Gly Ala Glu Asn Lys Phe Ile Cys Pro Cys His Gly  
165 170 175  
Ser Gln Tyr Asn Asn Gln Gly Lys Val Val Ala Gly Pro Phe Glu Ser  
180 185 190  
Met Lys Val Lys His Gly Arg Ser Lys Arg Val Trp Lys Asp Cys Arg  
195 200 205  
Cys

(2) INFORMATION FOR SEQ ID NO:3977:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..176
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579007

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3977:

Met Gly Arg Glu Arg Ala Gln Arg Ser Ile Val Cys Gln Ala Ala Ser  
1 5 10 15  
Ser Ile Ser Ala Asp Arg Val Pro Asp Met Glu Lys Arg Lys Leu Met  
20 25 30  
Asn Leu Leu Leu Leu Gly Ala Ile Ser Leu Pro Thr Val Gly Met Val  
35 40 45  
Val Pro Tyr Gly Ala Phe Phe Val Pro Ala Gly Ser Gly Asn Ala Gly  
50 55 60  
Gly Gly Thr Tyr Ala Lys Asp Lys Leu Gly Asn Asp Ile Thr Val Glu  
65 70 75 80  
Ala Trp Leu Asn Thr His Gly Pro Asn Asp Arg Thr Leu Ala Gln Gly  
85 90 95  
Leu Lys Gly Asp Pro Thr Tyr Leu Val Val Glu Gln Asp Lys Thr Leu  
100 105 110  
Ala Thr Tyr Gly Ile Asn Ala Val Cys Thr His Leu Gly Cys Val Val  
115 120 125  
Pro Trp Asn Gly Ala Glu Asn Lys Phe Ile Cys Pro Cys His Gly Ser  
130 135 140  
Gln Tyr Asn Asn Gln Gly Lys Val Val Ala Gly Pro Phe Glu Ser Met  
145 150 155 160



Lys Val Lys His Gly Arg Ser Lys Arg Val Trp Lys Asp Cys Arg Cys  
165 170 175

(2) INFORMATION FOR SEQ ID NO:3978:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 982 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..982
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579012

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3978:

catttgctcc aagtcccaaa tactagcarg cggcaggcgg ccaagaccgg tgtccctcga	60
cgacctgccg agtgccgagg caagcaagac gcgaggaggc tgtaagctgc catcagcagc	120
ggcgatggcg ggcgcggagg tgggagaaga caagtaccgc tccttcatcc acggcgaggg	180
cgagagggac accgtgtgga ggtacggcgc cccgcccaac tacgacgtgg tcaacaagct	240
cttcgaggag gagaggactc aggtgtggcc cgagggtcgc ctggaggaga aggtgcagcg	300
gttgctcaag agctgggaga tggagctggt gcacaargtg cggcccaggg accagaagac	360
cgtcaactcg gagaaatact ctgccagcac caacgggatg arcgctctra cccggggccga	420
ggtgatggcc atcggcggct acaacaactt cctgcgcacc aagctgcccc cggagcaccg	480
catctacgac cggacagcg agaccgtgga gtcCgccatg gccaccttca ccacggcctt	540
cccgcgggGC ttgcgCatcg aggtgctcga cgtctacagc ggcccggcca ggatcgcctt	600
caagttccgc cactggggct acatggaggg cccttcaagg gccacccgcc gcacggccag	660
cgggtcgagc tcttcggcgt ctgcatcttc catgttgacg aagacatgaa ggtggacaag	720
tcagagtact tctacgagcg cggcaacttc ctgcgcggct tcttgagtgc ccctgccct	780
gatggctcag gcggttgccc cgtgatgcgc gggaactgaa tgggcctgca atgggacatt	840
ggaagactag gcattggaac attgggatta ttagcattag cgatcccgaa tccgctttta	900
ttacggttta ataattccat catgtaacat gacacttgca tttgtgtttg aataaacatg	960
tcgttgcttc gacatattag cg	

(2) INFORMATION FOR SEQ ID NO:3979:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..235
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579013

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3979:

Ile Cys Ser Lys Ser Gln Ile Leu Ala Xaa Gly Arg Arg Pro Arg Pro	
1 5 10 15	
Val Ser Leu Asp Asp Leu Pro Ser Ala Glu Ala Ser Lys Thr Arg Gly	
20 25 30	
Gly Cys Lys Leu Pro Ser Ala Ala Ala Met Ala Gly Ala Glu Val Gly	
35 40 45	
Glu Asp Lys Tyr Arg Ser Phe Ile His Gly Glu Gly Glu Arg Asp Thr	
50 55 60	
Val Trp Arg Tyr Gly Ala Pro Pro Asn Tyr Asp Val Val Asn Lys Leu	
65 70 75 80	
Phe Glu Glu Glu Arg Thr Gln Val Trp Pro Glu Gly Ser Leu Glu Glu	
85 90 95	
Lys Val Gln Arg Leu Leu Lys Ser Trp Glu Met Glu Leu Val His Xaa	
100 105 110	
Val Arg Pro Glu Asp Gln Lys Thr Val Asn Ser Glu Lys Tyr Ser Ala	
115 120 125	

Ser Thr Asn Gly Met Xaa Ala Xaa Thr Arg Ala Glu Val Met Ala Ile  
130 135 140  
Gly Gly Tyr Asn Asn Phe Leu Arg Thr Lys Leu Pro Pro Glu His Arg  
145 150 155 160  
Ile Tyr Asp Pro Asp Ser Glu Thr Val Glu Ser Ala Met Ala Thr Phe  
165 170 175  
Thr Thr Ala Phe Pro Arg Gly Phe Ala Ile Glu Val Leu Asp Val Tyr  
180 185 190  
Ser Gly Pro Pro Arg Ile Ala Phe Lys Phe Arg His Trp Gly Tyr Met  
195 200 205  
Glu Gly Pro Ser Arg Ala Thr Arg Arg Thr Ala Ser Gly Ser Ser Ser  
210 215 220  
Ser Ala Ser Ala Ser Ser Met Leu Thr Lys Thr  
225 230 235

(2) INFORMATION FOR SEQ ID NO:3980:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..194
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579014

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3980:

Met Ala Gly Ala Glu Val Gly Glu Asp Lys Tyr Arg Ser Phe Ile His  
1 5 10 15  
Gly Glu Gly Glu Arg Asp Thr Val Trp Arg Tyr Gly Ala Pro Pro Asn  
20 25 30  
Tyr Asp Val Val Asn Lys Leu Phe Glu Glu Glu Arg Thr Gln Val Trp  
35 40 45  
Pro Glu Gly Ser Leu Glu Glu Lys Val Gln Arg Leu Leu Lys Ser Trp  
50 55 60  
Glu Met Glu Leu Val His Xaa Val Arg Pro Glu Asp Gln Lys Thr Val  
65 70 75 80  
Asn Ser Glu Lys Tyr Ser Ala Ser Thr Asn Gly Met Xaa Ala Xaa Thr  
85 90 95  
Arg Ala Glu Val Met Ala Ile Gly Gly Tyr Asn Asn Phe Leu Arg Thr  
100 105 110  
Lys Leu Pro Pro Glu His Arg Ile Tyr Asp Pro Asp Ser Glu Thr Val  
115 120 125  
Glu Ser Ala Met Ala Thr Phe Thr Thr Ala Phe Pro Arg Gly Phe Ala  
130 135 140  
Ile Glu Val Leu Asp Val Tyr Ser Gly Pro Pro Arg Ile Ala Phe Lys  
145 150 155 160  
Phe Arg His Trp Gly Tyr Met Glu Gly Pro Ser Arg Ala Thr Arg Arg  
165 170 175  
Thr Ala Ser Gly Ser Ser Ser Ser Ala Ser Ala Ser Ser Met Leu Thr  
180 185 190  
Lys Thr

(2) INFORMATION FOR SEQ ID NO:3981:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

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(B) LOCATION: 1..129

(D) OTHER INFORMATION: / Ceres Seq. ID 1579015

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3981:

Met Glu Leu Val His Xaa Val Arg Pro Glu Asp Gln Lys Thr Val Asn  
1 5 10 15  
Ser Glu Lys Tyr Ser Ala Ser Thr Asn Gly Met Xaa Ala Xaa Thr Arg  
20 25 30  
Ala Glu Val Met Ala Ile Gly Gly Tyr Asn Asn Phe Leu Arg Thr Lys  
35 40 45  
Leu Pro Pro Glu His Arg Ile Tyr Asp Pro Asp Ser Glu Thr Val Glu  
50 55 60  
Ser Ala Met Ala Thr Phe Thr Thr Ala Phe Pro Arg Gly Phe Ala Ile  
65 70 75 80  
Glu Val Leu Asp Val Tyr Ser Gly Pro Pro Arg Ile Ala Phe Lys Phe  
85 90 95  
Arg His Trp Gly Tyr Met Glu Gly Pro Ser Arg Ala Thr Arg Arg Thr  
100 105 110  
Ala Ser Gly Ser Ser Ser Ser Ala Ser Ser Met Leu Thr Lys  
115 120 125  
Thr

(2) INFORMATION FOR SEQ ID NO:3982:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1205 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1205

(D) OTHER INFORMATION: / Ceres Seq. ID 1579027

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3982:

ctctctgtcg catttcccgt cctgtccttc ccttaccgg cggtttaaac cctagttctc 60  
actcccatcg ccgcttcagc tccgccgcag cagatggagt tctgggggtct cgagggtcaag 120  
cctgggttcca ctgttaagtg tgagcctgga tatggctttg tgctgcacct ttcccaggct 180  
gctcttgggg aatcgaagaa gagtataat gccttgatgt atgtcaaaat tgatgatcag 240  
aaacttgcca ttggaaccct ctctgttgac aagaaccac acatacaatt tgatctgggt 300  
ttogataaag agtttgagct gtgcacaca tcaaaaacta ccagcgtctt cttcactggc 360  
tacaaggttg agcagccatt cgaggaagat gagccttctt ccacaatgga tcttgattct 420  
gaagatgaag acgaggagcg ggatgttcca gtatgcaagg aaaatggcaa agctgatggg 480  
aagaacaga aaagtcaaga aaaggcagtt gctgcacctt caaatcaag tccggattcc 540  
aagaagagca asgaTgacTg atgattctga tgaggaygag ackgaygatt ctgatgaggg 600  
tttatcttct gaagaaggcg atgatgattc aagtgatgaa gatgatacca gtgacgatga 660  
ggaggaagac actccaactc ctaagaagcc tgaggtaggc aagaagagag ctgctgaaaag 720  
ttcctgtctg aaaactctc tatctgataa gaaagcaaag gttgccacac cgtcatctca 780  
gaagacaggt ggcaagaagg gcgcgcgct ccatgtggca actccacacc cagcaaaaagg 840  
caagaccatt gtaaacaatg acaaatcggt caagtctcca aaatctgcgc caaatctgg 900  
tgtcccttgc aaatcgtgca gcaagtcatt catcagtcag acggcacttc aggctcactc 960  
gaaggcgaag catgggggca agtgagtcgc aggtccaata gagtcaacaa caaatgcgaa 1020  
acatgggaga ggagggtgaa cgagagtcctc gaaagagtg cggtggaagt aggcctaacc 1080  
ttattttgtt tagagacggg ctatgcgttc gatgtagcaa aacaaggctg tggtttgtgt 1140  
acttcaatat ttgggttgtg tgtttcgaat ttttttttga acgtgtctcg gattgttgtg 1200  
gtgcc

(2) INFORMATION FOR SEQ ID NO:3983:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 155 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..155

(D) OTHER INFORMATION: / Ceres Seq. ID 1579028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3983:

Met Glu Phe Trp Gly Leu Glu Val Lys Pro Gly Ser Thr Val Lys Cys  
1 5 10 15  
Glu Pro Gly Tyr Gly Phe Val Leu His Leu Ser Gln Ala Ala Leu Gly  
20 25 30  
Glu Ser Lys Lys Ser Asp Asn Ala Leu Met Tyr Val Lys Ile Asp Asp  
35 40 45  
Gln Lys Leu Ala Ile Gly Thr Leu Ser Val Asp Lys Asn Pro His Ile  
50 55 60  
Gln Phe Asp Leu Val Phe Asp Lys Glu Phe Glu Leu Ser His Thr Ser  
65 70 75 80  
Lys Thr Thr Ser Val Phe Phe Thr Gly Tyr Lys Val Glu Gln Pro Phe  
85 90 95  
Glu Glu Asp Glu Pro Ser Ser Thr Met Asp Leu Asp Ser Glu Asp Glu  
100 105 110  
Asp Glu Glu Arg Asp Val Pro Val Lys Glu Asn Gly Lys Ala Asp  
115 120 125  
Gly Lys Lys Gln Lys Ser Gln Glu Lys Ala Val Ala Ala Pro Ser Lys  
130 135 140  
Ser Ser Pro Asp Ser Lys Lys Ser Xaa Asp Asp  
145 150 155

(2) INFORMATION FOR SEQ ID NO:3984:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 173 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..173

(D) OTHER INFORMATION: / Ceres Seq. ID 1579029

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3984:

Met Ala Lys Leu Met Gly Arg Asn Arg Lys Val Lys Lys Arg Gln Leu  
1 5 10 15  
Leu His Leu Gln Asn Gln Val Arg Ile Pro Arg Arg Ala Xaa Met Thr  
20 25 30  
Asp Asp Ser Asp Glu Xaa Glu Xaa Xaa Asp Ser Asp Glu Gly Leu Ser  
35 40 45  
Ser Glu Glu Gly Asp Asp Asp Ser Ser Asp Glu Asp Asp Thr Ser Asp  
50 55 60  
Asp Glu Glu Glu Asp Thr Pro Thr Pro Lys Lys Pro Glu Val Gly Lys  
65 70 75 80  
Lys Arg Ala Ala Glu Ser Ser Val Leu Lys Thr Pro Leu Ser Asp Lys  
85 90 95  
Lys Ala Lys Val Ala Thr Pro Ser Ser Gln Lys Thr Gly Gly Lys Lys  
100 105 110  
Gly Ala Ala Val His Val Ala Thr Pro His Pro Ala Lys Gly Lys Thr  
115 120 125  
Ile Val Asn Asn Asp Lys Ser Val Lys Ser Pro Lys Ser Ala Pro Lys  
130 135 140  
Ser Gly Val Pro Cys Lys Ser Cys Ser Lys Ser Phe Ile Ser Gln Thr  
145 150 155 160  
Ala Leu Gln Ala His Ser Lys Ala Lys His Gly Gly Lys  
165 170

(2) INFORMATION FOR SEQ ID NO:3985:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..169  
(D) OTHER INFORMATION: / Ceres Seq. ID 1579030  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3985:

Met Gly Arg Asn Arg Lys Val Lys Lys Arg Gln Leu Leu His Leu Gln  
1 5 10 15  
Asn Gln Val Arg Ile Pro Arg Arg Ala Xaa Met Thr Asp Asp Ser Asp  
20 25 30  
Glu Xaa Glu Xaa Xaa Asp Ser Asp Glu Gly Leu Ser Ser Glu Glu Gly  
35 40 45  
Asp Asp Asp Ser Ser Asp Glu Asp Asp Thr Ser Asp Asp Glu Glu Glu  
50 55 60  
Asp Thr Pro Thr Pro Lys Lys Pro Glu Val Gly Lys Lys Arg Ala Ala  
65 70 75 80  
Glu Ser Ser Val Leu Lys Thr Pro Leu Ser Asp Lys Lys Ala Lys Val  
85 90 95  
Ala Thr Pro Ser Ser Gln Lys Thr Gly Gly Lys Lys Gly Ala Ala Val  
100 105 110  
His Val Ala Thr Pro His Pro Ala Lys Gly Lys Thr Ile Val Asn Asn  
115 120 125  
Asp Lys Ser Val Lys Ser Pro Lys Ser Ala Pro Lys Ser Gly Val Pro  
130 135 140  
Cys Lys Ser Cys Ser Lys Ser Phe Ile Ser Gln Thr Ala Leu Gln Ala  
145 150 155 160  
His Ser Lys Ala Lys His Gly Gly Lys  
165

(2) INFORMATION FOR SEQ ID NO:3986:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 835 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..835  
(D) OTHER INFORMATION: / Ceres Seq. ID 1579042

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3986:

attgtwcccg ccgctcttccc caattcgccg ccagscaggg taaaaaaaaa aaagaggaag 60  
aaaacctcct gcaattccca ttccatcgat ccagctccgg tccaagccaa agctttcttc 120  
gccccaaacc ttgttcaact ccaatgtcgg acttcttctt cgggagcccg ttccgcccgc 180  
tcttccacgc gcgccccttc catgcgctcg actggctctc cgccgcggcg gcggccatgg 240  
actgggtgga gaccccgctc tcccaogtgc tgcgcgtcaa cgtgccggga ctcggaagg 300  
acgacgtcaa ggtccaggtc gacgagggca aagtgtcac catcaggggc gccccgccc 360  
cggccaagga gaaggggaag gaggacgagg aggaggggac ggtgtggcac gtggcggaGc 420  
gcggcaagcc ggagttcgcg cgggcccgtg cgctgccgga gaacgtgcgc gtggacggga 480  
tcagggccgg cttggagaac ggggttctca ccgtcgttgt gccaaggaa gtcgccccg 540  
cccggcccaa gccaggtcc atcgccgtct ccagcaagct ctgatgagtc tgaggcgatg 600  
agtggcagag tgtacgggtc agtgtaaac catgccgcaa atggcgggta cgtctgaatt 660  
ctggtcgtgt gtgtgtccgt gtcacctaga aaacgcgcac cccgtgtaaa ttgcgataca 720  
atttcatgca agtaatccga gtgagtgaag atggctgcta gccaaaaacg gtcgattctg 780  
aatatgcagt ttgcaataaa ctaaattaaa aggaaaaggc atgtttgaat atgtg

(2) INFORMATION FOR SEQ ID NO:3987:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 218 amino acids

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- (B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..218  
(D) OTHER INFORMATION: / Ceres Seq. ID 1579043  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3987:

Ile Xaa Pro Ala Val Phe Pro Asn Ser Pro Pro Xaa Arg Val Lys Lys  
1 5 10 15  
Lys Lys Arg Lys Lys Thr Ser Cys Asn Ser His Ser Ile Asp Pro Ala  
20 25 30  
Pro Val Gln Ala Lys Ala Phe Phe Ala Pro Asn Leu Val Gln Leu Gln  
35 40 45  
Cys Arg Thr Ser Ser Ser Gly Ala Arg Ser Ala Ala Ser Ser Thr Arg  
50 55 60  
Ala Pro Ser Met Pro Ser Thr Gly Pro Pro Pro Arg Arg Arg Pro Trp  
65 70 75 80  
Thr Gly Trp Arg Pro Arg Pro Pro Thr Cys Cys Ala Ser Thr Cys Arg  
85 90 95  
Asp Ser Ala Arg Thr Thr Ser Arg Ser Arg Ser Thr Arg Ala Lys Cys  
100 105 110  
Ser Pro Ser Gly Ala Pro Arg Pro Arg Pro Arg Arg Arg Gly Arg Arg  
115 120 125  
Thr Arg Arg Arg Gly Arg Cys Gly Thr Trp Arg Ser Ala Ala Ser Arg  
130 135 140  
Ser Ser Arg Gly Pro Trp Arg Cys Arg Arg Thr Cys Ala Trp Thr Gly  
145 150 155 160  
Ser Gly Pro Ala Trp Arg Thr Gly Phe Ser Pro Ser Leu Cys Pro Arg  
165 170 175  
Lys Ser Pro Arg Pro Gly Pro Ser Pro Gly Pro Ser Pro Ser Pro Ala  
180 185 190  
Ser Ser Asp Glu Ser Glu Ala Met Ser Gly Arg Val Tyr Gly Ala Val  
195 200 205  
Leu Asn His Ala Ala Asn Gly Gly Tyr Val  
210 215

(2) INFORMATION FOR SEQ ID NO:3988:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 193 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..193  
(D) OTHER INFORMATION: / Ceres Seq. ID 1579044  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3988:

Cys Xaa Arg Arg Leu Pro Gln Phe Ala Ala Xaa Gln Gly Lys Lys Lys  
1 5 10 15  
Lys Glu Glu Glu Asn Leu Leu Gln Phe Pro Phe His Arg Ser Ser Ser  
20 25 30  
Gly Pro Ser Gln Ser Phe Leu Arg Pro Lys Pro Cys Ser Thr Pro Met  
35 40 45  
Ser Asp Phe Phe Phe Gly Ser Pro Phe Arg Arg Leu Phe His Ala Arg  
50 55 60  
Pro Phe His Ala Val Asp Trp Ser Ser Ala Ala Ala Ala Met Asp  
65 70 75 80  
Trp Val Glu Thr Pro Ser Ser His Val Leu Arg Val Asn Val Pro Gly  
85 90 95

(2) INFORMATION FOR SEQ ID NO:3989:

(A) LENGTH: 151 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..151

(D) OTHER INFORMATION: / Ceres Seq. ID 1579045

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3989:

(2) INFORMATION FOR SEQ ID NO:3990:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 827 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..827

(D) OTHER INFORMATION: / Ceres Seq. ID 1579078

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3990:

(X1) SEQUENCE DESCRIPTION: SEQ ID: NO: 1

gtcgccccc	cgctagtcgc	ccaaactacg	caaccgatat	attccccagc	acccccgttc	60
cagccgtcca	accgagacac	cgcgtgcgaa	ccaagcagac	cccagcagaa	gaagcgaagt	120
cgtcgcggga	gcaggaggaa	gagcgcagcag	caagatgtcg	tggcaggcgt	acgtcgatga	180

(2) INFORMATION FOR SEQ ID NO:3991:

- |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Pro | His | Ala | Ser | Arg | Pro | Asn | Tyr | Ala | Thr | Asp | Ile | Phe | Pro | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Pro | Val | Pro | Ala | Val | Gln | Pro | Arg | His | Arg | Val | Arg | Thr | Lys | Gln |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Pro | Ala | Glu | Glu | Ala | Lys | Ser | Ser | Pro | Glu | Gln | Glu | Glu | Glu | Arg |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Ala | Arg | Cys | Arg | Gly | Arg | Arg | Thr | Ser | Met | Thr | Thr | Cys | Cys | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Thr | Ser | Lys | Ala | Ser | Thr | Ser | Ala | Pro | Pro | Pro | Ser | Ser | Ala | Thr | Thr |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ala | Ala | Ser | Gly | His | Ser | Pro | Arg | Thr | Ser | Pro | Ser |     |     |     |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     |     |

(i) SEQUENCE CHARACTERISTICS:

- | Sequence Description |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|----------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met                  | Ser | Trp | Gln | Ala | Tyr | Val | Asp | Asp | His | Leu | Leu | Cys | Asp | Ile | Glu |
| 1                    |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly                  | Gln | His | Leu | Ser | Ala | Ala | Ala | Ile | Val | Gly | His | Asp | Gly | Ser | Val |
|                      |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Trp                  | Ala | Gln | Ser | Glu | Asn | Phe | Pro | Glu | Leu | Lys | Pro | Glu | Glu | Val | Ala |
|                      |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly                  | Met | Ile | Lys | Asp | Phe | Asp | Glu | Pro | Gly | Thr | Leu | Ala | Pro | Thr | Gly |
|                      | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu                  | Phe | Val | Gly | Gly | Thr | Lys | Tyr | Met | Val | Ile | Gln | Gly | Glu | Pro | Gly |
| 65                   |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Val                  | Val | Ile | Arg | Gly | Lys | Lys | Gly | Thr | Gly | Gly | Ile | Thr | Ile | Lys | Lys |
|                      |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Thr                  | Gly | Met | Ser | Leu | Ile | Ile | Gly | Ile | Tyr | Asp | Glu | Pro | Met | Thr | Pro |
|                      |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |



Gly Gln Cys Asn Met Val Val Glu Arg Leu Gly Asp Tyr Leu Ile Glu  
115 120 125  
Gln Gly Leu Leu Ser Leu Ser  
130 135

(2) INFORMATION FOR SEQ ID NO:3993:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..86
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579081

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3993:

Met Ile Lys Asp Phe Asp Glu Pro Gly Thr Leu Ala Pro Thr Gly Leu  
1 5 10 15  
Phe Val Gly Gly Thr Lys Tyr Met Val Ile Gln Gly Glu Pro Gly Val  
20 25 30  
Val Ile Arg Gly Lys Lys Gly Thr Gly Ile Thr Ile Lys Lys Thr  
35 40 45  
Gly Met Ser Leu Ile Ile Gly Ile Tyr Asp Glu Pro Met Thr Pro Gly  
50 55 60  
Gln Cys Asn Met Val Val Glu Arg Leu Gly Asp Tyr Leu Ile Glu Gln  
65 70 75 80  
Gly Leu Leu Ser Leu Ser  
85

(2) INFORMATION FOR SEQ ID NO:3994:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..833
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579082

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3994:

atcctagaag gaaacaggaa caggcagctc tgaaagactg aaactcacgg ccatggccat 60  
cctgggcgcc ctcaggctcg cgcggtctcc acccgccctc gccggcgctg cgccaccggc 120  
tacgtcgccg tctgcggctg tacgtcctc cgtgcacttc cacctcgcca atgccggcgc 180  
cgccgcgctc ngtcgccgcc tcgtcctctg ccgccgaccc cgccgtggct ttcattggag 240  
gaggaccgta cgggaagcag gtgacgcggg ggcaggacct caccggcaag gacttcagcg 300  
gccagacact catcaagcag gacttcaaga cgtctatact gaggcaggcg aacttcaaag 360  
gcgcgaacct gctcggcgcg aGcttcttcg atgcagacct cacaagcgct gatctctctg 420  
acgtgatct tagaggcgct gatttgctgc tggcgaattt aacgaaggca aacttatcaa 480  
atgccaactt agaaggggca cttgccactg ggaacacttc tttcaaaggt gccgacataa 540  
ctggggcaga ttttaccgat gtgccgctgc gagatgatca acgggagtac ctctgcaaaa 600  
tcgctgacgg agtaaattca accactggaa acccaacaaa ggagactctg ttctgcagct 660  
gatcgacgga aggacctggg acttggtgact tattcaacgt cttgataaac ttgcatctgc 720  
tgctgtaagc acgtgaggaa tgtaaattga gttatagagg gttcctagaa ataataactg 780  
gtaattacgt gtaaatcaac caacaataaa agtgtgtgct gccctttgaa tgt

(2) INFORMATION FOR SEQ ID NO:3995:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(A) NAME/KEY: peptide  
(B) LOCATION: 1..119  
(D) OTHER INFORMATION: / Ceres Seq. ID 1579083

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(A) NAME/KEY: peptide  
(B) LOCATION: 1..163  
(D) OTHER INFORMATION: / Ceres Seq. ID 1579084

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 871 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..871

(D) OTHER INFORMATION: / Ceres Seq. ID 1579106

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3997:

```
atcgatcgag cttggttgct cggcagcagc tagcaatggc cgccaagggg ggtgatgagc 60
tgaagctgct gggcgtgtgg aacagcccgt acgtcaacag ggtccagatc gtgctcaacc 120
tcaagggcct cagctacgag tacgtggagg aggacctcct cagcaagagc gagctcctcc 180
tcaagtccaa cccgggtgcac aagaaagtgc ccggtgctcat ccacgccggc aagccggctg 240
ccgagtcgca ggccatcatt cagtacctcg acgaggcttt ccccggcggc acgttcccgt 300
cggtcctccc agccgacccc tacgcacgtg ccaactgccg cttctggggc gccttcgctg 360
acgacaaggt cgggtctcca tggcacacgg tcctgttcgc gcgggaccac gggaagaagg 420
cggacgcggc gtcgcggatc gtcgcggcgc tggagacgct ggagggcgcg ttcaaggact 480
gtcgcggcgg gagggactac ttcggcggcg gcgCcatcgg cttcgtggac gtggctcctg 540
gcagctacct gggctgggtt aaggtgttcg agaagatggt cggcgtcagg gtcctggacg 600
tggcgaggac gccgctcctc gccgcgtggg gggagcggtt cggcgcgcgg gaagcggcca 660
aggacgtcct gccggatgac gttgacaagg tgctcgagtt ccttcagaag ttccctggact 720
aggtgcgcgc cagcgccacc atgtgtctcg gtgtccaact cccaatgttt gtttgctttg 780
gtcattttcg gtgcgtgtt aatggcctc agatgtttgc cagttgattt tatagaatta 840
agagctaatt tggtaatcac atttttttc g
```

(2) INFORMATION FOR SEQ ID NO:3998:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 239 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..239

(D) OTHER INFORMATION: / Ceres Seq. ID 1579107

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3998:

```
Arg Ser Ser Leu Val Ala Arg Gln Gln Leu Ala Met Ala Ala Lys Gly
1          5          10          15
Gly Asp Glu Leu Lys Leu Leu Gly Val Trp Asn Ser Pro Tyr Val Asn
20          25          30
Arg Val Gln Ile Val Leu Asn Leu Lys Gly Leu Ser Tyr Glu Tyr Val
35          40          45
Glu Glu Asp Leu Leu Ser Lys Ser Glu Leu Leu Leu Lys Ser Asn Pro
50          55          60
Val His Lys Lys Val Pro Val Leu Ile His Ala Gly Lys Pro Val Ala
65          70          75          80
Glu Ser Gln Ala Ile Ile Gln Tyr Leu Asp Glu Ala Phe Pro Gly Gly
85          90          95
Thr Phe Pro Ser Val Leu Pro Ala Asp Pro Tyr Ala Arg Ala Thr Ala
100         105         110
Arg Phe Trp Ala Ala Phe Val Asp Asp Lys Val Gly Ser Pro Trp His
115         120         125
Thr Val Leu Phe Ala Arg Asp His Gly Lys Lys Ala Asp Ala Ala Ser
130         135         140
Arg Ile Val Ala Ala Leu Glu Thr Leu Glu Gly Ala Phe Lys Asp Cys
145         150         155         160
Ser Gly Gly Arg Asp Tyr Phe Gly Gly Gly Ala Ile Gly Phe Val Asp
165         170         175
Val Val Leu Gly Ser Tyr Leu Gly Trp Phe Lys Val Phe Glu Lys Met
180         185         190
Val Gly Val Arg Val Leu Asp Val Ala Arg Thr Pro Leu Leu Ala Ala
195         200         205
Trp Gly Glu Arg Phe Ala Ala Glu Ala Ala Lys Asp Val Leu Pro
210         215         220
```

Asp Asp Val Asp Lys Val Leu Glu Phe Leu Gln Lys Phe Leu Asp  
225 230 235

(2) INFORMATION FOR SEQ ID NO:3999:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..228
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3999:

Met Ala Ala Lys Gly Gly Asp Glu Leu Lys Leu Leu Gly Val Trp Asn  
1 5 10 15  
Ser Pro Tyr Val Asn Arg Val Gln Ile Val Leu Asn Leu Lys Gly Leu  
20 25 30  
Ser Tyr Glu Tyr Val Glu Glu Asp Leu Leu Ser Lys Ser Glu Leu Leu  
35 40 45  
Leu Lys Ser Asn Pro Val His Lys Lys Val Pro Val Leu Ile His Ala  
50 55 60  
Gly Lys Pro Val Ala Glu Ser Gln Ala Ile Ile Gln Tyr Leu Asp Glu  
65 70 75 80  
Ala Phe Pro Gly Gly Thr Phe Pro Ser Val Leu Pro Ala Asp Pro Tyr  
85 90 95  
Ala Arg Ala Thr Ala Arg Phe Trp Ala Ala Phe Val Asp Asp Lys Val  
100 105 110  
Gly Ser Pro Trp His Thr Val Leu Phe Ala Arg Asp His Gly Lys Lys  
115 120 125  
Ala Asp Ala Ala Ser Arg Ile Val Ala Ala Leu Glu Thr Leu Glu Gly  
130 135 140  
Ala Phe Lys Asp Cys Ser Gly Gly Arg Asp Tyr Phe Gly Gly Gly Ala  
145 150 155 160  
Ile Gly Phe Val Asp Val Val Leu Gly Ser Tyr Leu Gly Trp Phe Lys  
165 170 175  
Val Phe Glu Lys Met Val Gly Val Arg Val Leu Asp Val Ala Arg Thr  
180 185 190  
Pro Leu Leu Ala Ala Trp Gly Glu Arg Phe Ala Ala Ala Glu Ala Ala  
195 200 205  
Lys Asp Val Leu Pro Asp Asp Val Asp Lys Val Leu Glu Phe Leu Gln  
210 215 220  
Lys Phe Leu Asp  
225

(2) INFORMATION FOR SEQ ID NO:4000:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 455 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..455
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4000:

acttcctccc ttcttacagc cgccgccgcc gcatcccagc ctccatcacc gtttcogtct 60  
cgttgccatg ggtaaggtgc acggatcggt ggcgcgcgcc gggaaggtcc gcgggcagac 120  
ccccaaggtg gcgaaGcagg acaagaagaa gaagccccgc ggccgcgcgc acaagaggat 180  
gcagtacaac cgccgcttcg tcaccgccgt cgtcggcttc ggcaagaagc gcgggcccaa 240  
ctcctccgag aagtaggcgc cgctcggttc gtaccggcttc ctcaccccttc ctgctctccg 300

tatgcttatg ctcttgatgg tactagtttc gttgttcgca agcagaggaa gaaccttctg 360  
tagattcggg tttgttggtcc atgtgctcag atgggaactt gagattgtat gaatttgaga 420  
tatgggtgata tgagctgatg atttttatta tgctt

(2) INFORMATION FOR SEQ ID NO:4001:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..84
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579117

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4001:

Leu Pro Pro Phe Leu Gln Pro Pro Pro Pro His Pro Ser Leu His His  
1 5 10 15  
Arg Phe Arg Leu Val Ala Met Gly Lys Val His Gly Ser Leu Ala Arg  
20 25 30  
Ala Gly Lys Val Arg Gly Gln Thr Pro Lys Val Ala Lys Gln Asp Lys  
35 40 45  
Lys Lys Lys Pro Arg Gly Arg Ala His Lys Arg Met Gln Tyr Asn Arg  
50 55 60  
Arg Phe Val Thr Ala Val Val Gly Phe Gly Lys Lys Arg Gly Pro Asn  
65 70 75 80  
Ser Ser Glu Lys

(2) INFORMATION FOR SEQ ID NO:4002:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579118

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4002:

Phe Leu Pro Ser Tyr Ser Arg Arg Arg Arg Ile Pro Ala Ser Ile Thr  
1 5 10 15  
Val Ser Val Ser Leu Pro Trp Val Arg Cys Thr Asp Arg Trp Arg Ala  
20 25 30  
Pro Gly Arg Ser Ala Gly Arg Pro Arg Trp Arg Ser Arg Thr Arg  
35 40 45  
Arg Arg Ser Pro Ala Ala Ala Arg Thr Arg Gly Cys Ser Thr Thr Ala  
50 55 60  
Ala Ser Ser Pro Pro Ser Ser Ala Ser Ala Arg Ser Ala Gly Pro Thr  
65 70 75 80  
Pro Pro Arg Ser Arg Arg Arg Ser Ala Arg Thr Gly Ser Ser Ser Phe  
85 90 95  
Leu Leu Ser Val Cys Leu Cys Ser  
100

(2) INFORMATION FOR SEQ ID NO:4003:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(2) INFORMATION FOR SEQ ID NO:4006:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 88 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..88  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1579130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4006:

Tyr Pro Val Gly Phe Ser Ser Arg Ala Ala Glu His Asn Thr Ala  
1                    5                    10                    15  
Pro His Tyr Pro Ala Glu Ser Ala His Pro His Pro Glu Gln Arg Arg  
                    20                    25                    30  
Tyr Val Ala Gly Glu Gly Arg Ser Val Glu Glu Gly Gly Gly Gly His  
                    35                    40                    45  
Gln Gly Val His His Gln Pro Gln Ala Pro Pro Arg Leu His Ile  
50                    55                    60  
Gln Glu Glu Gly Thr Gln Arg His Gln Gly Asp Gln Glu Val Cys Ala  
65                    70                    75                    80  
Glu Gly His Gly His His Gly His  
                    85

(2) INFORMATION FOR SEQ ID NO:4007:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 122 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..122  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1579131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4007:

Met Ser Gln Gly Lys Gly Gly Ala Ser Arg Lys Glu Glu Val Val Thr  
1                    5                    10                    15  
Arg Glu Tyr Thr Ile Asn Leu His Lys Arg Leu His Gly Cys Thr Phe  
                    20                    25                    30  
Lys Lys Lys Ala Pro Asn Ala Ile Lys Glu Ile Arg Lys Phe Ala Gln  
                    35                    40                    45  
Lys Ala Met Gly Thr Thr Asp Ile Arg Ile Asp Val Lys Leu Asn Lys  
50                    55                    60  
His Ile Trp Ser Ser Gly Ile Arg Ser Val Pro Arg Arg Val Arg Val  
65                    70                    75                    80  
Arg Ile Ala Arg Lys Arg Asn Asp Glu Glu Asp Ala Lys Glu Glu Leu  
                    85                    90                    95  
Tyr Ser Leu Val Thr Val Ala Glu Ile Pro Ala Glu Gly Leu Lys Gly  
                    100                    105                    110  
Leu Gly Thr Lys Val Val Asp Asp Thr Asp  
                    115                    120

(2) INFORMATION FOR SEQ ID NO:4008:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 1051 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..1051

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(D) OTHER INFORMATION: / Ceres Seq. ID 1579182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4008:

aatccaacga	actgaccaca	actacctaag	ctaaaagcta	accaccgtac	ccccggccat	60
ggcgctcgcg	cccacctccg	ctgccgtgct	caagaccccg	ttcctcgggg	ccaggcgcg	120
gctcgccaag	cccgcgcctc	gccgcgcgct	cgatcatgcc	gccgcggccg	ccgccaagaa	180
gtcgtggatc	ccggccatca	agagcgacgc	cgagatcgtc	aaccgcacct	ggctcgacgg	240
ctcgctcccc	ggcgacttcg	ggttcgaccc	gctggggctg	ggcaaggacc	cgcggttcct	300
caagtgttac	cgggaggcgg	astgatccac	gggcggtggg	cgatggcggc	cggtgtgggc	360
atcttcgtgg	ggcaggcggt	gagcggcatc	ccgtgggttc	argccggcgc	ggacccgagc	420
gccatcgcg	ccttctCctt	cgggtcgctg	ctgggcacgc	agctgctgct	gatgggggtg	480
gtggagtcga	agcggtggtg	ggactttctt	aaccgcgact	cccaggccgt	ggagtgggcc	540
acgccgtggt	cgcgcaccgc	tgagaacttc	gccaacttca	ccggcgagca	gggctacccg	600
ggcggcaagt	tcttcgaccc	gctcggcctc	gccggcaccc	tcaaggacgg	cgtctacatc	660
cccgcgctcg	acaagctcga	gcggctcaag	ctggccgaga	tcaagcacgc	ccgcatcgcc	720
atgcttgcca	tgctcgctt	ctacttcgag	gccgggcagg	gcaagacgcc	gctcggcgcg	780
ctcggcctat	gatttgcatg	ctgccggcga	ccgagtcagt	tctcgattgc	gcgggggtgg	840
tgagctccta	gggacgtacg	gctgcacggg	atcagacgcc	ttgcctcgca	gattggaggc	900
gaaagaagag	cgtagcagca	atctactgtc	tgtgttggtg	gtttagcgtg	cgtgaaccag	960
atgggggtgt	cctctctgtt	ttttctttct	ttcttttctg	tgtatgtatg	taccatgtaa	1020
tgtatagtat	ggatcgattt	tcattgcatt	g			

(2) INFORMATION FOR SEQ ID NO:4009:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..88

(D) OTHER INFORMATION: / Ceres Seq. ID 1579183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4009:

Met	Ala	Leu	Ala	Pro	Thr	Ser	Ala	Ala	Val	Leu	Lys	Thr	Pro	Phe	Leu
1				5					10					15	
Gly	Ala	Arg	Arg	Ala	Leu	Ala	Lys	Pro	Ala	Pro	Arg	Arg	Ala	Leu	Val
			20						25					30	
Ile	Ala	Ala	Ala	Ala	Ala	Ala	Lys	Lys	Ser	Trp	Ile	Pro	Ala	Ile	Lys
			35					40						45	
Ser	Asp	Ala	Glu	Ile	Val	Asn	Pro	Pro	Trp	Leu	Asp	Gly	Ser	Leu	Pro
	50					55					60				
Gly	Asp	Phe	Gly	Phe	Asp	Pro	Leu	Gly	Leu	Gly	Lys	Asp	Pro	Ala	Phe
65					70					75				80	
Leu	Lys	Trp	Tyr	Arg	Glu	Ala	Xaa								
							85								

(2) INFORMATION FOR SEQ ID NO:4010:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..149

(D) OTHER INFORMATION: / Ceres Seq. ID 1579184

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4010:

Met	Ala	Ala	Val	Leu	Gly	Ile	Phe	Val	Gly	Gln	Ala	Trp	Ser	Gly	Ile
1				5					10					15	
Pro	Trp	Phe	Xaa	Ala	Gly	Ala	Asp	Pro	Ser	Ala	Ile	Ala	Pro	Phe	Ser
			20						25					30	
Phe	Gly	Ser	Leu	Leu	Gly	Thr	Gln	Leu	Leu	Leu	Met	Gly	Trp	Val	Glu



35 40 45  
Ser Lys Arg Trp Val Asp Phe Phe Asn Pro Asp Ser Gln Ala Val Glu  
50 55 60  
Trp Ala Thr Pro Trp Ser Arg Thr Ala Glu Asn Phe Ala Asn Phe Thr  
65 70 75 80  
Gly Glu Gln Gly Tyr Pro Gly Gly Lys Phe Phe Asp Pro Leu Gly Leu  
85 90 95  
Ala Gly Thr Val Lys Asp Gly Val Tyr Ile Pro Asp Val Asp Lys Leu  
100 105 110  
Glu Arg Leu Lys Leu Ala Glu Ile Lys His Ala Arg Ile Ala Met Leu  
115 120 125  
Ala Met Leu Ala Phe Tyr Phe Glu Ala Gly Gln Gly Lys Thr Pro Leu  
130 135 140  
Gly Ala Leu Gly Leu  
145

(2) INFORMATION FOR SEQ ID NO:4011:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 106 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..106

(D) OTHER INFORMATION: / Ceres Seq. ID 1579185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4011:

Met Gly Trp Val Glu Ser Lys Arg Trp Val Asp Phe Phe Asn Pro Asp  
1 5 10 15  
Ser Gln Ala Val Glu Trp Ala Thr Pro Trp Ser Arg Thr Ala Glu Asn  
20 25 30  
Phe Ala Asn Phe Thr Gly Glu Gln Gly Tyr Pro Gly Gly Lys Phe Phe  
35 40 45  
Asp Pro Leu Gly Leu Ala Gly Thr Val Lys Asp Gly Val Tyr Ile Pro  
50 55 60  
Asp Val Asp Lys Leu Glu Arg Leu Lys Leu Ala Glu Ile Lys His Ala  
65 70 75 80  
Arg Ile Ala Met Leu Ala Met Leu Ala Phe Tyr Phe Glu Ala Gly Gln  
85 90 95  
Gly Lys Thr Pro Leu Gly Ala Leu Gly Leu  
100 105

(2) INFORMATION FOR SEQ ID NO:4012:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 760 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..760

(D) OTHER INFORMATION: / Ceres Seq. ID 1579249

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4012:

atgaggaggc aagtrcgag gagccaata aaaagaacaa gaaaaagaag gcacatgata 60  
taagcagaag tgaagtcag gcaggaactg gacttggtga gtcagatagc aaggaaccac 120  
tccaaacacg gacgtttgcc aatggtatga tgattcagga gttagagatg ggcaaacctg 180  
atggtaaaaa ggccagccgt gggaagaagg tttctgttag atatattggc aagctaaaga 240  
atggcactat tttcgactcc aacgtcagtg gaagaccttt tgagtttaga ctaggtgttg 300  
ggcaggttat cagtggctgg gacgttggcg tcaatggtat gcgggttggg gacaaaagga 360  
gactcaccat tccaccttcc atggggtatg ggagcaaaaag agtggggcag ataccacaga 420  
actcaactct catcttcgat gtggagctgg tgaacgtaaa atgaagtgag aagatccacg 480

agaaaactgcg gcagttttcac aaatttttGct acgcatcatt ttccttgggc aatgctgttt 540  
cgtaggcata ggggcatgtt aagtggattc atctctgtcg ctatcatact ttcgaactga 600  
gtttcagaag gaaaaaaact gtggactgtt gccatctggg ataattcctg ggctgcagca 660  
ttcgccatcc ttctcccggt tccttcaggg tcattttgac attcttgtga taccctcaga 720  
accttttgaa ctgatgaaat ggtaaggtg gagtacgtgc

(2) INFORMATION FOR SEQ ID NO:4013:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1579250

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4013:

Glu Glu Ala Ser Xaa Gln Glu Ala Asn Lys Lys Asn Lys Lys Lys Lys  
1 5 10 15  
Ala His Asp Ile Ser Arg Ser Glu Ser Gln Ala Gly Thr Gly Leu Gly  
20 25 30  
Glu Ser Asp Ser Lys Glu Pro Leu Gln Thr Arg Thr Phe Ala Asn Gly  
35 40 45  
Met Met Ile Gln Glu Leu Glu Met Gly Lys Pro Asp Gly Lys Lys Ala  
50 55 60  
Ser Arg Gly Lys Lys Val Ser Val Arg Tyr Ile Gly Lys Leu Lys Asn  
65 70 75 80  
Gly Thr Ile Phe Asp Ser Asn Val Ser Gly Arg Pro Phe Glu Phe Arg  
85 90 95  
Leu Gly Val Gly Gln Val Ile Ser Gly Trp Asp Val Gly Val Asn Gly  
100 105 110  
Met Arg Val Gly Asp Lys Arg Arg Leu Thr Ile Pro Pro Ser Met Gly  
115 120 125  
Tyr Gly Ser Lys Arg Val Gly Gln Ile Pro Gln Asn Ser Thr Leu Ile  
130 135 140  
Phe Asp Val Glu Leu Val Asn Val Lys  
145 150

(2) INFORMATION FOR SEQ ID NO:4014:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..105

(D) OTHER INFORMATION: / Ceres Seq. ID 1579251

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4014:

Met Met Ile Gln Glu Leu Glu Met Gly Lys Pro Asp Gly Lys Lys Ala  
1 5 10 15  
Ser Arg Gly Lys Lys Val Ser Val Arg Tyr Ile Gly Lys Leu Lys Asn  
20 25 30  
Gly Thr Ile Phe Asp Ser Asn Val Ser Gly Arg Pro Phe Glu Phe Arg  
35 40 45  
Leu Gly Val Gly Gln Val Ile Ser Gly Trp Asp Val Gly Val Asn Gly  
50 55 60  
Met Arg Val Gly Asp Lys Arg Arg Leu Thr Ile Pro Pro Ser Met Gly  
65 70 75 80  
Tyr Gly Ser Lys Arg Val Gly Gln Ile Pro Gln Asn Ser Thr Leu Ile  
85 90 95

(2) INFORMATION FOR SEQ ID NO:4015:

(A) LENGTH: 104 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4015:

(2) INFORMATION FOR SEQ ID NO:4016:

(A) LENGTH: 525 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..525

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4016:

(2) INFORMATION FOR SEQ ID NO:4017:

(A) LENGTH: 72 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..72

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4017:

(2) INFORMATION FOR SEQ ID NO:4018:

(A) LENGTH: 104 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..104

(D) OTHER INFORMATION: / Ceres Seq. ID 1579258

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..77

(D) OTHER INFORMATION: / Ceres Seq. ID 1579259

Met	Ala	Gly	Gly	Arg	Val	Ala	His	Ala	Thr	Leu	Lys	Gly	Pro	Ser	Val
1				5					10					15	
Val	Lys	Glu	Ile	Phe	Ile	Gly	Leu	Thr	Leu	Gly	Leu	Ile	Ala	Gly	Gly
			20					25					30		
Met	Trp	Lys	Met	His	His	Trp	Asn	Glu	Gln	Arg	Lys	Thr	Arg	Ser	Phe
		35					40					45			
Tyr	Asp	Met	Leu	Asp	Lys	Gly	Gln	Ile	Ser	Val	Val	Val	Glu	Asp	Gln
	50					55					60				
Asp	Asp	Gln	Lys	Gln	Glu	Gln	Pro	Pro	Leu	Pro	Pro	Val			
65					70					75					

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 906 base pairs

[illegible]

- (B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..906  
(D) OTHER INFORMATION: / Ceres Seq. ID 1579263  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4020:

```
attatctatt tatctcgtag tatctcttct taacagaacc cctataaatt ccctacgatac      60
gatcccttgg ctccacctat cacttttctt tccgatcaga tcctctcagt tatcatggcg      120
ggcggcgctt tcaccgagaa gggcaagcaa tatccgggga agatgacggg gtctcgtcttc      180
ctgcctgcc tcgtcgcttc ctccggcggc ctcatcttcg gatacgacat tggcatctca      240
ggcggcggtga cgtccatgga cccgttcttg aagcgcttct tcccgtcggg gtacgccaaag      300
gagcaggagg tgggtggagac caaccagtac tgcaagttcg acagcgtgct gCtgacgctc      360
ttcacctcct cgctctacct cgcggcgctc gtcgcctccc tcttcgccgg ctacatcacc      420
aagaggtgog gccgcaggGt gtccatgctc ggcgggcgcg cCatcttctt cgtcggcgcc      480
gtcctcaacg gcctcgccca gaacgtggcc atgctcatca tcggcaggat ctttctcggc      540
attggcgctg gattcagcaa tcagccggat gcatggatct gcgtcgcgat ttatttttgg      600
aaccgtttct ctgatcgggt ggctttttta gcgggcaact gaaacttgct gccaaagtgcc      660
aacagagacc aaacttccct gcaactgtaga gtatgctgca tgtgttgtgt gcagccgcac      720
ctggaagagc atgcactgcc agaagctcct agatttattt ntcaacttacg ttttttcagt      780
gctagccagt atttcacatt tctacttacg gttatttttg aaccgtcatc acaaatgggt      840
ttcttaagtc aactgtcaat aaaaatagca tttttatttg cgttttctt tatgaaaccc      900
aagtgg
```

(2) INFORMATION FOR SEQ ID NO:4021:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 175 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..175  
(D) OTHER INFORMATION: / Ceres Seq. ID 1579264  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4021:

```
Met Ala Gly Gly Ala Phe Thr Glu Lys Gly Lys Gln Tyr Pro Gly Lys
1      5      10      15
Met Thr Val Phe Val Phe Leu Ala Cys Leu Val Ala Ser Ser Gly Gly
20     25     30
Leu Ile Phe Gly Tyr Asp Ile Gly Ile Ser Gly Gly Val Thr Ser Met
35     40     45
Asp Pro Phe Leu Lys Arg Phe Phe Pro Ser Val Tyr Ala Lys Glu Gln
50     55     60
Glu Val Val Glu Thr Asn Gln Tyr Cys Lys Phe Asp Ser Val Leu Leu
65     70     75     80
Thr Leu Phe Thr Ser Ser Leu Tyr Leu Ala Ala Leu Val Ala Ser Leu
85     90     95
Phe Ala Gly Tyr Ile Thr Lys Arg Cys Gly Arg Arg Val Ser Met Leu
100    105    110
Gly Gly Gly Ala Ile Phe Leu Val Gly Ala Val Leu Asn Gly Leu Ala
115    120    125
Gln Asn Val Ala Met Leu Ile Gly Arg Ile Phe Leu Gly Ile Gly
130    135    140
Val Gly Phe Ser Asn Gln Pro Asp Ala Trp Ile Cys Val Ala Ile Tyr
145    150    155    160
Phe Trp Asn Arg Phe Ser Asp Arg Leu Ala Phe Leu Ala Gly Asn
165    170    175
```

(2) INFORMATION FOR SEQ ID NO:4022:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..159  
(D) OTHER INFORMATION: / Ceres Seq. ID 1579265  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4022:

Met Thr Val Phe Val Phe Leu Ala Cys Leu Val Ala Ser Ser Gly Gly  
1 5 10 15  
Leu Ile Phe Gly Tyr Asp Ile Gly Ile Ser Gly Gly Val Thr Ser Met  
20 25 30  
Asp Pro Phe Leu Lys Arg Phe Phe Pro Ser Val Tyr Ala Lys Glu Gln  
35 40 45  
Glu Val Val Glu Thr Asn Gln Tyr Cys Lys Phe Asp Ser Val Leu Leu  
50 55 60  
Thr Leu Phe Thr Ser Ser Leu Tyr Leu Ala Ala Leu Val Ala Ser Leu  
65 70 75 80  
Phe Ala Gly Tyr Ile Thr Lys Arg Cys Gly Arg Arg Val Ser Met Leu  
85 90 95  
Gly Gly Gly Ala Ile Phe Leu Val Gly Ala Val Leu Asn Gly Leu Ala  
100 105 110  
Gln Asn Val Ala Met Leu Ile Ile Gly Arg Ile Phe Leu Gly Ile Gly  
115 120 125  
Val Gly Phe Ser Asn Gln Pro Asp Ala Trp Ile Cys Val Ala Ile Tyr  
130 135 140  
Phe Trp Asn Arg Phe Ser Asp Arg Leu Ala Phe Leu Ala Gly Asn  
145 150 155

(2) INFORMATION FOR SEQ ID NO:4023:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 128 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..128  
(D) OTHER INFORMATION: / Ceres Seq. ID 1579266  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4023:

Met Asp Pro Phe Leu Lys Arg Phe Phe Pro Ser Val Tyr Ala Lys Glu  
1 5 10 15  
Gln Glu Val Val Glu Thr Asn Gln Tyr Cys Lys Phe Asp Ser Val Leu  
20 25 30  
Leu Thr Leu Phe Thr Ser Ser Leu Tyr Leu Ala Ala Leu Val Ala Ser  
35 40 45  
Leu Phe Ala Gly Tyr Ile Thr Lys Arg Cys Gly Arg Arg Val Ser Met  
50 55 60  
Leu Gly Gly Gly Ala Ile Phe Leu Val Gly Ala Val Leu Asn Gly Leu  
65 70 75 80  
Ala Gln Asn Val Ala Met Leu Ile Ile Gly Arg Ile Phe Leu Gly Ile  
85 90 95  
Gly Val Gly Phe Ser Asn Gln Pro Asp Ala Trp Ile Cys Val Ala Ile  
100 105 110  
Tyr Phe Trp Asn Arg Phe Ser Asp Arg Leu Ala Phe Leu Ala Gly Asn  
115 120 125

(2) INFORMATION FOR SEQ ID NO:4024:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 783 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..783  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1579270  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4024:

atgtgtgtgt	cccaacagct	gagtggcatg	gacatggacc	aaaggcttca	gtgcatgttt	60
aagagagttcc	gggagacct	cgacgctgcg	acagaaggca	tcaagacaaa	ctactatggc	120
ataaagcatg	tgatcgaagc	cttgctgcct	ctgcttcaag	cttcctccga	tgggaggatc	180
gttaacgtct	cctctgagtt	cggcctgcta	aggctgatca	acaacgagga	gctaaggcag	240
gagctaaacg	acgtggagan	gctcaccgar	gagargctgg	acgargtgct	ggccgcgtac	300
ctgaragact	tgcagccv	cnargtkggg	gcrcgcgggt	kgccggtgga	cttctcgccc	360
tacaargtgg	ccaaggtggc	catgaacgcg	tacacgagga	tcctagcgag	gaggcaccs	420
gggstgcgcg	tcaactgcgc	gcaccccgcc	tacgtgagca	ccgacatgac	cgtccacacc	480
gggcytytca	cgcccgagca	aggcgcgccc	aacgtcgtga	aggtggcgct	gatgccggag	540
ggcgcccgca	ccggcgcgta	cttcgcgttg	ggagaggagg	cgtcctttgt	gtgacgaaag	600
caccgtcgtc	gttaagttcg	tcgttggttcg	ccaactccct	gtcagtcgat	ttctaaatcg	660
acgtacaatg	aaatacatca	tcgctgcaaa	ctcacaatg	aaaacagtta	agggaacctt	720
ttgtagcaaa	aaaaaaagtg	gacagaataa	tgaataatca	tgtcaaatat	cgcttgagta	780
tct						

(2) INFORMATION FOR SEQ ID NO:4025:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 197 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..197  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1579271  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4025:

Met	Cys	Val	Ser	Gln	Leu	Ser	Gly	Met	Asp	Met	Asp	Gln	Arg	Leu
1			5				10					15		
Gln	Cys	Met	Phe	Lys	Arg	Val	Arg	Glu	Thr	Tyr	Asp	Ala	Ala	Thr
			20				25					30		
Gly	Ile	Lys	Thr	Asn	Tyr	Tyr	Gly	Ile	Lys	His	Val	Ile	Glu	Ala
			35				40					45		
Leu	Pro	Leu	Leu	Gln	Ala	Ser	Ser	Asp	Gly	Arg	Ile	Val	Asn	Val
			50				55					60		
Ser	Glu	Phe	Gly	Leu	Leu	Arg	Leu	Ile	Asn	Asn	Glu	Glu	Leu	Arg
							70				75			80
Glu	Leu	Asn	Asp	Val	Glu	Xaa	Leu	Thr	Xaa	Glu	Xaa	Leu	Asp	Xaa
							85				90			95
Leu	Ala	Ala	Tyr	Leu	Xaa	Asp	Phe	Asp	Ala	Xaa	Xaa	Xaa	Gly	Xaa
							100				105			110
Gly	Xaa	Pro	Val	Asp	Phe	Ser	Ala	Tyr	Xaa	Val	Ala	Lys	Val	Ala
							115				120			125
Asn	Ala	Tyr	Thr	Arg	Ile	Leu	Ala	Arg	Arg	His	Xaa	Gly	Xaa	Arg
							130				135			140
Asn	Cys	Ala	His	Pro	Gly	Tyr	Val	Ser	Thr	Asp	Met	Thr	Val	His
							145				150			155
Gly	Xaa	Xaa	Thr	Pro	Glu	Gln	Gly	Ala	Ala	Asn	Val	Val	Lys	Val
							165				170			175
Leu	Met	Pro	Glu	Gly	Gly	Pro	Thr	Gly	Ala	Tyr	Phe	Ala	Leu	Gly
							180				185			190

Glu Ala Ser Phe Val  
195

(2) INFORMATION FOR SEQ ID NO:4026:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..188
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4026:

Met Asp Met Asp Gln Arg Leu Gln Cys Met Phe Lys Arg Val Arg Glu  
1 5 10 15  
Thr Tyr Asp Ala Ala Thr Glu Gly Ile Lys Thr Asn Tyr Tyr Gly Ile  
20 25 30  
Lys His Val Ile Glu Ala Leu Leu Pro Leu Leu Gln Ala Ser Ser Asp  
35 40 45  
Gly Arg Ile Val Asn Val Ser Ser Glu Phe Gly Leu Leu Arg Leu Ile  
50 55 60  
Asn Asn Glu Glu Leu Arg Gln Glu Leu Asn Asp Val Glu Xaa Leu Thr  
65 70 75 80  
Xaa Glu Xaa Leu Asp Xaa Val Leu Ala Ala Tyr Leu Xaa Asp Phe Asp  
85 90 95  
Ala Xaa Xaa Xaa Gly Xaa Arg Gly Xaa Pro Val Asp Phe Ser Ala Tyr  
100 105 110  
Xaa Val Ala Lys Val Ala Met Asn Ala Tyr Thr Arg Ile Leu Ala Arg  
115 120 125  
Arg His Xaa Gly Xaa Arg Val Asn Cys Ala His Pro Gly Tyr Val Ser  
130 135 140  
Thr Asp Met Thr Val His Thr Gly Xaa Xaa Thr Pro Glu Gln Gly Ala  
145 150 155 160  
Ala Asn Val Val Lys Val Ala Leu Met Pro Glu Gly Gly Pro Thr Gly  
165 170 175  
Ala Tyr Phe Ala Leu Gly Glu Glu Ala Ser Phe Val  
180 185

(2) INFORMATION FOR SEQ ID NO:4027:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 655 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..655
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579274

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4027:

cactaccacc agtaccacac cactccgcgc tastgaggac ggtacagcgg cacagaggtg 60  
cgacgtacga cgacgacgac gcargcgcca cacatggcat cccagctctc cgccgccgtg 120  
ccccggttcc acggcctccg gggctacgcc gcgcccaggt ccgcggtggc agcgctgccg 180  
tccgtgaggg tgggcaggaa gaggtcgctcg tcgcagggca tccgctgcga ctacatybgC 240  
tccgccacca acctgatcat ggtgacgacg acgacgctga tgctgttcgc rgggcggttc 300  
GggctggCgc cgtcggCgaa ccgcaaggcg acggcggggc tgaagctgga ggcgcgcgac 360  
tccggcctgc agacgggtga ccccgccggg ttaccctcg ccgacacgct gGCctgcggc 420  
gccgtcggcc acatcctcgg cgtcggcatc gtgctcgggc tcaagaacac cggcgccctc 480  
gaccagatca tcggctagat ccctacgtcg tcgttggttaa gatcagactc agcagcctcg 540  
atcgcgccgc cggccggcag gtgcctgcag gtggtgactt tgtaacgtgt gtgcgtgcgt 600  
acgtgtacat tgcatccatc ttggttccaa tggacatata gtcctgttg ctct



(2) INFORMATION FOR SEQ ID NO:4028:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..125
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579275

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4028:

Leu Pro Pro Val Pro His His Ser Ala Leu Xaa Arg Thr Val Gln Arg  
1 5 10 15  
His Arg Gly Ala Thr Tyr Asp Asp Asp Ala Xaa Ala Thr His Gly  
20 25 30  
Ile Pro Ala Leu Arg Arg Arg Ala Pro Val Pro Arg Pro Gly Leu  
35 40 45  
Arg Arg Ala Gln Val Arg Gly Gly Ser Ala Ala Val Arg Glu Gly Gly  
50 55 60  
Gln Glu Glu Val Val Val Ala Gly His Pro Leu Arg Leu His Xaa Leu  
65 70 75 80  
Arg His Gln Pro Asp His Gly Asp Asp Asp Ala Asp Ala Val Arg  
85 90 95  
Xaa Ala Val Arg Ala Gly Ala Val Gly Glu Pro Gln Gly Asp Gly Gly  
100 105 110  
Ala Glu Ala Gly Gly Ala Arg Leu Arg Pro Ala Asp Gly  
115 120 125

(2) INFORMATION FOR SEQ ID NO:4029:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..134
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4029:

Met Ala Ser Gln Leu Ser Ala Ala Val Pro Arg Phe His Gly Leu Arg  
1 5 10 15  
Gly Tyr Ala Ala Pro Arg Ser Ala Val Ala Ala Leu Pro Ser Val Arg  
20 25 30  
Val Gly Arg Lys Arg Ser Ser Ser Gln Gly Ile Arg Cys Asp Tyr Xaa  
35 40 45  
Xaa Ser Ala Thr Asn Leu Ile Met Val Thr Thr Thr Thr Leu Met Leu  
50 55 60  
Phe Xaa Gly Arg Phe Gly Leu Ala Pro Ser Ala Asn Arg Lys Ala Thr  
65 70 75 80  
Ala Gly Leu Lys Leu Glu Ala Arg Asp Ser Gly Leu Gln Thr Gly Asp  
85 90 95  
Pro Ala Gly Phe Thr Leu Ala Asp Thr Leu Ala Cys Gly Ala Val Gly  
100 105 110  
His Ile Leu Gly Val Gly Ile Val Leu Gly Leu Lys Asn Thr Gly Ala  
115 120 125  
Leu Asp Gln Ile Ile Gly  
130

(2) INFORMATION FOR SEQ ID NO:4030:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..79
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1579277
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4030:

Met Val Thr Thr Thr Thr Leu Met Leu Phe Xaa Gly Arg Phe Gly Leu  
1 5 10 15  
Ala Pro Ser Ala Asn Arg Lys Ala Thr Ala Gly Leu Lys Leu Glu Ala  
20 25 30  
Arg Asp Ser Gly Leu Gln Thr Gly Asp Pro Ala Gly Phe Thr Leu Ala  
35 40 45  
Asp Thr Leu Ala Cys Gly Ala Val Gly His Ile Leu Gly Val Gly Ile  
50 55 60  
Val Leu Gly Leu Lys Asn Thr Gly Ala Leu Asp Gln Ile Ile Gly  
65 70 75

(2) INFORMATION FOR SEQ ID NO:4031:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 851 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..851
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579278

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4031:

ctccccaatc cccaggtcct catcggcctc ctctctctcg gtctcgccag atctcccccac 60  
ggaaccctac ccgagcatca gccatggcaa tcgcggcgcg cgccctgcgc cgcctcccgc 120  
ttcacctctc cccctcgatc tcccgctcct tctgcgcggt ttccccggcc gcgcctcctcg 180  
ctacctcggc cccgcgcgcc gcgtccgccca aggtcgtctga ccgcatcggt gcggtcctcg 240  
ccatcgatcc cgacggggcg cgcccgatg tggtcggcct ctcggggcag acactccttc 300  
gcgctctggc caacgcgggG ctcatcgagc cggcctccca ccgcctcgag gatatcgacg 360  
cgtgCtccgc cgagtgcgag gtccacatcg cgcaggagtg gcttgacaag ctgccaccac 420  
cgctctacga ggagcgatac gtgtctacgc gcgcgtccag gaaccgcgag ctcaacaagy 480  
acgcgcgcct gggctgccag gtgtctctcg cgccggagct gcaggggatg gtgtcgcca 540  
tccccgagcc taagccgtgg gacatcccat aatggcctgc cgacgaaag taaggtgcgg 600  
cttttgacgc tgtgagcctt ccttaattcc cttggctcgg tcaagctgtg cgcctgtgcc 660  
atcccccttt atattgttac gatttagtga agaataataa tttgatgagc aaaacttggc 720  
attggttaac ttttgttcct agtatatgga tgctctaag tggaatcctt ttgcaactac 780  
cgcagtttaa tgtttcatgg tttgaagttt tgtacattgt gatgaatggt tgattaatct 840  
tttcatttcc t

(2) INFORMATION FOR SEQ ID NO:4032:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 204 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..204
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579279

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4032:

Leu Pro Asn Pro Gln Val Leu Ile Gly Leu Leu Ser Leu Gly Leu Ala  
1 5 10 15  
Arg Ser Pro His Gly Thr Leu Pro Glu His Gln Pro Trp Gln Ser Arg

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20 25 30  
Arg Ala Pro Cys Ala Ala Ser Arg Phe Thr Ser Pro Pro Arg Ser Pro  
35 40 45  
Ala Pro Ser Ala Arg Phe Pro Arg Pro Pro Pro Arg Leu Pro Arg Pro  
50 55 60  
Pro Pro Pro Arg Pro Pro Arg Ser Leu Thr Ala Ser Cys Ala Ser Ser  
65 70 75 80  
Pro Ser Ile Pro Thr Gly Arg Ala Ala Met Trp Ser Ala Ser Arg Gly  
85 90 95  
Arg His Ser Phe Ala Leu Trp Pro Thr Arg Gly Ser Ser Ser Arg Pro  
100 105 110  
Pro Thr Ala Ser Arg Ile Ser Thr Arg Ala Pro Pro Ser Ala Arg Ser  
115 120 125  
Thr Ser Arg Arg Ser Gly Leu Thr Ser Cys His His Arg Pro Thr Arg  
130 135 140  
Ser Asp Thr Cys Ser Arg Ala Arg Pro Gly Thr Ala Ser Ser Thr Xaa  
145 150 155 160  
Thr Arg Ala Trp Ala Ala Arg Ser Ser Ser Arg Arg Ser Cys Arg Gly  
165 170 175  
Trp Ser Ser Pro Ser Pro Ser Leu Ser Arg Gly Thr Ser His Asn Gly  
180 185 190  
Leu Pro Thr Lys Gly Lys Val Arg Leu Leu Thr Leu  
195 200

(2) INFORMATION FOR SEQ ID NO:4033:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 189 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..189

(D) OTHER INFORMATION: / Ceres Seq. ID 1579280

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4033:

Pro Gln Ser Pro Gly Pro His Arg Pro Pro Leu Ser Arg Ser Arg Gln  
1 5 10 15  
Ile Ser Pro Arg Asn Pro Thr Arg Ala Ser Ala Met Ala Ile Ala Ala  
20 25 30  
Arg Ala Leu Arg Arg Leu Pro Leu His Leu Ser Pro Ser Ile Ser Arg  
35 40 45  
Ser Phe Cys Ala Val Ser Pro Ala Ala Ala Ser Ala Thr Ser Ala Pro  
50 55 60  
Ala Ala Ala Ser Ala Lys Val Ala Asp Arg Ile Val Arg Val Leu Ala  
65 70 75 80  
Ile Asp Pro Asp Gly Ala Arg Arg Asp Val Val Gly Leu Ser Gly Gln  
85 90 95  
Thr Leu Leu Arg Ala Leu Ala Asn Ala Gly Leu Ile Glu Pro Ala Ser  
100 105 110  
His Arg Leu Glu Asp Ile Asp Ala Cys Ser Ala Glu Cys Glu Val His  
115 120 125  
Ile Ala Gln Glu Trp Leu Asp Lys Leu Pro Pro Pro Ser Tyr Glu Glu  
130 135 140  
Arg Tyr Val Leu Thr Arg Ala Ser Arg Asn Arg Glu Leu Asn Lys Xaa  
145 150 155 160  
Ala Arg Leu Gly Cys Gln Val Val Leu Ala Pro Glu Leu Gln Gly Met  
165 170 175  
Val Val Ala Ile Pro Glu Pro Lys Pro Trp Asp Ile Pro  
180 185

(2) INFORMATION FOR SEQ ID NO:4034:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..162  
(D) OTHER INFORMATION: / Ceres Seq. ID 1579281  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4034:

Met Ala Ile Ala Ala Arg Ala Leu Arg Leu Pro Leu His Leu Ser  
1 5 10 15  
Pro Ser Ile Ser Arg Ser Phe Cys Ala Val Ser Pro Ala Ala Ala Ser  
20 25 30  
Ala Thr Ser Ala Pro Ala Ala Ala Ser Ala Lys Val Ala Asp Arg Ile  
35 40 45  
Val Arg Val Leu Ala Ile Asp Pro Asp Gly Ala Arg Arg Asp Val Val  
50 55 60  
Gly Leu Ser Gly Gln Thr Leu Leu Arg Ala Leu Ala Asn Ala Gly Leu  
65 70 75 80  
Ile Glu Pro Ala Ser His Arg Leu Glu Asp Ile Asp Ala Cys Ser Ala  
85 90 95  
Glu Cys Glu Val His Ile Ala Gln Glu Trp Leu Asp Lys Leu Pro Pro  
100 105 110  
Pro Ser Tyr Glu Glu Arg Tyr Val Leu Thr Arg Ala Ser Arg Asn Arg  
115 120 125  
Glu Leu Asn Lys Xaa Ala Arg Leu Gly Cys Gln Val Val Leu Ala Pro  
130 135 140  
Glu Leu Gln Gly Met Val Val Ala Ile Pro Glu Pro Lys Pro Trp Asp  
145 150 155 160  
Ile Pro

(2) INFORMATION FOR SEQ ID NO:4035:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 843 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..843  
(D) OTHER INFORMATION: / Ceres Seq. ID 1579303

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4035:

tcttcaccca cattataaag atcctccact tcgcactttc gccgccgcct ctctccttcc 60  
cgagcaggag gcgacaagg taagcagcaa tcgcaggaac cctagcgccg ccgcacccgc 120  
aggaatgggt atcgacctcg tcgccggtgg gaggrrkaag aagaccaagc gcactgcgcc 180  
caagtctgac gatgtctacc tcAagctcct cgtcaagctc taccgtttcN ttggtcagga 240  
ggaccaagag caatttcaac gctgtcattc tcaagaggct tttcatgagt aaaaccaacc 300  
gaccaccaat ctccatgcgc cgccttgtca agtttatgga aggaaaggag aagaacattg 360  
ctgtcattgt tggcacagtc acagatgaca aaaggatcca ggaggttcca gcaatgaagg 420  
ttactgccct gaggttcacg gagacagcaa gggccaggat tgtcaatgct ggtggcgagt 480  
gcctcacatt tgaccagctt gctcttcgtg ctccacttgg cgagaacacg gtcctcttga 540  
ggggcccca gaatgcccg gaggcagtga ggcactttgg caaggctcct ggagtgccgc 600  
acagccacac caagccgtat gtgcgctcca agggaaggaa gttcgagaag gctcgtggca 660  
ggaggaacag ccgtggattc aagggtttaa acaaattgtg gccctccgtg ttscatcag 720  
catmstgcaa ccgttgtgtt tgatcagtcg acagtaatta gtcatcactc tgtaccgaga 780  
ttmstagcac aatttgttgt cctggytga attytsgaag atatttgatg tcgtctccyt 840  
att

(2) INFORMATION FOR SEQ ID NO:4036:

- (i) SEQUENCE CHARACTERISTICS:

[illegible]

130

(2) INFORMATION FOR SEQ ID NO:4038:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..124
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579306

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4038:

Met Arg Arg Leu Val Lys Phe Met Glu Gly Lys Glu Lys Asn Ile Ala  
1 5 10 15  
Val Ile Val Gly Thr Val Thr Asp Asp Lys Arg Ile Gln Glu Val Pro  
20 25 30  
Ala Met Lys Val Thr Ala Leu Arg Phe Thr Glu Thr Ala Arg Ala Arg  
35 40 45  
Ile Val Asn Ala Gly Gly Glu Cys Leu Thr Phe Asp Gln Leu Ala Leu  
50 55 60  
Arg Ala Pro Leu Gly Glu Asn Thr Val Leu Leu Arg Gly Pro Lys Asn  
65 70 75 80  
Ala Arg Glu Ala Val Arg His Phe Gly Lys Ala Pro Gly Val Pro His  
85 90 95  
Ser His Thr Lys Pro Tyr Val Arg Ser Lys Gly Arg Lys Phe Glu Lys  
100 105 110  
Ala Arg Gly Arg Arg Asn Ser Arg Gly Phe Lys Val  
115 120

(2) INFORMATION FOR SEQ ID NO:4039:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..819
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579307

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4039:

aaatccccac gaaaacccta aaccctcgct acccggcggc ggctacaagc tcttcgctcg 60  
ttcagcacca tgargccacc ggctagagga ggacgtggtg ggaggggtgg caggttcgat 120  
ggcggcgggc tctgtcgcg cggecggtgc atcgccccct gcctcaccgt tctcttcctt 180  
ctcgcgctcg cgggcttcct cctctggccc gcggaaccgg acatctccct ggccgcctc 240  
cacctagcgc acgtctccgt cgtggcacgc cctgccgtcg ccgtcactat atCcgccacg 300  
ctcaaggttc gcgttcgcaa tctgacctc ttgcgctcg actacaccgg cctcgacgtc 360  
gctatcggct aCcgcggtgc Ggggcttggc cgggtaacat ccggcgggcg acgggtccgg 420  
gcgcgcgctg tctcgtagct cgacgccaac ctgcagctcg acggcatacg cgtcgtcgag 480  
gacgcgatgt acctgctcga ggacctcgcg caaggatccg tgcccttcga caccatcgcc 540  
gaggtcgagg gccacctcca ctcccttttc ctcagcatcc cgggtcaaggg gagaatatct 600  
tgcgtaaatgc atattaatcc acacaaccaa accatagtac atcaggactg ctatcctgag 660  
tgaattgctt atggcggtga aatgtggaag ggtgtaagct atgttgctt gcgaatggat 720  
cgtttgattt gtttctaacc tttgcttcca gtcgtggtt taaaagtaag aaccaactaa 780  
ggggtgtttg aatgtaatta agctaatagt tagttcgct

(2) INFORMATION FOR SEQ ID NO:4040:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..197  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1579308  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4040:

Met Xaa Pro Pro Ala Arg Gly Gly Arg Gly Gly Arg Gly Gly Arg Phe  
1                    5                    10                    15  
Asp Gly Gly Gly Leu Cys Arg Gly Gly Arg Cys Ile Val Pro Cys Leu  
                    20                    25                    30  
Thr Val Leu Phe Leu Leu Ala Leu Ala Gly Phe Leu Leu Trp Pro Ala  
                    35                    40                    45  
Asp Pro Asp Ile Ser Leu Ala Arg Leu His Leu Ala His Val Ser Val  
                    50                    55                    60  
Val Ala Arg Pro Ala Val Ala Val Thr Ile Ser Ala Thr Leu Lys Val  
65                    70                    75                    80  
Arg Val Arg Asn Pro Asp Leu Phe Ala Leu Asp Tyr Thr Arg Leu Asp  
                    85                    90                    95  
Val Ala Ile Gly Tyr Arg Gly Ala Gly Leu Gly Arg Val Thr Ser Gly  
                    100                    105                    110  
Gly Gly Arg Val Arg Ala Arg Ala Val Ser Tyr Val Asp Ala Asn Leu  
                    115                    120                    125  
Gln Leu Asp Gly Ile Arg Val Val Glu Asp Ala Met Tyr Leu Leu Glu  
130                    135                    140  
Asp Leu Ala Gln Gly Ser Val Pro Phe Asp Thr Ile Ala Glu Val Glu  
145                    150                    155                    160  
Gly His Leu His Phe Leu Phe Leu Ser Ile Pro Val Lys Gly Arg Ile  
                    165                    170                    175  
Ser Cys Val Met His Ile Asn Pro His Asn Gln Thr Ile Val His Gln  
                    180                    185                    190  
Asp Cys Tyr Pro Glu  
                    195

(2) INFORMATION FOR SEQ ID NO:4041:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 628 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:

- (A) NAME/KEY: -  
    (B) LOCATION: 1..628  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1579351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4041:

ataaaaaagct gttcttctcc cctcatcgca tacggcatac cacactagaa ccgccgccgc 60  
tgccgtttcg cgcaccgtac cctagccctc gtcagcggcg gtttcgagct cctccagcca 120  
tgacgttcaa gcggaggaat ggcggacgca acaagcacgg gcgcggccac gtcaagtaca 180  
tccgctgctc caactgcgcc aagtgcgtgcc ccaaggataa ggctatcaag cggttcttgg 240  
tgaggaacat tgttgagcag gctgccgtga gagatgtgca ggaggcctgt gtacatgatg 300  
gatatgttct acccaaattg tatgcaaagg ttcatactg tgtctcatgc gcaatccatg 360  
cgcacattgt ccgtgtccgc tctcgtgaga acaggaggaa ccgtgagccc ccgcagcgct 420  
tcagacgccg ggatgatggc ccaaggcctg gtcagggccc gccgcgcccc ggcggtgcag 480  
ctcctgCagc tgcagctgct getgctcctc gtacctaatg tctggaatta gtttcggggc 540  
ttagttttgt gaaacattac ctgttttgag aaaccattgt tactgtatcc ccttgatgtc 600  
aaacttttta gcacaatttg tggttctg

(2) INFORMATION FOR SEQ ID NO:4042:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 171 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

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(A) LENGTH: 85 amino acids

[illegible]



- (B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..85  
(D) OTHER INFORMATION: / Ceres Seq. ID 1579354  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4044:

Met Cys Arg Arg Pro Val Tyr Met Met Asp Met Phe Tyr Pro Asn Cys  
1 5 10 15  
Met Gln Arg Phe Ile Thr Val Ser His Ala Gln Ser Met Arg Thr Leu  
20 25 30  
Ser Val Ser Ala Leu Val Arg Thr Gly Gly Thr Val Ser Pro Arg Ser  
35 40 45  
Ala Ser Asp Ala Gly Met Met Ala Gln Gly Leu Val Arg Ala Arg Arg  
50 55 60  
Ala Gln Ala Val Gln Leu Leu Gln Leu Gln Leu Leu Leu Leu Val  
65 70 75 80  
Pro Lys Phe Trp Asn  
85

(2) INFORMATION FOR SEQ ID NO:4045:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 804 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..804  
(D) OTHER INFORMATION: / Ceres Seq. ID 1579355  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4045:

tttgc tgaag tacaccaaac aaggcatact cctgtacagt ctcagatttg ggtcggttgt 60  
gttgcagcag tcatggcagg cctctttaat gtgcgtgtgc tctcacatat tctttccgtc 120  
ggcactctga ccggttattc agttgtatca gcttgtgtga tcacactaag atggaatgac 180  
aaaggaacta gtcgtcgctc ccttggaagt atgtcaattt ggcaagaggg tgttctaagt 240  
cttgcacatg ttgctctttg tggttttata gtgggacttt gctatcgctt taactatgct 300  
atagccttta ttggtgttagc ttttgtgata gctgttgctg ccagtttcgc tctccagttt 360  
cgtcaggctc atgtggatcc acctggcctt tcttgtcctg gggtagcggt ggttcccatt 420  
atttctgttt tcttcaacat ggtcctgttt gctcagctac atgaagaagc gtggtataga 480  
tttgcattc ttagttctcat cgtgtgggga gttTatgccg gctatggtca gtacaatgct 540  
gttccttcca gtcagaaca ctctactatt ggttaccatg gcgttccttc tgaagccgca 600  
tgagctatgt tcatccccgg agttcttcga acatactgta cggtagcaac atacaccatg 660  
gtcaccgaag tttgaacctg ttgctttttt cttgatgttt tgcacagtgc atactcttgt 720  
agttacgctt agtactccta tatgtagaca gtgaatttcg cagcctgtgt tgtgccacc 780  
acaccattcg tcaggaagct tgcc

(2) INFORMATION FOR SEQ ID NO:4046:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 200 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..200  
(D) OTHER INFORMATION: / Ceres Seq. ID 1579356  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4046:

Phe Ala Glu Val His Pro Thr Arg His Thr Pro Val Gln Ser Gln Ile  
1 5 10 15

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Trp Val Gly Cys Val Ala Ala Val Met Ala Gly Leu Phe Asn Val Arg  
20 25 30  
Val Leu Ser His Ile Leu Ser Val Gly Thr Leu Thr Gly Tyr Ser Val  
35 40 45  
Val Ser Ala Cys Val Ile Thr Leu Arg Trp Asn Asp Lys Gly Thr Ser  
50 55 60  
Arg Arg Ser Leu Gly Ser Met Ser Ile Trp Gln Glu Gly Val Leu Ser  
65 70 75 80  
Leu Val Ile Val Ala Leu Cys Gly Phe Ile Val Gly Leu Cys Tyr Arg  
85 90 95  
Phe Asn Tyr Ala Ile Ala Phe Met Val Val Ala Phe Val Ile Ala Val  
100 105 110  
Ala Ala Ser Phe Ala Leu Gln Phe Arg Gln Val Tyr Val Asp Pro Pro  
115 120 125  
Gly Phe Ser Cys Pro Gly Val Pro Leu Val Pro Ile Ile Ser Val Phe  
130 135 140  
Phe Asn Met Val Leu Phe Ala Gln Leu His Glu Glu Ala Trp Tyr Arg  
145 150 155 160  
Phe Val Ile Leu Ser Leu Ile Ala Val Gly Val Tyr Ala Gly Tyr Gly  
165 170 175  
Gln Tyr Asn Ala Val Pro Ser Ser Ser Glu His Ser Thr Ile Gly Tyr  
180 185 190  
His Gly Val Pro Ser Glu Ala Ala  
195 200

(2) INFORMATION FOR SEQ ID NO:4047:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..176
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4047:

Met Ala Gly Leu Phe Asn Val Arg Val Leu Ser His Ile Leu Ser Val  
1 5 10 15  
Gly Thr Leu Thr Gly Tyr Ser Val Val Ser Ala Cys Val Ile Thr Leu  
20 25 30  
Arg Trp Asn Asp Lys Gly Thr Ser Arg Arg Ser Leu Gly Ser Met Ser  
35 40 45  
Ile Trp Gln Glu Gly Val Leu Ser Leu Val Ile Val Ala Leu Cys Gly  
50 55 60  
Phe Ile Val Gly Leu Cys Tyr Arg Phe Asn Tyr Ala Ile Ala Phe Met  
65 70 75 80  
Val Val Ala Phe Val Ile Ala Val Ala Ala Ser Phe Ala Leu Gln Phe  
85 90 95  
Arg Gln Val Tyr Val Asp Pro Pro Gly Phe Ser Cys Pro Gly Val Pro  
100 105 110  
Leu Val Pro Ile Ile Ser Val Phe Phe Asn Met Val Leu Phe Ala Gln  
115 120 125  
Leu His Glu Glu Ala Trp Tyr Arg Phe Val Ile Leu Ser Leu Ile Ala  
130 135 140  
Val Gly Val Tyr Ala Gly Tyr Gly Gln Tyr Asn Ala Val Pro Ser Ser  
145 150 155 160  
Ser Glu His Ser Thr Ile Gly Tyr His Gly Val Pro Ser Glu Ala Ala  
165 170 175

(2) INFORMATION FOR SEQ ID NO:4048:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 130 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..130  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1579358  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4048:  
Met Ser Ile Trp Gln Glu Gly Val Leu Ser Leu Val Ile Val Ala Leu  
1                  5                  10                  15  
Cys Gly Phe Ile Val Gly Leu Cys Tyr Arg Phe Asn Tyr Ala Ile Ala  
                  20                  25                  30  
Phe Met Val Val Ala Phe Val Ile Ala Val Ala Ala Ser Phe Ala Leu  
                  35                  40                  45  
Gln Phe Arg Gln Val Tyr Val Asp Pro Pro Gly Phe Ser Cys Pro Gly  
50                  55                  60  
Val Pro Leu Val Pro Ile Ile Ser Val Phe Phe Asn Met Val Leu Phe  
65                  70                  75                  80  
Ala Gln Leu His Glu Glu Ala Trp Tyr Arg Phe Val Ile Leu Ser Leu  
                  85                  90                  95  
Ile Ala Val Gly Val Tyr Ala Gly Tyr Gly Gln Tyr Asn Ala Val Pro  
                  100                  105                  110  
Ser Ser Ser Glu His Ser Thr Ile Gly Tyr His Gly Val Pro Ser Glu  
                  115                  120                  125  
Ala Ala  
130

(2) INFORMATION FOR SEQ ID NO:4049:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 650 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..650  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1579359  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4049:  
attatatttat cgggtgctoga ggttcagggtt tcacgcagkc ggcgagagct ggcagccatg 60  
aagarggggga gcccattggtc gctgcggctg ctaatttgct gcgcggcaat ggtggccatc 120  
gcgcttctcc cccaacaagg aggccaggcc gcttggttcg tgccgacgcc ggttccagct 180  
ccggcaccgc ccggtctctc cgcgacgaac acgaacgact cctccgctgc tcctcggcca 240  
gccaagccca gcgcattccc accccaatg tacggtggtg tcacccccgg cagtctccag 300  
ccacacgagt gcggcgggcg gtgcgcgggg cgggtgctcg cgacggcgta ccagaagccg 360  
tgccctcttct tctgcgcgaa gtvCtgcgcg gcgtgcctgt gcgtgcgcgc gggcacctac 420  
ggcaacaaga acacctgccc ctgctacaac aactggaaga ccaagcgggg aggccccaag 480  
tgcccctagt agccctccct ctoggtctac ttgatgagat cttctgttca aaaaatcaaa 540  
aggtaagaat ctgtttaacc atcttttagat ttcacaaata aaacagggtt caatttatct 600  
ttgtagttaa acgcttgcaa ctcatgtgtg aatctcatcc aatattagt

(2) INFORMATION FOR SEQ ID NO:4050:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 162 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide

(B) LOCATION: 1..162

(D) OTHER INFORMATION: / Ceres Seq. ID 1579360

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4050:

Ile	Ile	Leu	Ser	Val	Leu	Glu	Val	Gln	Val	Ser	Arg	Xaa	Arg	Arg	Glu
1			5					10						15	
Leu	Ala	Ala	Met	Lys	Xaa	Gly	Ser	Pro	Trp	Ser	Leu	Arg	Leu	Leu	Ile
		20						25					30		
Cys	Cys	Ala	Ala	Met	Val	Ala	Ile	Ala	Leu	Leu	Pro	Gln	Gln	Gly	Gly
		35					40					45			
Gln	Ala	Ala	Cys	Phe	Val	Pro	Thr	Pro	Gly	Pro	Ala	Pro	Ala	Pro	Pro
	50					55					60				
Gly	Ser	Ser	Ala	Thr	Asn	Thr	Asn	Asp	Ser	Ser	Ala	Ala	Pro	Arg	Pro
65				70						75				80	
Ala	Lys	Pro	Ser	Ala	Phe	Pro	Pro	Pro	Met	Tyr	Gly	Gly	Val	Thr	Pro
			85					90						95	
Gly	Ser	Leu	Gln	Pro	His	Glu	Cys	Gly	Gly	Arg	Cys	Ala	Gly	Arg	Cys
		100						105					110		
Ser	Ala	Thr	Ala	Tyr	Gln	Lys	Pro	Cys	Leu	Phe	Phe	Cys	Arg	Lys	Xaa
	115					120						125			
Cys	Ala	Ala	Cys	Leu	Cys	Val	Pro	Pro	Gly	Thr	Tyr	Gly	Asn	Lys	Asn
	130					135					140				
Thr	Cys	Pro	Cys	Tyr	Asn	Asn	Trp	Lys	Thr	Lys	Arg	Gly	Gly	Pro	Lys
145				150						155				160	
Cys	Pro														

(2) INFORMATION FOR SEQ ID NO:4051:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..192

(D) OTHER INFORMATION: / Ceres Seq. ID 1579361

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4051:

Tyr	Phe	Ile	Gly	Ala	Arg	Gly	Ser	Gly	Phe	Thr	Gln	Xaa	Ala	Arg	Ala
1			5					10						15	
Gly	Ser	His	Glu	Xaa	Gly	Glu	Pro	Met	Val	Ala	Ala	Ala	Ala	Asn	Leu
		20						25					30		
Leu	Arg	Gly	Asn	Gly	Gly	His	Arg	Ala	Ser	Pro	Pro	Thr	Arg	Arg	Pro
		35				40						45			
Gly	Arg	Leu	Phe	Arg	Ala	Asp	Ala	Gly	Ser	Ser	Ser	Gly	Thr	Ala	Arg
	50					55					60				
Leu	Leu	Arg	Asp	Glu	His	Glu	Arg	Leu	Leu	Arg	Cys	Ser	Ser	Ala	Ser
65			70							75				80	
Gln	Ala	Gln	Arg	Ile	Pro	Thr	Pro	Asn	Val	Arg	Trp	Cys	His	Pro	Arg
		85						90						95	
Gln	Ser	Pro	Ala	Thr	Arg	Val	Arg	Arg	Pro	Val	Arg	Gly	Ala	Val	Leu
	100							105					110		
Gly	Asp	Gly	Val	Pro	Glu	Ala	Val	Pro	Leu	Leu	Leu	Pro	Gln	Xaa	Leu
	115					120						125			
Arg	Gly	Val	Pro	Val	Arg	Ala	Ala	Gly	His	Leu	Arg	Gln	Gln	Glu	His
	130					135					140				
Leu	Pro	Leu	Leu	Gln	Gln	Leu	Glu	Asp	Gln	Ala	Gly	Arg	Pro	Gln	Val
145				150						155				160	
Pro	Leu	Val	Ala	Leu	Pro	Leu	Gly	Leu	Leu	Asp	Glu	Ile	Phe	Cys	Ser
			165					170						175	
Lys	Asn	Gln	Lys	Val	Arg	Ile	Cys	Leu	Thr	Ile	Phe	Arg	Phe	His	Lys
		180						185					190		

(2) INFORMATION FOR SEQ ID NO:4052:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..168
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579362

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4052:

Met Val Ala Ala Ala Asn Leu Leu Arg Gly Asn Gly Gly His Arg  
1 5 10 15  
Ala Ser Pro Pro Thr Arg Arg Pro Gly Arg Leu Phe Arg Ala Asp Ala  
20 25 30  
Gly Ser Ser Ser Gly Thr Ala Arg Leu Leu Arg Asp Glu His Glu Arg  
35 40 45  
Leu Leu Arg Cys Ser Ser Ala Ser Gln Ala Gln Arg Ile Pro Thr Pro  
50 55 60  
Asn Val Arg Trp Cys His Pro Arg Gln Ser Pro Ala Thr Arg Val Arg  
65 70 75 80  
Arg Pro Val Arg Gly Ala Val Leu Gly Asp Gly Val Pro Glu Ala Val  
85 90 95  
Pro Leu Leu Leu Pro Gln Xaa Leu Arg Gly Val Pro Val Arg Ala Ala  
100 105 110  
Gly His Leu Arg Gln Gln Glu His Leu Pro Leu Leu Gln Leu Glu  
115 120 125  
Asp Gln Ala Gly Arg Pro Gln Val Pro Leu Val Ala Leu Pro Leu Gly  
130 135 140  
Leu Leu Asp Glu Ile Phe Cys Ser Lys Asn Gln Lys Val Arg Ile Cys  
145 150 155 160  
Leu Thr Ile Phe Arg Phe His Lys  
165

(2) INFORMATION FOR SEQ ID NO:4053:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 570 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..570
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579366

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4053:

ggagcgattt attaagrcr cctccgcaa ccgcactctg cccgccgaaa gcgtcgctcg 60  
gccacctcgc actcgcgcgc gcctcaaaga tgcacaggca gctcagcctc tccgccagcm 120  
cgaagcagca gcagccgcct cctgamggca ccarcaccgg angcggcgac gcggcgggcga 180  
aggcgatggc ggcgggcgag gacgagtcgt cggcctcgca ctccagctcc aaggccagca 240  
gggggtggtc ggcgaggac gagaggcca tccacctegt cccgctgctc accttctct 300  
gcttctctct gctcttctc tgctcccacg acccgctccc cgccgatatg toagCttcg 360  
ctggaggcgg cggcgaggga ggaggagcga gatctgggaa ccggagggtta aggatgcttt 420  
agtgtgcgta ttacctacc attggagtat tattatcgcg atgcggatgt tgtacttgct 480  
cagcagtaac caagtatggg accaaagtat gtcaccatac aaaacactct tgctgtggta 540  
atactaccaa cctacatcag catgttctct

(2) INFORMATION FOR SEQ ID NO:4054:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..139
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1579367
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4054:

Thr His Leu Leu Ser Xaa Pro Pro Pro Thr Ala Leu Cys Pro Pro Lys  
1 5 10 15  
Ala Ser Ser Gly His Leu Ala Leu Ala Arg Ala Ser Lys Met His Arg  
20 25 30  
Gln Leu Ser Leu Ser Ala Ser Xaa Lys Gln Gln Gln Pro Pro Pro Xaa  
35 40 45  
Gly Thr Xaa Thr Gly Xaa Gly Asp Ala Ala Ala Lys Ala Met Ala Ala  
50 55 60  
Ala Glu Asp Glu Ser Ser Ala Ser His Ser Ser Lys Ala Ser Arg  
65 70 75 80  
Gly Trp Ser Ala Arg Asp Glu Arg Ala Ile His Leu Val Pro Leu Leu  
85 90 95  
Thr Phe Leu Cys Phe Leu Leu Leu Phe Leu Cys Ser His Asp Pro Ser  
100 105 110  
Pro Ala Asp Met Ser Ser Phe Ala Gly Gly Gly Gly Gly Gly Gly Gly  
115 120 125  
Ala Arg Ser Gly Asn Arg Arg Leu Arg Met Leu  
130 135

(2) INFORMATION FOR SEQ ID NO:4055:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 110 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..110
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1579368
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4055:

Met His Arg Gln Leu Ser Leu Ser Ala Ser Xaa Lys Gln Gln Gln Pro  
1 5 10 15  
Pro Pro Xaa Gly Thr Xaa Thr Gly Xaa Gly Asp Ala Ala Ala Lys Ala  
20 25 30  
Met Ala Ala Ala Glu Asp Glu Ser Ser Ala Ser His Ser Ser Ser Lys  
35 40 45  
Ala Ser Arg Gly Trp Ser Ala Arg Asp Glu Arg Ala Ile His Leu Val  
50 55 60  
Pro Leu Leu Thr Phe Leu Cys Phe Leu Leu Leu Phe Leu Cys Ser His  
65 70 75 80  
Asp Pro Ser Pro Ala Asp Met Ser Ser Phe Ala Gly Gly Gly Gly Gly  
85 90 95  
Gly Gly Gly Ala Arg Ser Gly Asn Arg Arg Leu Arg Met Leu  
100 105 110

(2) INFORMATION FOR SEQ ID NO:4056:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 78 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..78  
(D) OTHER INFORMATION: / Ceres Seq. ID 1579369

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4056:

Met	Ala	Ala	Ala	Glu	Asp	Glu	Ser	Ser	Ala	Ser	His	Ser	Ser	Ser	Lys
1				5					10					15	
Ala	Ser	Arg	Gly	Trp	Ser	Ala	Arg	Asp	Glu	Arg	Ala	Ile	His	Leu	Val
			20					25					30		
Pro	Leu	Leu	Thr	Phe	Leu	Cys	Phe	Leu	Leu	Leu	Phe	Leu	Cys	Ser	His
		35					40					45			
Asp	Pro	Ser	Pro	Ala	Asp	Met	Ser	Ser	Phe	Ala	Gly	Gly	Gly	Gly	Gly
	50				55						60				
Gly	Gly	Gly	Ala	Arg	Ser	Gly	Asn	Arg	Arg	Leu	Arg	Met	Leu		
65				70						75					

(2) INFORMATION FOR SEQ ID NO:4057:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 618 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..618  
(D) OTHER INFORMATION: / Ceres Seq. ID 1579382

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4057:

agcaatsccc	aacagcgcca	ctgtccagtg	cgcgcgtsaa	gcttgcttag	stagccgcca	60
tggcctccct	cgccgcgcgc	tccgtgaagc	ccgtggccat	caagggtctc	gccggcagct	120
ctatctccgg	aaggaagctc	gccgtcgcca	gGccgtcggc	ccgctccatc	cgcaggcccc	180
gcgcagcCgc	cgtgggtggc	aagtacggcg	acaagagcgt	ctacttcgac	ctcgacgaca	240
tcggcaacac	caccggacag	tgggacctct	acggctctga	cgcgcctcgc	ccctacaacc	300
cgctacagag	caagttcttc	gagacgttcg	cggctccgtt	caccaagaga	ggtctgctgc	360
tcaagttcct	gctgctgggc	ggcggctcac	ttctggccta	cgtcagcgcg	tcggcgtcac	420
cggacctcct	gccgatcaag	aaggacctc	aggagccgcc	gcagcctggc	ccgcgcggca	480
agatctaagc	tcagctactc	catttgcatg	gtctagtagt	agcttgcttt	gtactstagg	540
gccggtcgat	ccgtcgcaat	cgtcatggat	catctctcta	tcttggtgtt	acgctgttca	600
taatttggtg	tattcgcc					

(2) INFORMATION FOR SEQ ID NO:4058:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..92  
(D) OTHER INFORMATION: / Ceres Seq. ID 1579383

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4058:

Ala	Xaa	Pro	Asn	Ser	Ala	Thr	Val	Gln	Cys	Ala	Arg	Xaa	Ala	Cys	Leu
1			5					10						15	
Xaa	Ser	Arg	His	Gly	Leu	Pro	Arg	Arg	Leu	Arg	Glu	Ala	Arg	Gly	
			20					25				30			
His	Gln	Gly	Ser	Arg	Arg	Gln	Leu	Tyr	Leu	Arg	Lys	Glu	Ala	Arg	Arg
		35				40					45				
Arg	Gln	Ala	Val	Gly	Pro	Leu	His	Pro	Gln	Ala	Pro	Arg	Ser	Arg	Arg
	50				55					60					
Gly	Gly	Gln	Val	Arg	Arg	Gln	Glu	Arg	Leu	Leu	Arg	Pro	Arg	Arg	His
65				70					75					80	
Arg	Gln	His	His	Arg	Thr	Val	Gly	Pro	Leu	Arg	Leu				
			85					90							

(2) INFORMATION FOR SEQ ID NO:4059:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..142
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4059:

Met Ala Ser Leu Ala Ala Val Ser Val Lys Pro Val Ala Ile Lys Gly  
1 5 10 15  
Leu Ala Gly Ser Ser Ile Ser Gly Arg Lys Leu Ala Val Ala Arg Pro  
20 25 30  
Ser Ala Arg Ser Ile Arg Arg Pro Arg Ala Ala Ala Val Val Ala Lys  
35 40 45  
Tyr Gly Asp Lys Ser Val Tyr Phe Asp Leu Asp Asp Ile Gly Asn Thr  
50 55 60  
Thr Gly Gln Trp Asp Leu Tyr Gly Ser Asp Ala Pro Ser Pro Tyr Asn  
65 70 75 80  
Pro Leu Gln Ser Lys Phe Phe Glu Thr Phe Ala Ala Pro Phe Thr Lys  
85 90 95  
Arg Gly Leu Leu Leu Lys Phe Leu Leu Leu Gly Gly Gly Ser Leu Leu  
100 105 110  
Ala Tyr Val Ser Ala Ser Ala Ser Pro Asp Leu Leu Pro Ile Lys Lys  
115 120 125  
Gly Pro Gln Glu Pro Pro Gln Pro Gly Pro Arg Gly Lys Ile  
130 135 140

(2) INFORMATION FOR SEQ ID NO:4060:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 771 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..771
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579398

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4060:

atcacaaattc acagcgctca agttctcgcg cccagagcca aattttttctc cactcaatca 60  
ctgcagccat gnacgccagc ngascggtag caaggcgaag aagggggcgg ctgggcgcaa 120  
ggctggcggc cccaggaaga agtcggtgtc gcggtccgtc aaggccgggc tgcagttccc 180  
cgtcggccgg atcgggcgct acctcaagaa gggccggtac gcgcagcgCG tgggcaccgg 240  
cgcccccggt tatctcgccg ccgtgtttga gtacctcgcc gccgaggtgc tggagctggc 300  
cggcaacgcg gcgaaggaca acaagaagac gcgcacgtc ccgcgccacg tgctcctggc 360  
gatccgcaac gacgttgagc tcggcaagct gctggctggc gtcaccatcg cgcacggcgg 420  
tgtcctcccc aacatcaacc cggttctcct gcccaagaag gtggcggaga aggcgtctag 480  
cggcggcagc aaggagagca agtccccctaa gaaggccgcc aagtccccaa agaaggcagc 540  
caagtccccg aagaaggctt agaaattagt cactccacta gcgctctgct gtagcatggt 600  
cgtgtttaga tctgtggatg ttatgtgttc cggcctaatt tcctctttgc cttgtggctt 660  
ctgatattgt catcgcatg tttgcggtg tgtgtttcct tggtctgatt ttgcaattca 720  
tcattctggt gaatgaactt actatcgga aatgaagcat aataacgatg c

(2) INFORMATION FOR SEQ ID NO:4061:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear



- (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..186  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1579399  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4061:

Ser Gln Phe Thr Ala Leu Lys Phe Ser Arg Pro Glu Pro Asn Phe Ser  
1                  5                  10                  15  
Pro Leu Asn His Cys Ser His Xaa Arg Gln Xaa Xaa Gly Ser Lys Ala  
                  20                  25                  30  
Lys Lys Gly Ala Ala Gly Arg Lys Ala Gly Gly Pro Arg Lys Lys Ser  
                  35                  40                  45  
Val Ser Arg Ser Val Lys Ala Gly Leu Gln Phe Pro Val Gly Arg Ile  
50                  55                  60  
Gly Arg Tyr Leu Lys Lys Gly Arg Tyr Ala Gln Arg Val Gly Thr Gly  
65                  70                  75                  80  
Ala Pro Val Tyr Leu Ala Ala Val Leu Glu Tyr Leu Ala Ala Glu Val  
                  85                  90                  95  
Leu Glu Leu Ala Gly Asn Ala Ala Lys Asp Asn Lys Lys Thr Arg Ile  
                  100                  105                  110  
Val Pro Arg His Val Leu Leu Ala Ile Arg Asn Asp Val Glu Leu Gly  
                  115                  120                  125  
Lys Leu Leu Ala Gly Val Thr Ile Ala His Gly Gly Val Leu Pro Asn  
130                  135                  140  
Ile Asn Pro Val Leu Leu Pro Lys Lys Val Ala Glu Lys Ala Ser Ser  
145                  150                  155                  160  
Gly Gly Ser Lys Glu Ser Lys Ser Pro Lys Lys Ala Ala Lys Ser Pro  
                  165                  170                  175  
Lys Lys Ala Ala Lys Ser Pro Lys Lys Ala  
                  180                  185

(2) INFORMATION FOR SEQ ID NO:4062:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 188 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..188  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1579400  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4062:

His Asn Ser Gln Arg Ser Ser Ser Arg Ala Gln Ser Gln Ile Phe Leu  
1                  5                  10                  15  
His Ser Ile Thr Ala Ala Met Xaa Ala Ser Xaa Xaa Val Ala Arg Arg  
                  20                  25                  30  
Arg Arg Gly Arg Leu Gly Ala Arg Leu Ala Ala Pro Gly Arg Ser Arg  
                  35                  40                  45  
Cys Arg Gly Pro Ser Arg Pro Gly Cys Ser Ser Pro Ser Ala Gly Ser  
50                  55                  60  
Gly Ala Thr Ser Arg Arg Ala Gly Thr Arg Ser Ala Trp Ala Pro Ala  
65                  70                  75                  80  
Pro Pro Ser Ile Ser Pro Pro Cys Leu Ser Thr Ser Pro Pro Arg Cys  
                  85                  90                  95  
Trp Ser Trp Pro Ala Thr Arg Arg Arg Thr Thr Arg Arg Arg Ala Ser  
                  100                  105                  110  
Ser Arg Ala Thr Cys Ser Trp Arg Ser Ala Thr Thr Leu Ser Ser Ala  
                  115                  120                  125  
Ser Cys Trp Leu Ala Ser Pro Ser Arg Thr Ala Val Ser Ser Pro Thr  
130                  135                  140  
Ser Thr Arg Phe Ser Cys Pro Arg Arg Trp Arg Arg Arg Arg Leu Ala

(2) INFORMATION FOR SEO ID NO:4063:

(A) LENGTH: 166 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

MOLECULE TYPE: peptid

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..166

(D) OTHER INFORMATION: / Ceres Seq. ID 1579401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4063:

(2) INFORMATION FOR SEO ID NO:4064:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 782 base pairs

(B) TYPE: nucleic acid

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(C) STRANDEDNESS: single
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(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..782

(D) OTHER INFORMATION: / Ceres Seq. ID 1579402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4064:

asattcagcc	cacaagcaca	taacaacata	gcaccccccc	tagggtttca	caacatatgt	60
accctctcgc	gcaaacactc	ctctttccgc	rcmgcctccc	ctcccgccca	cttgctccgc	120
cggcgcggcc	accgcgcgcg	caccgcagca	gccagtcagc	agatcgtaac	catggcggat	180
tctaaggcgg	ctgcggcggt	gacctccgc	acgcgcaagt	tcatgaccaa	cgccttctc	240
tcgcgcaagc	agttcgtgct	cgaGgtcatc	caccccggcc	gccccaacgt	ctccaaggcg	300
gaGbtcaagg	agaggctggc	gaagatctac	gaggtgaagg	acccaaactg	catcttcgtc	360
ttcaagtttc	ggaccaactt	cggaggcgcc	aagtccaccg	gtctcggtct	catctacgac	420
aaccttgagg	ccgccaagaa	gttcgagccc	aagtaccgcc	tcttcaggaa	cggccttgct	480
accaaggtag	agaagtcacg	aaagcagatg	aaggaacgta	agracagggc	gaagaaaatc	540
cgtggtgtga	aqaaagacaaa	agcgggagat	gccaaagaaga	agtaaggggag	gaagttactt	600

gccttgccat ttctcatctt aggccttggg ttgtttaggg tgggctcctt ccggcaatgc 660  
tgaatgtgtt tagttagaag tagagaagat tttgccaatc acccattacg ttgagtttct 720  
cgttgcacct tctgttcagt tttgaggcac tttgtcagac acaagaatat atatacctgg 780  
tc

(2) INFORMATION FOR SEQ ID NO:4065:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..194
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4065:

Xaa Phe Ser Pro Gln Ala His Asn Asn Ile Ala Pro Pro Leu Gly Phe  
1 5 10 15  
His Asn Ile Cys Thr Leu Ser Arg Lys His Ser Ser Phe Arg Xaa Ala  
20 25 30  
Ser Pro Pro Ala His Leu Leu Arg Arg Arg Gly His Arg Arg Arg Thr  
35 40 45  
Ala Ala Ala Ser Gln Gln Ile Val Thr Met Ala Asp Ser Lys Ala Ala  
50 55 60  
Ala Ala Val Thr Leu Arg Thr Arg Lys Phe Met Thr Asn Arg Leu Leu  
65 70 75 80  
Ser Arg Lys Gln Phe Val Leu Glu Val Ile His Pro Gly Arg Pro Asn  
85 90 95  
Val Ser Lys Ala Glu Xaa Lys Glu Arg Leu Ala Lys Ile Tyr Glu Val  
100 105 110  
Lys Asp Pro Asn Cys Ile Phe Val Phe Lys Phe Arg Thr Asn Phe Gly  
115 120 125  
Gly Gly Lys Ser Thr Gly Phe Gly Leu Ile Tyr Asp Asn Leu Glu Ala  
130 135 140  
Ala Lys Lys Phe Glu Pro Lys Tyr Arg Leu Ile Arg Asn Gly Leu Ala  
145 150 155 160  
Thr Lys Val Glu Lys Ser Arg Lys Gln Met Lys Glu Arg Lys Xaa Arg  
165 170 175  
Ala Lys Lys Ile Arg Gly Val Lys Lys Thr Lys Ala Gly Asp Ala Lys  
180 185 190  
Lys Lys

(2) INFORMATION FOR SEQ ID NO:4066:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..137
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4066:

Met Ala Asp Ser Lys Ala Ala Ala Val Thr Leu Arg Thr Arg Lys  
1 5 10 15  
Phe Met Thr Asn Arg Leu Leu Ser Arg Lys Gln Phe Val Leu Glu Val  
20 25 30  
Ile His Pro Gly Arg Pro Asn Val Ser Lys Ala Glu Xaa Lys Glu Arg  
35 40 45  
Leu Ala Lys Ile Tyr Glu Val Lys Asp Pro Asn Cys Ile Phe Val Phe

50 55 60  
Lys Phe Arg Thr Asn Phe Gly Gly Gly Lys Ser Thr Gly Phe Gly Leu  
65 70 75 80  
Ile Tyr Asp Asn Leu Glu Ala Ala Lys Lys Phe Glu Pro Lys Tyr Arg  
85 90 95  
Leu Ile Arg Asn Gly Leu Ala Thr Lys Val Glu Lys Ser Arg Lys Gln  
100 105 110  
Met Lys Glu Arg Lys Xaa Arg Ala Lys Lys Ile Arg Gly Val Lys Lys  
115 120 125  
Thr Lys Ala Gly Asp Ala Lys Lys Lys  
130 135

(2) INFORMATION FOR SEQ ID NO:4067:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..120
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4067:

Met Thr Asn Arg Leu Leu Ser Arg Lys Gln Phe Val Leu Glu Val Ile  
1 5 10 15  
His Pro Gly Arg Pro Asn Val Ser Lys Ala Glu Xaa Lys Glu Arg Leu  
20 25 30  
Ala Lys Ile Tyr Glu Val Lys Asp Pro Asn Cys Ile Phe Val Phe Lys  
35 40 45  
Phe Arg Thr Asn Phe Gly Gly Gly Lys Ser Thr Gly Phe Gly Leu Ile  
50 55 60  
Tyr Asp Asn Leu Glu Ala Ala Lys Lys Phe Glu Pro Lys Tyr Arg Leu  
65 70 75 80  
Ile Arg Asn Gly Leu Ala Thr Lys Val Glu Lys Ser Arg Lys Gln Met  
85 90 95  
Lys Glu Arg Lys Xaa Arg Ala Lys Lys Ile Arg Gly Val Lys Lys Thr  
100 105 110  
Lys Ala Gly Asp Ala Lys Lys Lys  
115 120

(2) INFORMATION FOR SEQ ID NO:4068:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 650 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..650
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4068:

attcacgctc cacgttccat atggcttccct gcaggatggc actcctcctt ggcttgcctgc 60  
tgctagtagt aGcttcgccc gcgatcgctg atgacgactc cggatatctac taccagctgg 120  
ctcttatgtg gccaggagca tactgcgagc agaccagcgc tgggtgctgc aaGccgacca 180  
ccggcgtctc ccggrcgccg gacttctaca taacgggctt caccgtcctt aacgcgacca 240  
ccgacgctgc agtgacggga tgcagcaaca aagttcctta cgaccctaac ctgattaccg 300  
gcacccaagg cctgaatcag tactggagca acatcagggtg ccccagcaac aacgggcaga 360  
gcagctggaa gaacgcctgg aagaaggccg gcgcctgatc ttgctccaga ggggtgtgttt 420  
gggaattggg agggggaaaa aaagaggaaa ttgctgcata gagtcagacg gtgtatcagc 480  
ttgtacgcca tcaatcaagt gctgtaaaca tgccctgggaa ataattgggg acctggattt 540  
gaataagatt tgagttgttg ggggcggacg tgctacatta ggccttggtc gggttattcct 600

aataccttcg gtgcaataaaa ggaaatcatc ttgcgcgtga ccgagcgtgc

(2) INFORMATION FOR SEQ ID NO:4069:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..131

(D) OTHER INFORMATION: / Ceres Seq. ID 1579407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4069:

Ser Pro Ser Thr Phe His Met Ala Ser Cys Arg Met Ala Leu Leu Leu  
1 5 10 15  
Gly Leu Leu Leu Leu Val Val Ala Ser Pro Ala Ile Ala Asp Asp Asp  
20 25 30  
Ser Gly Ile Tyr Tyr Gln Leu Ala Leu Met Trp Pro Gly Ala Tyr Cys  
35 40 45  
Glu Gln Thr Ser Ala Gly Cys Cys Lys Pro Thr Thr Gly Val Ser Pro  
50 55 60  
Xaa Arg Asp Phe Tyr Ile Thr Gly Phe Thr Val Leu Asn Ala Thr Thr  
65 70 75 80  
Asp Ala Ala Val Thr Gly Cys Ser Asn Lys Val Pro Tyr Asp Pro Asn  
85 90 95  
Leu Ile Thr Gly Ile Gln Gly Leu Asn Gln Tyr Trp Ser Asn Ile Arg  
100 105 110  
Cys Pro Ser Asn Asn Gly Gln Ser Ser Trp Lys Asn Ala Trp Lys Lys  
115 120 125  
Ala Gly Ala  
130

(2) INFORMATION FOR SEQ ID NO:4070:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..125

(D) OTHER INFORMATION: / Ceres Seq. ID 1579408

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4070:

Met Ala Ser Cys Arg Met Ala Leu Leu Leu Gly Leu Leu Leu Val  
1 5 10 15  
Val Ala Ser Pro Ala Ile Ala Asp Asp Ser Gly Ile Tyr Tyr Gln  
20 25 30  
Leu Ala Leu Met Trp Pro Gly Ala Tyr Cys Glu Gln Thr Ser Ala Gly  
35 40 45  
Cys Cys Lys Pro Thr Thr Gly Val Ser Pro Xaa Arg Asp Phe Tyr Ile  
50 55 60  
Thr Gly Phe Thr Val Leu Asn Ala Thr Thr Asp Ala Ala Val Thr Gly  
65 70 75 80  
Cys Ser Asn Lys Val Pro Tyr Asp Pro Asn Leu Ile Thr Gly Ile Gln  
85 90 95  
Gly Leu Asn Gln Tyr Trp Ser Asn Ile Arg Cys Pro Ser Asn Asn Gly  
100 105 110  
Gln Ser Ser Trp Lys Asn Ala Trp Lys Lys Ala Gly Ala  
115 120 125

(2) INFORMATION FOR SEQ ID NO:4071:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..120
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1579409
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4071:

Met Ala Leu Leu Gly Leu Leu Leu Val Val Ala Ser Pro Ala  
1 5 10 15  
Ile Ala Asp Asp Asp Ser Gly Ile Tyr Tyr Gln Leu Ala Leu Met Trp  
20 25 30  
Pro Gly Ala Tyr Cys Glu Gln Thr Ser Ala Gly Cys Cys Lys Pro Thr  
35 40 45  
Thr Gly Val Ser Pro Xaa Arg Asp Phe Tyr Ile Thr Gly Phe Thr Val  
50 55 60  
Leu Asn Ala Thr Thr Asp Ala Ala Val Thr Gly Cys Ser Asn Lys Val  
65 70 75 80  
Pro Tyr Asp Pro Asn Leu Ile Thr Gly Ile Gln Gly Leu Asn Gln Tyr  
85 90 95  
Trp Ser Asn Ile Arg Cys Pro Ser Asn Asn Gly Gln Ser Ser Trp Lys  
100 105 110  
Asn Ala Trp Lys Lys Ala Gly Ala  
115 120

- (2) INFORMATION FOR SEQ ID NO:4072:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 635 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..635
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1579440

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4072:

atttatattt atttattgct gccgcgtcca ccgtccgtcc ccaaacccta ccgcagtcgc 60  
cgccaccgtc tcccctcctg atccaatcca atggcgcgcc tccacctcgt ggccgtggca 120  
atgggcttgc tcttggcctt gacgacggcg caggcaccgg gcgcgtccac gatgcccgCg 180  
cccatggcgC agntccggcg acctcggcgc ctccctcgtcc cgcgccatcc ccgaccaga 240  
agaccgctcc agctccggcg cccaatgcca cggtaccgcg ccccgccctcG ccgccggcgc 300  
cgagctctat cgggcagacg ccgaccgagg cgccgtcctc ccctccgccg ccagcgccg 360  
cgtccagcgt tgccctccgcc ttgtacgtgg Nccgccgcta tggcgGctgt cgtgtttttc 420  
ttctgaggtc ggtactcggc gccgatggat ccgccgccta tggatggta cggtcgggtg 480  
tggatttgac acgatggctc ccCgctaccg ctggtcgagt ttgcttatta ggatactagt 540  
agttaattaa tagttgggtt gatcagatca gatctagcgt ttttgttgag tggggatatt 600  
atttcttcta cggatctgca cactagggtt atgtc

- (2) INFORMATION FOR SEQ ID NO:4073:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 178 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..178
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1579441
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4073:

Leu Tyr Leu Phe Ile Ala Ala Ala Ser Thr Val Arg Pro Gln Thr Leu  
1 5 10 15  
Pro Gln Ser Pro Pro Pro Ser Pro Leu Leu Ile Gln Ser Asn Gly Ala  
20 25 30  
Pro Pro Pro Arg Gly Arg Gly Asn Gly Leu Ala Leu Gly Leu Asp Asp  
35 40 45  
Gly Ala Gly Thr Gly Arg Val His Asp Ala Arg Ala His Gly Ala Xaa  
50 55 60  
Pro Ala Thr Ser Ala Pro Pro Arg Pro Ala Pro Ser Pro Thr Gln Lys  
65 70 75 80  
Thr Ala Pro Ala Pro Ala Pro Asn Ala Thr Val Pro Ala Pro Ala Ser  
85 90 95  
Pro Pro Ala Pro Ser Ser Ile Gly Gln Thr Pro Thr Glu Ala Pro Ser  
100 105 110  
Ser Pro Pro Pro Pro Ser Ala Ala Ser Ser Val Ala Ser Ala Leu Tyr  
115 120 125  
Val Xaa Arg Arg Tyr Gly Gly Cys Arg Val Phe Leu Leu Arg Ser Val  
130 135 140  
Leu Gly Ala Asp Gly Ser Ala Ala Tyr Gly Met Val Arg Cys Gly Val  
145 150 155 160  
Asp Leu Thr Arg Trp Leu Pro Ala Thr Ala Gly Arg Val Cys Leu Leu  
165 170 175  
Gly Tyr

(2) INFORMATION FOR SEQ ID NO:4074:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..111

(D) OTHER INFORMATION: / Ceres Seq. ID 1579442

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4074:

Met Ala Arg Leu His Leu Val Ala Val Ala Met Gly Leu Leu Leu Ala  
1 5 10 15  
Leu Thr Thr Ala Gln Ala Pro Gly Ala Ser Thr Met Pro Ala Pro Met  
20 25 30  
Ala Gln Xaa Arg Arg Pro Arg Arg Leu Leu Val Pro Arg His Pro Arg  
35 40 45  
Pro Arg Arg Pro Leu Gln Leu Arg Arg Pro Met Pro Arg Tyr Pro Pro  
50 55 60  
Pro Pro Arg Arg Arg Arg Ala Leu Ser Gly Arg Arg Arg Pro Arg  
65 70 75 80  
Arg Arg Pro Pro Leu Arg Arg Pro Ala Pro Arg Pro Ala Leu Pro Pro  
85 90 95  
Pro Cys Thr Trp Xaa Ala Ala Met Ala Ala Val Val Phe Phe Phe  
100 105 110

(2) INFORMATION FOR SEQ ID NO:4075:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 101 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..101

(D) OTHER INFORMATION: / Ceres Seq. ID 1579443

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4075:

```
Met Gly Leu Leu Leu Ala Leu Thr Thr Ala Gln Ala Pro Gly Ala Ser
1          5          10          15
Thr Met Pro Ala Pro Met Ala Gln Xaa Arg Arg Pro Arg Arg Leu Leu
20          25          30
Val Pro Arg His Pro Arg Pro Arg Arg Pro Leu Gln Leu Arg Arg Pro
35          40          45
Met Pro Arg Tyr Pro Pro Pro Pro Arg Arg Arg Arg Arg Ala Leu Ser
50          55          60
Gly Arg Arg Arg Pro Arg Arg Arg Pro Pro Leu Arg Arg Pro Ala Pro
65          70          75          80
Arg Pro Ala Leu Pro Pro Pro Cys Thr Trp Xaa Ala Ala Met Ala Ala
85          90          95
Val Val Phe Phe Phe
100
```

(2) INFORMATION FOR SEQ ID NO:4076:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 780 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..780
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579447

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4076:

```
actcagccca ctacctttca gatttttctt catctgccgc cgcctgcacc caacaagcct      60
ctcgacgcta gtcattggcgc cttccaacgg cgccgcscgg tcgacgagac cgtcgccgcc      120
accgactccg tgcaggagcc tcccagaag atctccaaga tctctcccct gctcaagggtg      180
aagaagctct ccgagaaggc cgtgctgccg tcccgcggct ccgctctcgc cgccggctac      240
gacctctcga gcgcgagga gatggtggtg ccggcgcggtg gcaaggcgct cgtgccgacc      300
gacctcagcg tcgcatccc gcacggaacc tacgcgCgca tcgcGCCcag gtcggggctg      360
gcgctgaagc actccatcga cgtgggcgcc ggcgtgatcg acgcggacta ccgaggcccc      420
gtcggcgcca tcctcttcaa ccaactccgac gccgacttcg ccgtgaagcc cggcgacagg      480
atcgcgcaga tgatcatcga ggtgatcgcg acgcccagag tcgcggaggt ggaggacctc      540
gacgccaccg tccgtggggg cggagggttc ggggtccaccg gcgtctgaag ggattcgggtg      600
tctaggttag gatggcgatg caagccttgg tgtcttttgt tggctctaag aaatcgtgat      660
gttcaccatc actatcctgc tatcgataat tagtattgag attagtagct aggttgcgta      720
gttagctcga tgcacgtact attgtcgaga actcgctatt ctgtgatgtt gaaaatgtct      780
```

(2) INFORMATION FOR SEQ ID NO:4077:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..195
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579448

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4077:

```
Thr Gln Pro Thr Thr Phe Gln Ile Phe Pro His Leu Pro Pro Pro Ala
1          5          10          15
Pro Asn Lys Pro Leu Asp Ala Ser His Gly Arg Phe Gln Arg Arg Arg
20          25          30
Xaa Val Asp Glu Thr Val Ala Ala Thr Asp Ser Val Gln Glu Pro Pro
35          40          45
Gln Lys Ile Ser Lys Ile Ser Pro Leu Leu Lys Val Lys Lys Leu Ser
50          55          60
```



Glu Lys Ala Val Leu Pro Ser Arg Gly Ser Ala Leu Ala Ala Gly Tyr  
65 70 75 80  
Asp Leu Ser Ser Ala Glu Glu Met Val Val Pro Ala Arg Gly Lys Ala  
85 90 95  
Leu Val Pro Thr Asp Leu Ser Val Ala Ile Pro His Gly Thr Tyr Ala  
100 105 110  
Arg Ile Ala Pro Arg Ser Gly Leu Ala Leu Lys His Ser Ile Asp Val  
115 120 125  
Gly Ala Gly Val Ile Asp Ala Asp Tyr Arg Gly Pro Val Gly Val Ile  
130 135 140  
Leu Phe Asn His Ser Asp Ala Asp Phe Ala Val Lys Pro Gly Asp Arg  
145 150 155 160  
Ile Ala Gln Met Ile Ile Glu Val Ile Ala Thr Pro Glu Val Ala Glu  
165 170 175  
Val Glu Asp Leu Asp Ala Thr Val Arg Gly Asp Gly Gly Phe Gly Ser  
180 185 190  
Thr Gly Val  
195

(2) INFORMATION FOR SEQ ID NO:4078:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..108
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579449

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4078:

Met Val Val Pro Ala Arg Gly Lys Ala Leu Val Pro Thr Asp Leu Ser  
1 5 10 15  
Val Ala Ile Pro His Gly Thr Tyr Ala Arg Ile Ala Pro Arg Ser Gly  
20 25 30  
Leu Ala Leu Lys His Ser Ile Asp Val Gly Ala Gly Val Ile Asp Ala  
35 40 45  
Asp Tyr Arg Gly Pro Val Gly Val Ile Leu Phe Asn His Ser Asp Ala  
50 55 60  
Asp Phe Ala Val Lys Pro Gly Asp Arg Ile Ala Gln Met Ile Ile Glu  
65 70 75 80  
Val Ile Ala Thr Pro Glu Val Ala Glu Val Glu Asp Leu Asp Ala Thr  
85 90 95  
Val Arg Gly Asp Gly Gly Phe Gly Ser Thr Gly Val  
100 105

(2) INFORMATION FOR SEQ ID NO:4079:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..469
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579454

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4079:

atccgttgct catctcacca gaagcgaaGc cggaggaggg aggaaggaga tccgcgagcag	60
ccggagccgg aggcCgagag gatgaagacg ttcgaccggt ggccggtctt cttccgccgg	120
gagtggaaagc gcaactggcc cttcctcacg gggttcgcca tcaccggctt catcatcacc	180
aagatgacgg ccaacttcac cgaggaggac ctcaagaact ccaagtctgt ccaggaacac	240
aagaagcgct gaccaaccgg gagtcgtccg aatcgctctgc ggatgaaaaa ttagccccct	300

atttatcttg tctttttttt tatctagatg cgtgcactct attgtaataa tgtaataaga 360  
ggcaattgga ttgatccaac agcaaccggc ttctgatttt gaTcygcttc gctgacataa 420  
tatgtgcctt ttttctggat gttggattgc atctaactct gttgaattg

(2) INFORMATION FOR SEQ ID NO:4080:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..83
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579455

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4080:

Ile Arg Cys Ser Ser His Gln Lys Arg Ser Arg Arg Arg Glu Glu Gly  
1 5 10 15  
Asp Arg Glu Gln Pro Glu Pro Glu Ala Glu Arg Met Lys Thr Phe Asp  
20 25 30  
Pro Trp Pro Val Phe Phe Arg Arg Glu Trp Lys Arg Asn Trp Pro Phe  
35 40 45  
Leu Thr Gly Phe Ala Ile Thr Gly Phe Ile Ile Thr Lys Met Thr Ala  
50 55 60  
Asn Phe Thr Glu Glu Asp Leu Lys Asn Ser Lys Phe Val Gln Glu His  
65 70 75 80  
Lys Lys Arg

(2) INFORMATION FOR SEQ ID NO:4081:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..114
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579456

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4081:

Pro Leu Leu Ile Ser Pro Glu Ala Lys Pro Glu Glu Gly Gly Arg Arg  
1 5 10 15  
Ser Arg Ala Ala Gly Ala Gly Gly Arg Glu Asp Glu Asp Val Arg Pro  
20 25 30  
Val Ala Gly Leu Leu Pro Pro Gly Val Glu Ala Gln Leu Ala Leu Pro  
35 40 45  
His Gly Val Arg His His Arg Leu His His His Gln Asp Asp Gly Gln  
50 55 60  
Leu His Arg Gly Gly Pro Gln Glu Leu Gln Val Arg Pro Gly Thr Gln  
65 70 75 80  
Glu Ala Leu Thr Asn Arg Glu Ser Ser Glu Ser Pro Ala Asp Glu Lys  
85 90 95  
Leu Ala Pro Tyr Leu Ser Cys Leu Phe Tyr Leu Asp Ala Cys Thr  
100 105 110  
Leu Leu

(2) INFORMATION FOR SEQ ID NO:4082:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 741 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..741

(D) OTHER INFORMATION: / Ceres Seq. ID 1579457

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4082:

```
ccttcttccc ccactgtcgc cgtcctcgt ctccactct ctccactttg ctgcttcttc      60
tcccttatta atgctcgtgg gctcctatga tccgccctcc gccgcgggtt tcttgatcca      120
tccccggccc aaggaagcgg accccggcga aactcctga cagattcgcc cCgtccgccg      180
ctccctcgat tcggtccCTt ccccgtcagc ggcaggtgtt taggGacctc tgcagcatag      240
catctggtcc gtccctggag atgtccggcg tacaggagca gttcgagatc aagttccggG      300
ctgccggacg gcaccgacat cggaccNcag gcggttcccg ccgrcgtcca ccgtcgccac      360
gctcaaggag accatcatcg cccagtggcc cgatgatggt gaaggctctg cagcgcaagc      420
cggcgatgta tactggcggc ggcggcggcg gcgagcaaag cgggaggagc agctggtgag      480
gagattgaga ctgtggtggt gcgtggcgtg tactgttcat cgttcagaca gatgacttgc      540
tggccCatgc tgtgggctca ggaactgctt cttoacagtg gcgatgttct gatctgtaat      600
gcacgaagca cgatactatt tgttgtatat gtatgtatgt gtaactacag ataagattag      660
gaacggtgtg aaagaataaa gaaaccgatg gaataagtga tttgggaaca atctcagaat      720
caatttatgc agtcctttag g
```

(2) INFORMATION FOR SEQ ID NO:4083:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..52

(D) OTHER INFORMATION: / Ceres Seq. ID 1579458

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4083:

```
Leu Leu Pro Pro Leu Ser Pro Leu Leu Val Phe His Ser Leu His Phe
1           5           10          15
Ala Ala Ser Ser Pro Leu Leu Met Leu Val Gly Ser Tyr Asp Pro Pro
20          25          30
Ser Ala Ala Gly Phe Leu Ile His Pro Arg Pro Lys Glu Ala Asp Pro
35          40          45
Gly Glu His Ser
50
```

(2) INFORMATION FOR SEQ ID NO:4084:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..72

(D) OTHER INFORMATION: / Ceres Seq. ID 1579459

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4084:

```
Met Ser Gly Val Gln Glu Gln Phe Glu Ile Lys Phe Arg Ala Ala Gly
1           5           10          15
Arg His Arg His Arg Thr Xaa Gly Gly Ser Arg Xaa Arg Pro Pro Ser
20          25          30
Pro Arg Ser Arg Arg Pro Ser Ser Pro Ser Gly Pro Met Met Val Lys
35          40          45
Ala Leu Gln Arg Lys Pro Ala Met Tyr Thr Gly Gly Gly Gly Gly Gly
50          55          60
Glu Gln Ser Gly Arg Ser Ser Trp
65          70
```

(2) INFORMATION FOR SEQ ID NO:4085:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..40
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579460

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4085:

Met Thr Cys Trp Pro Met Leu Trp Ala Gln Glu Leu Leu Leu His Ser  
1 5 10 15  
Gly Asp Val Leu Ile Cys Asn Ala Arg Ser Thr Ile Leu Phe Val Val  
20 25 30  
Tyr Val Cys Met Cys Asn Tyr Arg  
35 40

(2) INFORMATION FOR SEQ ID NO:4086:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 629 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..629
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579468

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4086:

aaaaagaggt gtccatggtg ctcaagctca gccaaagcaaa taagacgact tgttttcattg 60  
attcttgaag agatcgagct tcttttgcac cacaagggtcg aggatgtctt gcaactgagg 120  
atcaagctgc ggctgcggct caagctgcaa gtgcggcaag aagtaccctg acctggagga 180  
gacgagcacc gccgcgcagg ccaccgctgt cctcggcggtg gcccgcggaga agaaggccgc 240  
gcccgcagttc gtcgaggccg cggcggagtc cggcggaggcc gcccAcgAcc tgcggctgcg 300  
gtagcaGctg caagtgcgac ccctgcaact gctgatcaca tcgatcgacg accatggata 360  
tgattattat ctatctagct tgtggtggtg gttgaacaat aataagcgag gccgagctgg 420  
ctgccataca taggtattgt gtggtgtgtg agagagagag agaaacagag ttcttcagtt 480  
tgctatctct ctctctgcat gtttggcgtc agtctttgtg ctcatgtacg tgtgtctaca 540  
tgcattgttg ttgatccgat tgcgtctgct gtaaccatat attaattggt ccacgatgat 600  
atgatttgat actatatata tatatatat

(2) INFORMATION FOR SEQ ID NO:4087:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..56
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579469

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4087:

Lys Lys Arg Cys Pro Trp Cys Ser Ser Ala Lys Gln Ile Arg Arg  
1 5 10 15  
Leu Val Ser Leu Ile Leu Glu Glu Ile Glu Leu Leu Leu His His Lys  
20 25 30  
Val Glu Asp Val Leu Gln Leu Arg Ile Lys Leu Arg Leu Arg Leu Lys  
35 40 45  
Leu Gln Val Arg Gln Glu Val Pro  
50 55

(2) INFORMATION FOR SEQ ID NO:4088:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..66
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579470

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4088:

```
Met Ser Cys Asn Cys Gly Ser Ser Cys Gly Cys Gly Ser Ser Cys Lys
1          5          10          15
Cys Gly Lys Lys Tyr Pro Asp Leu Glu Glu Thr Ser Thr Ala Ala Gln
          20          25          30
Ala Thr Val Val Leu Gly Val Ala Pro Glu Lys Lys Ala Ala Pro Glu
          35          40          45
Phe Val Glu Ala Ala Ala Glu Ser Gly Glu Ala Ala His Asp Leu Arg
          50          55          60
Leu Arg
65
```

(2) INFORMATION FOR SEQ ID NO:4089:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 676 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..676
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579471

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4089:

```
actcctccaa accctagccc agagcagccg catcgaactc tacctgcctt tctctcgtcc      60
ctggcggcgg cggcaggatg gcggttctta ctgcgaggac ggtgaaggat gtgaaccccc      120
acgagtttgt caaggcctac tccgcccata tcaaacgctc cggcaagatg gagcttcctg      180
agtgggttga cattgtgaag actgcgaggt tcaaggagct ccctccttat gacctgact      240
ggtactacat cagggctgca tctgtagcaa ggaagatcta cttgagacaa ggcattggtg      300
ttggtggctt ccagaagatt tatggtggcc gccagaggaa tgGctcacgc ccacctcact      360
tctgcaagag cagtggtgcc atttcacgca acatcctcca gcagctgcag gagatgggca      420
tcattgatgt cgatcccaag ggtggacggc gcatcacctc ccaggggaagg cgtgatctgg      480
accaggtggc tggaaaggggt gctgttgaag cttgagcaat ctcatatttg gtttctatga      540
tgtcatgttt gattgttgag atggctacac tttatttgca ctttgatta ggatttttgt      600
gttaagagaa ctcaaggcat tctagctatg gttcacactg tattttccct gagtacctat      660
ttatcaaaac ctattc
```

(2) INFORMATION FOR SEQ ID NO:4090:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..145
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579472

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4090:

```
Met Ala Ala Ser Thr Ala Arg Thr Val Lys Asp Val Asn Pro His Glu
1          5          10          15
Phe Val Lys Ala Tyr Ser Ala His Leu Lys Arg Ser Gly Lys Met Glu
```

20 25 30  
Leu Pro Glu Trp Val Asp Ile Val Lys Thr Ala Arg Phe Lys Glu Leu  
35 40 45  
Pro Pro Tyr Asp Pro Asp Trp Tyr Tyr Ile Arg Ala Ala Ser Val Ala  
50 55 60  
Arg Lys Ile Tyr Leu Arg Gln Gly Ile Gly Val Gly Gly Phe Gln Lys  
65 70 75 80  
Ile Tyr Gly Gly Arg Gln Arg Asn Gly Ser Arg Pro Pro His Phe Cys  
85 90 95  
Lys Ser Ser Gly Ala Ile Ser Arg Asn Ile Leu Gln Gln Leu Gln Glu  
100 105 110  
Met Gly Ile Ile Asp Val Asp Pro Lys Gly Gly Arg Arg Ile Thr Ser  
115 120 125  
Gln Gly Arg Arg Asp Leu Asp Gln Val Ala Gly Arg Val Ala Val Glu  
130 135 140  
Ala  
145

(2) INFORMATION FOR SEQ ID NO:4091:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..115

(D) OTHER INFORMATION: / Ceres Seq. ID 1579473

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4091:

Met Glu Leu Pro Glu Trp Val Asp Ile Val Lys Thr Ala Arg Phe Lys  
1 5 10 15  
Glu Leu Pro Pro Tyr Asp Pro Asp Trp Tyr Tyr Ile Arg Ala Ala Ser  
20 25 30  
Val Ala Arg Lys Ile Tyr Leu Arg Gln Gly Ile Gly Val Gly Gly Phe  
35 40 45  
Gln Lys Ile Tyr Gly Gly Arg Gln Arg Asn Gly Ser Arg Pro Pro His  
50 55 60  
Phe Cys Lys Ser Ser Gly Ala Ile Ser Arg Asn Ile Leu Gln Gln Leu  
65 70 75 80  
Gln Glu Met Gly Ile Ile Asp Val Asp Pro Lys Gly Gly Arg Arg Ile  
85 90 95  
Thr Ser Gln Gly Arg Arg Asp Leu Asp Gln Val Ala Gly Arg Val Ala  
100 105 110  
Val Glu Ala  
115

(2) INFORMATION FOR SEQ ID NO:4092:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..72

(D) OTHER INFORMATION: / Ceres Seq. ID 1579474

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4092:

Met Val Ala Ala Arg Gly Met Ala His Ala His Leu Thr Ser Ala Arg  
1 5 10 15  
Ala Val Val Pro Phe His Ala Thr Ser Ser Ser Ser Cys Arg Arg Trp  
20 25 30

Ala Ser Leu Met Ser Ile Pro Arg Val Asp Gly Ala Ser Pro Pro Arg  
35 40 45  
Glu Gly Val Ile Trp Thr Arg Trp Leu Glu Gly Leu Leu Leu Lys Leu  
50 55 60  
Glu Gln Ser His Ile Trp Phe Leu  
65 70

(2) INFORMATION FOR SEQ ID NO:4093:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..321
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579490

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4093:

aaataggaca cgccggctag tactgcgcca gccCactcca gcgctgaagg cctgcagcgc	60
cagcgcagcg cytctctgct actgtgntcg ctgacgccgg tggggtgtga gccaactgcg	120
agctgtgcc acccctgctg ccgcgkctga ccgccggccc cggaccgaga tggacgctcg	180
gtgggcggtg ctgctcgcgc tgctggtcgc cagcggcggc gtccgtgtct gcgcgcgcgc	240
tgkggccaaag ggcgccaaact ggctgggcgg gctgagccgc gcgtcgttcc ccaaggggtt	300
cgtgttcggg acggcgacgt c	

(2) INFORMATION FOR SEQ ID NO:4094:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4094:

Asn Arg Thr Arg Leu Val Leu Arg Gln Pro Thr Pro Ala Leu Lys	
1 5 10 15	
Ala Cys Ser Ala Ser Ala Ala Xaa Leu Cys Tyr Cys Xaa Cys	
20 25 30	

(2) INFORMATION FOR SEQ ID NO:4095:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..50
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579492

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4095:

Met Asp Ala Arg Trp Ala Val Leu Leu Ala Leu Leu Val Ala Ser Gly	
1 5 10 15	
Gly Val Arg Val Cys Ala Ala Ala Xaa Ala Lys Gly Ala Asn Trp Leu	
20 25 30	
Gly Gly Leu Ser Arg Ala Ser Phe Pro Lys Gly Phe Val Phe Gly Thr	
35 40 45	
Ala Thr	
50	

(2) INFORMATION FOR SEQ ID NO:4096:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4096:

(2) INFORMATION FOR SEO ID NO:4097:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4097:

(2) INFORMATION FOR SEO ID NO:4098:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4098:

Ala	His	Pro	Ser	Pro	Phe	Pro	Pro	Pro	Arg	Arg	Arg	Glu	Thr	Pro	Thr
1				5					10					15	
Pro	Pro	Ile	His	His	His	Val	Ala	Pro	Pro	Pro	His	Pro	Ser	Pro	Arg
			20					25					30		
Leu	Ala	Gln	Gly	Tyr	Arg	Arg	Arg	Arg	Arg	Gly	Pro	Cys	Gly	Val	Arg
		35					40					45			
Leu	Leu	Cys	Ser	Pro	Arg	Arg	Pro	Ala	Leu	Leu	Gly	Gly	Arg	Arg	Phe
	50					55					60				



(2) INFORMATION FOR SEQ ID NO:4099:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..67  
(D) OTHER INFORMATION: / Ceres Seq. ID 1579496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4099:

[illegible]

(2) INFORMATION FOR SEO ID NO:4100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 737 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..737  
(D) OTHER INFORMATION: / Ceres Seq. ID 1579503

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4100:

atagaaagtt	gaaaggatga	agttagagga	tctcgttcca	ctgcgctacg	agacggcagc	60
gctgcggaac	aacaatggcg	atgatgcctc	ctgcagcggc	gtcatccctc	gcctccactc	120
cccgcggcat	cgcgcgtccg	cctactcgca	cggcatccct	gtgcatccgc	ttaggtgtcg	180
tgacggcgac	gctgttcgct	ggactggcgg	cggcgtcgca	gccagtggag	cgtcacgcgc	240
cggtggtggt	cgcgatggcg	aagagggagc	aggagctgga	ggggatccag	gccatcacga	300
cggaacagct	ggaggaggag	gtggtagacc	tcaaggggga	gcttttctcG	cttcgcctta	360
aGcgctcggc	gcgccaggag	tccaagaaca	gcgagttcgg	cgcgatgcgc	aagaggattg	420
ctcgtatggt	gactgtgaaa	agagagcggg	aaactgaaca	aggaataaac	aagagattgt	480
ccagggagct	tgataggaaa	tggaaagcagg	gcatttgtgt	cagaccacca	ccatctctaa	540
gggagaacaa	agaggagtag	agagctgcaa	aagaagcaat	ctgcaaaagt	cgtttcatgc	600
aagagtgttg	caagaagggt	cctttgtgat	tccaaacttt	atttcattgt	tacgtattcc	660
atgtttacat	tttactaagc	attgctatcc	gaatctgaat	ttcagtcggt	agtctcttct	720
gtaaatttga	tttatct					

(2) INFORMATION FOR SEQ ID NO:4101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..161  
(D) OTHER INFORMATION: / Ceres Seq. ID 1579504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4101:

[illegible]



(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..158

(D) OTHER INFORMATION: / Ceres Seq. ID 1579506

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4103:

Met Pro Pro Ala Ala Ala Ser Ser Leu Ala Ser Thr Pro Arg Gly Ile  
1 5 10 15  
Ala Ala Pro Pro Thr Arg Thr Ala Ser Leu Cys Ile Arg Leu Gly Val  
20 25 30  
Val Thr Ala Thr Leu Phe Ala Gly Leu Ala Ala Ala Ser Gln Pro Val  
35 40 45  
Glu Arg His Ala Ala Val Val Val Ala Met Ala Lys Arg Glu Gln Glu  
50 55 60  
Leu Glu Gly Ile Gln Ala Met Thr Thr Glu Gln Leu Glu Glu Glu Val  
65 70 75 80  
Val Asp Leu Lys Gly Glu Leu Phe Leu Leu Arg Leu Lys Arg Ser Ala  
85 90 95  
Arg Gln Glu Phe Lys Asn Ser Glu Phe Gly Arg Met Arg Lys Arg Ile  
100 105 110  
Ala Arg Met Leu Thr Val Lys Arg Glu Arg Glu Thr Glu Gln Gly Ile  
115 120 125  
Asn Lys Arg Leu Ser Arg Glu Leu Asp Arg Lys Trp Lys Gln Gly Ile  
130 135 140  
Val Val Arg Pro Pro Pro Ser Leu Arg Glu Asn Lys Glu Glu  
145 150 155

(2) INFORMATION FOR SEQ ID NO:4104:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 456 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..456

(D) OTHER INFORMATION: / Ceres Seq. ID 1579543

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4104:

agccgtcatc gtttcgcgctc tgcctcagcc cgccgcaagg agaggagaca tcttcgagaa 60  
gctgaaatgg ctccctaaagc tgctcctgcc aagaagggtg atgccaagac ccaggccttg 120  
aagggttgcca aggctgtgaa gtctggggca gccaagaaga agaccaagaa gatccgcacg 180  
tgtgtgacat ttcaccgccc cagcaccctg aagaaggcta gggaccccaa gtaccacga 240  
atcagcacta ccggaaggaa caagcttgat cagtaccaa ttctcaagta ccccttacc 300  
acagaatcag cgatgaagaa gattgaagat aacaacactc tggctctcat tgttgacctc 360  
aaggcagaca agaagaagat caaggctgcc gtcaagaaga tgtatgacat ccaggcaaa 420  
aaggtaaca ccttgatcag gcctgatggg aagaag

(2) INFORMATION FOR SEQ ID NO:4105:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 152 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..152

(D) OTHER INFORMATION: / Ceres Seq. ID 1579544

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4105:

Ser Arg His Arg Phe Ala Ser Ala Ser Ala Arg Arg Lys Glu Arg Arg  
1 5 10 15  
His Leu Arg Glu Ala Glu Met Ala Pro Lys Ala Ala Pro Ala Lys Lys  
20 25 30

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Gly Asp Ala Lys Thr Gln Ala Leu Lys Val Ala Lys Ala Val Lys Ser  
35 40 45  
Gly Ala Ala Lys Lys Lys Thr Lys Lys Ile Arg Thr Ser Val Thr Phe  
50 55 60  
His Arg Pro Thr Thr Leu Lys Lys Ala Arg Asp Pro Lys Tyr Pro Arg  
65 70 75 80  
Ile Ser Thr Thr Gly Arg Asn Lys Leu Asp Gln Tyr Gln Ile Leu Lys  
85 90 95  
Tyr Pro Leu Thr Thr Glu Ser Ala Met Lys Lys Ile Glu Asp Asn Asn  
100 105 110  
Thr Leu Val Phe Ile Val Asp Leu Lys Ala Asp Lys Lys Lys Ile Lys  
115 120 125  
Ala Ala Val Lys Lys Met Tyr Asp Ile Gln Ala Lys Lys Val Asn Thr  
130 135 140  
Leu Ile Arg Pro Asp Gly Lys Lys  
145 150

(2) INFORMATION FOR SEQ ID NO:4106:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 130 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..130

(D) OTHER INFORMATION: / Ceres Seq. ID 1579545

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4106:

Met Ala Pro Lys Ala Ala Pro Ala Lys Lys Gly Asp Ala Lys Thr Gln  
1 5 10 15  
Ala Leu Lys Val Ala Lys Ala Val Lys Ser Gly Ala Ala Lys Lys Lys  
20 25 30  
Thr Lys Lys Ile Arg Thr Ser Val Thr Phe His Arg Pro Thr Thr Leu  
35 40 45  
Lys Lys Ala Arg Asp Pro Lys Tyr Pro Arg Ile Ser Thr Thr Gly Arg  
50 55 60  
Asn Lys Leu Asp Gln Tyr Gln Ile Leu Lys Tyr Pro Leu Thr Thr Glu  
65 70 75 80  
Ser Ala Met Lys Lys Ile Glu Asp Asn Asn Thr Leu Val Phe Ile Val  
85 90 95  
Asp Leu Lys Ala Asp Lys Lys Lys Ile Lys Ala Ala Val Lys Lys Met  
100 105 110  
Tyr Asp Ile Gln Ala Lys Lys Val Asn Thr Leu Ile Arg Pro Asp Gly  
115 120 125  
Lys Lys  
130

(2) INFORMATION FOR SEQ ID NO:4107:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 445 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..445

(D) OTHER INFORMATION: / Ceres Seq. ID 1579546

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4107:

aaaaaaacc	tactaacgc	gtctcctctc	cagcgccgc	cgtcgccgc	gccctcctct	60
tggtccgc	gtccgtcgag	gtcatcatgg	tgagggtcag	tgtgctcaac	gatgcgtca	120
agtccatgta	caatgcagag	aagaggggca	agaggcaggt	catgatcagg	ccgtcgtcca	180



tggttcgcgc agcaccagca ccacgaggcc gccttcgcgc cgcgcgcga cgccgagctc 300  
gacgtgcgcg cgctcctccc cgacgactcc gtcgacctcc tcgacaccga cgacctcttc 360  
tacgcgcctg acgtccacca cccccacaac gccaaagccg cgctgctgcc cgggtacgac 420  
ctcgacatgc tcagggcgct gaggctcagc tccccccggg ccg

(2) INFORMATION FOR SEQ ID NO:4111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..115

(D) OTHER INFORMATION: / Ceres Seq. ID 1579570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4111:

Met Ala Thr Ser Ser Leu Asn Pro Asn Ala Pro Leu Phe Ile Pro Ala  
1 5 10 15  
Ala Tyr Arg Gln Val Glu Glu Phe Ser Pro Glu Trp Tyr Glu Leu Val  
20 25 30  
Asn Thr Thr Ala Trp Phe Arg Asp His Trp Phe Arg Gln His Gln His  
35 40 45  
His Glu Ala Ala Phe Ala Ala Ala Ala Asp Ala Glu Leu Asp Val Ala  
50 55 60  
Ala Leu Leu Pro Asp Asp Ser Val Asp Leu Leu Asp Thr Asp Asp Leu  
65 70 75 80  
Phe Tyr Ala Pro Asp Val His His Pro His Asn Ala Lys Pro Ala Leu  
85 90 95  
Leu Pro Gly Tyr Asp Leu Asp Met Leu Arg Ala Leu Ser Leu Ser Ser  
100 105 110  
Pro Arg Ala  
115

(2) INFORMATION FOR SEQ ID NO:4112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..79

(D) OTHER INFORMATION: / Ceres Seq. ID 1579571

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4112:

Met Ser Ser Ser Thr Pro Pro Pro Gly Ser Gly Thr Thr Gly Ser Ala  
1 5 10 15  
Ser Thr Ser Thr Thr Arg Pro Pro Ser Pro Pro Pro Pro Thr Pro Ser  
20 25 30  
Ser Thr Ser Pro Arg Ser Ser Pro Thr Thr Pro Ser Thr Ser Ser Thr  
35 40 45  
Pro Thr Thr Ser Ser Thr Arg Leu Thr Ser Thr Thr Pro Thr Thr Pro  
50 55 60  
Ser Arg Arg Cys Cys Pro Gly Thr Thr Ser Thr Cys Ser Gly Arg  
65 70 75

(2) INFORMATION FOR SEQ ID NO:4113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..478

(D) OTHER INFORMATION: / Ceres Seq. ID 1579576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4113:

aaaaaaacgc	ccaccacgcc	gccactcgca	accgcacacc	agccctcgca	acccaccacc	60
acgtccgaga	cgcccgagat	ggagttcctc	gccgcgtacc	tgctgccgtg	cctgggcgcc	120
ggccccggccc	ccacgctccc	gaccaaggac	gacgtgcgtc	gcattcctgag	atccgtcagc	180
gccgaggtgg	aggaggaccg	cctcgacctg	gtcttcgccc	tcctagaggt	taaggacatc	240
gccgagctga	tcgccacggg	cggggagcat	ctcgcctacg	cgccgtcagg	agccgctgct	300
gccgtcgttg	ccactcctgc	cgtgcgcgag	gtcgaggagg	aggccacgaa	ggaggaggat	360
gaggacatcg	ccctcttcaa	cctcttcgac	tgatcgtgca	accctacgtg	gaccgatcga	420
tgccatcctc	gtccttgcc	gtgcgcgttt	gcttggtgct	ctgattgtac	attgtagt	

(2) INFORMATION FOR SEQ ID NO:4114:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 130 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..130

(D) OTHER INFORMATION: / Ceres Seq. ID 1579577

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4114:

Lys	Lys	Thr	Pro	Thr	Thr	Pro	Pro	Leu	Ala	Thr	Ala	His	Gln	Pro	Ser	
1			5					10						15		
Gln	Pro	Thr	Thr	Ser	Glu	Thr	Ser	Glu	Met	Glu	Phe	Leu	Ala	Ala		
			20					25				30				
Tyr	Leu	Leu	Pro	Cys	Leu	Gly	Ala	Gly	Pro	Ala	Pro	Thr	Leu	Pro	Thr	
			35				40					45				
Lys	Asp	Asp	Val	Arg	Arg	Ile	Leu	Arg	Ser	Val	Ser	Ala	Glu	Val	Glu	
			50				55				60					
Glu	Asp	Arg	Leu	Asp	Leu	Val	Phe	Ala	Leu	Leu	Glu	Val	Lys	Asp	Ile	
65						70				75					80	
Ala	Glu	Leu	Ile	Ala	Thr	Gly	Gly	Glu	His	Leu	Ala	Tyr	Ala	Pro	Ser	
			85						90					95		
Gly	Ala	Ala	Ala	Ala	Val	Val	Ala	Thr	Pro	Ala	Ala	Ala	Glu	Val	Glu	
			100					105					110			
Glu	Glu	Ala	Thr	Lys	Glu	Glu	Asp	Glu	Asp	Ile	Ala	Leu	Phe	Asn	Leu	
			115				120					125				
Phe	Asp															
130																

(2) INFORMATION FOR SEQ ID NO:4115:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 76 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..76

(D) OTHER INFORMATION: / Ceres Seq. ID 1579578

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4115:

Lys	Asn	Ala	His	His	Ala	Ala	Thr	Arg	Asn	Arg	Thr	Pro	Ala	Leu	Ala	
1			5						10					15		
Thr	His	His	His	Val	Arg	Asp	Val	Arg	Asp	Gly	Val	Pro	Arg	Arg	Val	
			20					25				30				
Pro	Ala	Ala	Val	Pro	Gly	Arg	Arg	Pro	Gly	Pro	His	Ala	Pro	Asp	Gln	
			35				40					45				

Gly Arg Arg Ala Ser His Pro Glu Ile Arg Gln Arg Arg Gly Gly Gly  
50 55 60  
Gly Pro Pro Arg Pro Gly Leu Arg Pro Pro Arg Gly  
65 70 75

(2) INFORMATION FOR SEQ ID NO:4116:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 104 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..104
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1579579
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4116:

Met Glu Phe Leu Ala Ala Tyr Leu Leu Pro Cys Leu Gly Ala Gly Pro  
1 5 10 15  
Ala Pro Thr Leu Pro Thr Lys Asp Asp Val Arg Arg Ile Leu Arg Ser  
20 25 30  
Val Ser Ala Glu Val Glu Glu Asp Arg Leu Asp Leu Val Phe Ala Leu  
35 40 45  
Leu Glu Val Lys Asp Ile Ala Glu Leu Ile Ala Thr Gly Gly Glu His  
50 55 60  
Leu Ala Tyr Ala Pro Ser Gly Ala Ala Ala Val Val Ala Thr Pro  
65 70 75 80  
Ala Ala Ala Glu Val Glu Glu Glu Ala Thr Lys Glu Glu Asp Glu Asp  
85 90 95  
Ile Ala Leu Phe Asn Leu Phe Asp  
100

(2) INFORMATION FOR SEQ ID NO:4117:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 448 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..448
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1579584
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4117:

gctgtctttc ttctgctctt ccacgcgcgc agtggttttga gaagctggtc ggcgctccta	60
gatcccttcg cctctctcgc gttcgaggct aggtagccgc caccatgagc cgctcggggc	120
agcctocgga tctcaagaag tacatggaca agaagcttca gattaagctg aatgcaaacc	180
gtgttggttat tggcacactt cggggattcg accagttcat gaatctggtg atcgacaaca	240
ctgtggagggt caatggaaat gacaagacag atattggaat ggtgggttatc aggggaaaca	300
gtgttggtcat gatcgaggca ctggagccag ttgccaagtc gcagtgaatc cttatttttc	360
agctgatata gtcgcagcat gaaaactgat gtaaagtcta tgagtgaacc ctgttggtact	420
tgcatttgta attgaagtct gtcgcttt	

(2) INFORMATION FOR SEQ ID NO:4118:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 80 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..80
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1579585



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4118:

Met	Ser	Arg	Ser	Gly	Gln	Pro	Pro	Asp	Leu	Lys	Lys	Tyr	Met	Asp	Lys
1				5					10					15	
Lys	Leu	Gln	Ile	Lys	Leu	Asn	Ala	Asn	Arg	Val	Val	Ile	Gly	Thr	Leu
			20					25					30		
Arg	Gly	Phe	Asp	Gln	Phe	Met	Asn	Leu	Val	Ile	Asp	Asn	Thr	Val	Glu
		35					40					45			
Val	Asn	Gly	Asn	Asp	Lys	Thr	Asp	Ile	Gly	Met	Val	Val	Ile	Arg	Gly
	50					55				60					
Asn	Ser	Val	Val	Met	Ile	Glu	Ala	Leu	Glu	Pro	Val	Ala	Lys	Ser	Gln
65					70					75					80

(2) INFORMATION FOR SEQ ID NO:4119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..67
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579586

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4119:

Met	Asp	Lys	Lys	Leu	Gln	Ile	Lys	Leu	Asn	Ala	Asn	Arg	Val	Val	Ile
1				5					10					15	
Gly	Thr	Leu	Arg	Gly	Phe	Asp	Gln	Phe	Met	Asn	Leu	Val	Ile	Asp	Asn
			20					25					30		
Thr	Val	Glu	Val	Asn	Gly	Asn	Asp	Lys	Thr	Asp	Ile	Gly	Met	Val	Val
		35					40					45			
Ile	Arg	Gly	Asn	Ser	Val	Val	Met	Ile	Glu	Ala	Leu	Glu	Pro	Val	Ala
	50					55				60					
Lys	Ser	Gln													
65															

(2) INFORMATION FOR SEQ ID NO:4120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..42
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579587

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4120:

Met	Asn	Leu	Val	Ile	Asp	Asn	Thr	Val	Glu	Val	Asn	Gly	Asn	Asp	Lys
1				5					10					15	
Thr	Asp	Ile	Gly	Met	Val	Val	Ile	Arg	Gly	Asn	Ser	Val	Val	Met	Ile
			20					25					30		
Glu	Ala	Leu	Glu	Pro	Val	Ala	Lys	Ser	Gln						
		35					40								

(2) INFORMATION FOR SEQ ID NO:4121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 517 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..517

(D) OTHER INFORMATION: / Ceres Seq. ID 1579596

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4121:

ccgtgaaacc aacgcccctc tctccccgcg cagagaccc atcgcgaaatg gaagttgctc	60
ctgcggtgaa gcaactcctc cccatggcgc agggcccca ctccccgtcc tctccacca	120
cctcctcctc gccctcgccc tcggccgcgc cgcggtcccc gccgcccgcg cagcagcagt	180
cgcagtcgca ggcgcccgtg ccgcgcacatc togcacaccac gcccttcccc accaccttcg	240
tgcaggccga cacggccagc ttcaaggagg tgcgtccagag gctcaccggc tccgacacgc	300
cgccgcctgc ccagaagccc gccaaagccc acggccacca ccaccaccac cacggcggcg	360
gcggcgctcg gcccaagaag ccggccttca agctctacga gcgccggatc ggcaagaaca	420
acctcaagat gatcgcgccg ctggcggggc cgtcgccgcg gaaggcggcg ccggagggtc	480
tgctgcccag cgtgctcgac ttccctttcn ctggcgc	

(2) INFORMATION FOR SEQ ID NO:4122:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 172 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..172

(D) OTHER INFORMATION: / Ceres Seq. ID 1579597

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4122:

Arg	Glu	Thr	Asn	Ala	Pro	Leu	Ser	Pro	Arg	Thr	Arg	Pro	Ile	Ala	Asn	
1			5					10						15		
Gly	Ser	Cys	Ser	Cys	Gly	Glu	Ala	Thr	Pro	Pro	His	Gly	Ala	Gly	Pro	
			20					25				30				
Gln	Leu	Pro	Val	Leu	Leu	His	His	Leu	Leu	Leu	Ala	Leu	Ala	Leu	Gly	
			35				40					45				
Arg	Arg	Ala	Val	Pro	Ala	Ala	Ala	Pro	Ala	Ala	Val	Ala	Val	Ala	Gly	
			50				55				60					
Ala	Arg	Ala	Ala	His	His	Arg	His	His	Ala	Leu	Pro	His	His	Leu	Arg	
65						70				75				80		
Ala	Gly	Arg	His	Gly	Gln	Leu	Gln	Gly	Gly	Arg	Pro	Glu	Ala	His	Arg	
			85					90						95		
Leu	Arg	His	Ala	Ala	Ala	Cys	Pro	Glu	Ala	Arg	Gln	Asp	Pro	Arg	Pro	
			100					105					110			
Pro	Pro	Pro	Pro	Pro	Arg	Arg	Arg	Arg	Arg	Arg	Ala	Gln	Glu	Ala	Gly	
			115					120					125			
Leu	Gln	Ala	Leu	Arg	Ala	Pro	Asp	Arg	Gln	Glu	Gln	Pro	Gln	Asp	Asp	
			130				135				140					
Arg	Ala	Ala	Gly	Gly	Ala	Val	Ala	Ala	Glu	Gly	Ala	Gly	Gly	Ala		
145					150				155					160		
Val	Ala	Gln	Arg	Ala	Arg	Leu	Pro	Phe	Xaa	Trp	Arg					
			165					170								

(2) INFORMATION FOR SEQ ID NO:4123:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 171 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..171

(D) OTHER INFORMATION: / Ceres Seq. ID 1579598

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4123:

Val	Lys	Pro	Thr	Pro	Leu	Ser	Pro	Arg	Ala	Arg	Asp	Pro	Ser	Arg	Met	
1				5				10					15			

Glu Val Ala Pro Ala Val Lys Gln Leu Leu Pro Met Ala Gln Gly Pro  
20 25 30  
Asn Ser Pro Ser Ser Ser Thr Thr Ser Ser Ser Pro Ser Pro Ser Ala  
35 40 45  
Ala Ala Pro Ser Pro Pro Pro Arg Gln Gln Gln Ser Gln Ser Gln Ala  
50 55 60  
Pro Val Pro Arg Ile Ile Asp Thr Thr Pro Phe Pro Thr Thr Phe Val  
65 70 75 80  
Gln Ala Asp Thr Ala Ser Phe Lys Glu Val Val Gln Arg Leu Thr Gly  
85 90 95  
Ser Asp Thr Pro Pro Pro Ala Gln Lys Pro Ala Lys Thr His Gly His  
100 105 110  
His His His His His Gly Gly Gly Gly Val Gly Pro Lys Lys Pro Ala  
115 120 125  
Phe Lys Leu Tyr Glu Arg Arg Ile Gly Lys Asn Asn Leu Lys Met Ile  
130 135 140  
Ala Pro Leu Ala Gly Pro Ser Pro Arg Lys Ala Ala Pro Glu Val Leu  
145 150 155 160  
Ser Pro Ser Val Leu Asp Phe Pro Phe Xaa Gly  
165 170

(2) INFORMATION FOR SEQ ID NO:4124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..156
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579599

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4124:

Met Glu Val Ala Pro Ala Val Lys Gln Leu Leu Pro Met Ala Gln Gly  
1 5 10 15  
Pro Asn Ser Pro Ser Ser Ser Thr Thr Ser Ser Ser Pro Ser Pro Ser  
20 25 30  
Ala Ala Ala Pro Ser Pro Pro Pro Arg Gln Gln Gln Ser Gln Ser Gln  
35 40 45  
Ala Pro Val Pro Arg Ile Ile Asp Thr Thr Pro Phe Pro Thr Thr Phe  
50 55 60  
Val Gln Ala Asp Thr Ala Ser Phe Lys Glu Val Val Gln Arg Leu Thr  
65 70 75 80  
Gly Ser Asp Thr Pro Pro Pro Ala Gln Lys Pro Ala Lys Thr His Gly  
85 90 95  
His His His His His Gly Gly Gly Gly Val Gly Pro Lys Lys Pro  
100 105 110  
Ala Phe Lys Leu Tyr Glu Arg Arg Ile Gly Lys Asn Asn Leu Lys Met  
115 120 125  
Ile Ala Pro Leu Ala Gly Pro Ser Pro Arg Lys Ala Ala Pro Glu Val  
130 135 140  
Leu Ser Pro Ser Val Leu Asp Phe Pro Phe Xaa Gly  
145 150 155

(2) INFORMATION FOR SEQ ID NO:4125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..487

(D) OTHER INFORMATION: / Ceres Seq. ID 1579610

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4125:

attccgagtc tactattgta cctctccgtg gggcgcatcc gccatttgtg ccaattctag	60
catcagcgtc cgatcgacca ggagtgtgaa gtaggtgtgg gagatcaagg gcacgagcga	120
cccggccaag tttagtgtgg attttaaaat caagttcctt acagttggtg gaaagaaact	180
aaagttgaca atatgggata ccgctggcca ggagaggttt aggacaataa ctagttctta	240
ctacagaggt gctcagggaa ttattttagt atatgatgtc acaaagagag agagtttctc	300
aaatttggct gatgtttgga ctaaggaaat agaagcaaac tcaacaaaca aagactgcat	360
aaaaatgctt gttggaaaca aagttgacaa ggatgatgaa agaatggtca cagaagaaga	420
aggtcttgct tttgctgaag aatctggttg tctgtttctt gagagcagtg caaaacacga	480
gaaaatg	

(2) INFORMATION FOR SEQ ID NO:4126:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..30

(D) OTHER INFORMATION: / Ceres Seq. ID 1579611

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4126:

Phe Arg Val Tyr Tyr Cys Thr Ser Pro Trp Gly Arg Ser Ala Ile Cys	
1 5 10 15	
Ala Asn Ser Ser Ile Ser Val Arg Ser Thr Arg Ser Val Lys	
20 25 30	

(2) INFORMATION FOR SEQ ID NO:4127:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..41

(D) OTHER INFORMATION: / Ceres Seq. ID 1579612

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4127:

Met Leu Val Gly Asn Lys Val Asp Lys Asp Asp Glu Arg Met Val Thr	
1 5 10 15	
Glu Glu Glu Gly Leu Ala Phe Ala Glu Ser Gly Cys Leu Phe Leu	
20 25 30	
Glu Ser Ser Ala Lys His Glu Lys Met	
35 40	

(2) INFORMATION FOR SEQ ID NO:4128:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..31

(D) OTHER INFORMATION: / Ceres Seq. ID 1579613

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4128:

Met Met Lys Glu Trp Ser Gln Lys Lys Lys Val Leu Leu Leu Lys	
1 5 10 15	
Asn Leu Val Val Cys Phe Leu Arg Ala Val Gln Asn Thr Arg Lys	

```

(2) INFORMATION FOR SEQ ID NO:4130:
  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 127 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS:
      (D) TOPOLOGY: linear
  (ii) MOLECULE TYPE: peptide
  (ix) FEATURE:
      (A) NAME/KEY: peptide
      (B) LOCATION: 1..127
      (D) OTHER INFORMATION: / Ceres Seq. ID 1579615
  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4130:
Met Ser Ile Leu Arg Ala Pro Pro Pro Cys Phe Ser Ser Pro Leu Arg
1          5          10          15
Leu Arg Val Ala Val Ala Lys Pro Leu Ala Ala Pro Met Arg Arg Gln
          20          25          30
Leu Leu Arg Ala Gln Ala Thr Tyr Asn Val Lys Leu Ile Thr Pro Glu
          35          40          45
Gly Glu Val Glu Leu Gln Val Pro Asp Asp Val Tyr Ile Leu Asp Phe
          50          55          60
Ala Glu Glu Glu Gly Ile Asp Leu Pro Phe Ser Cys Arg Ala Gly Ser
65          70          75          80
Cys Ser Ser Cys Ala Gly Lys Val Val Ser Gly Ser Val Asp Gln Ser
          85          90          95
Asp Gln Ser Phe Leu Asn Asp Asn Gln Val Ala Asp Gly Trp Val Leu
          100         105         110
Thr Ala Leu Arg Thr Pro Pro Thr Ser Ser Ser Arg Arg Thr
          115         120         125

```

```
(2) INFORMATION FOR SEQ ID NO:4131:
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 99 amino acids
            (B) TYPE: amino acid
            (C) STRANDEDNESS:
            (D) TOPOLOGY: linear
      (ii) MOLECULE TYPE: peptide
      (ix) FEATURE:
            (A) NAME/KEY: peptide
            (B) LOCATION: 1..99
            (D) OTHER INFORMATION: / Ceres Seq. ID 1579616
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4131:

```
Met Arg Arg Gln Leu Leu Arg Ala Gln Ala Thr Tyr Asn Val Lys Leu
1          5          10          15
Ile Thr Pro Glu Gly Glu Val Glu Leu Gln Val Pro Asp Asp Val Tyr
          20          25          30
Ile Leu Asp Phe Ala Glu Glu Glu Gly Ile Asp Leu Pro Phe Ser Cys
          35          40          45
Arg Ala Gly Ser Cys Ser Ser Cys Ala Gly Lys Val Val Ser Gly Ser
          50          55          60
Val Asp Gln Ser Asp Gln Ser Phe Leu Asn Asp Asn Gln Val Ala Asp
65          70          75          80
Gly Trp Val Leu Thr Ala Leu Arg Thr Pro Pro Pro Thr Ser Ser Ser
          85          90          95
Arg Arg Thr
```

(2) INFORMATION FOR SEQ ID NO:4132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..468
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579618

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4132:

```
acacaatttc accgaaatcc tccaatacc caccctacga atcttcttct cgggctcctt      60
ctgcgccatc ttctggctca agaagcgcg cctcatgccg ggcctcactt tctctaata      120
gctcatctcc cgggacgagg gcctccactg cgacttcgcc tgccctcctt atgacctcct      180
tcggggcaag ctcgatgagt cccgcgtccg cgagatcggt gccgacgccg tcgacatcga      240
gcgtgagttc gtttgcgacg cgctccccgt cgcgctggtc ggaatgaacg gcgggctcat      300
gagccagtac atcgagttcg tcgcgcaccg cctgctcatg gcgctggggc acaggaagat      360
gtacaacgtc gccaacccct tcgactggat ggagctcatt tccctgcagg ccaaagacta      420
acttctttga gaagcgcgtc gggwagtacc agaagcgctc cgtaatgt
```

(2) INFORMATION FOR SEQ ID NO:4133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..139
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579619

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4133:

```
His Asn Phe Thr Glu Ile Leu Gln Tyr Pro Thr Leu Arg Ile Phe Phe
1          5          10          15
Ser Gly Ser Phe Cys Ala Ile Phe Trp Leu Lys Lys Arg Gly Leu Met
          20          25          30
Pro Gly Leu Thr Phe Ser Asn Glu Leu Ile Ser Arg Asp Glu Gly Leu
          35          40          45
His Cys Asp Phe Ala Cys Leu Leu Tyr Asp Leu Leu Arg Gly Lys Leu
50          55          60
Asp Glu Ser Arg Val Arg Glu Ile Val Ala Asp Ala Val Asp Ile Glu
65          70          75          80
Arg Glu Phe Val Cys Asp Ala Leu Pro Val Ala Leu Val Gly Met Asn
          85          90          95
Gly Gly Leu Met Ser Gln Tyr Ile Glu Phe Val Ala Asp Arg Leu Leu
          100          105          110
```

Met Ala Leu Gly His Arg Lys Met Tyr Asn Val Ala Asn Pro Phe Asp  
115 120 125

Trp Met Glu Leu Ile Ser Leu Gln Ala Lys Asp  
130 135

(2) INFORMATION FOR SEQ ID NO:4134:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 94 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..94

(D) OTHER INFORMATION: / Ceres Seq. ID 1579620

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4134:

Thr Ile Ser Pro Lys Ser Ser Asn Thr Pro Pro Tyr Glu Ser Ser Ser  
1 5 10 15  
Arg Ala Pro Ser Ala Pro Ser Ser Gly Ser Arg Ser Ala Ala Ser Cys  
20 25 30  
Arg Ala Ser Leu Ser Leu Met Ser Ser Ser Pro Gly Thr Arg Ala Ser  
35 40 45  
Thr Ala Thr Ser Pro Ala Ser Phe Met Thr Ser Phe Gly Ala Ser Ser  
50 55 60  
Met Ser Pro Ala Ser Ala Arg Ser Leu Pro Thr Pro Ser Thr Ser Ser  
65 70 75 80  
Val Ser Ser Phe Ala Thr Arg Ser Pro Ser Arg Trp Ser Glu  
85 90

(2) INFORMATION FOR SEQ ID NO:4135:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..108

(D) OTHER INFORMATION: / Ceres Seq. ID 1579621

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4135:

Met Pro Gly Leu Thr Phe Ser Asn Glu Leu Ile Ser Arg Asp Glu Gly  
1 5 10 15  
Leu His Cys Asp Phe Ala Cys Leu Leu Tyr Asp Leu Leu Arg Gly Lys  
20 25 30  
Leu Asp Glu Ser Arg Val Arg Glu Ile Val Ala Asp Ala Val Asp Ile  
35 40 45  
Glu Arg Glu Phe Val Cys Asp Ala Leu Pro Val Ala Leu Val Gly Met  
50 55 60  
Asn Gly Gly Leu Met Ser Gln Tyr Ile Glu Phe Val Ala Asp Arg Leu  
65 70 75 80  
Leu Met Ala Leu Gly His Arg Lys Met Tyr Asn Val Ala Asn Pro Phe  
85 90 95  
Asp Trp Met Glu Leu Ile Ser Leu Gln Ala Lys Asp  
100 105

(2) INFORMATION FOR SEQ ID NO:4136:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 445 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..445

(D) OTHER INFORMATION: / Ceres Seq. ID 1579629

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4136:

aaggccagtc	tgagtgtg	cg	ttcgattcgc	ttgtgctgca	gctaggggtt	agagggtttc	60
tggg	cg	cgga	g	gggaggcg	gcggcg	gcta	120
aggagccgct	ggatctgata	cg	cctcagcc	tgcacgagcg	catctacgtc	aagctccgat	180
ccgaccgcga	gctgcgcggc	aagctccatg	cgtatgatca	acatttaa	ac	atgatacttg	240
gagatgttga	agaggtcgtg	acaactgttg	agatagatga	tgaacatat	ga	ga	300
tgcgcgataa	tctttgcaga	ccacgaaacg	cactatcccc	tttctttttg	tccgaggtga		360
tggtgtcata	ttggtttctc	cacccttcg	tacggcayga	astttgaagt	tagatcatgc		420
tggttggttaa	ttatgataac	tggtg					

(2) INFORMATION FOR SEQ ID NO:4137:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 134 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..134

(D) OTHER INFORMATION: / Ceres Seq. ID 1579630

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4137:

Gly	Gln	Ser	Glu	Cys	Ala	Phe	Asp	Ser	Leu	Val	Leu	Gln	Leu	Gly	Phe
1			5						10					15	
Arg	Gly	Phe	Leu	Gly	Ala	Glu	Arg	Glu	Ala	Ala	Ala	Ala	Met	Ala	Ala
			20					25					30		
Ala	Glu	Glu	Glu	Ile	Ala	Val	Lys	Glu	Pro	Leu	Asp	Leu	Ile	Arg	Leu
			35				40					45			
Ser	Leu	Asp	Glu	Arg	Ile	Tyr	Val	Lys	Leu	Arg	Ser	Asp	Arg	Glu	Leu
			50			55					60				
Arg	Gly	Lys	Leu	His	Ala	Tyr	Asp	Gln	His	Leu	Asn	Met	Ile	Leu	Gly
65					70					75				80	
Asp	Val	Glu	Glu	Val	Thr	Thr	Val	Glu	Ile	Asp	Asp	Glu	Thr	Tyr	
				85				90					95		
Glu	Glu	Ile	Val	Arg	Asp	Asn	Leu	Cys	Arg	Pro	Arg	Asn	Ala	Leu	Ser
			100				105					110			
Pro	Phe	Phe	Leu	Ser	Glu	Val	Met	Val	Ser	Tyr	Trp	Phe	Leu	His	Pro
			115				120					125			
Phe	Val	Arg	Xaa	Glu	Xaa										
			130												

(2) INFORMATION FOR SEQ ID NO:4138:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..105

(D) OTHER INFORMATION: / Ceres Seq. ID 1579631

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4138:

Met	Ala	Ala	Ala	Glu	Glu	Glu	Ile	Ala	Val	Lys	Glu	Pro	Leu	Asp	Leu
1				5					10					15	
Ile	Arg	Leu	Ser	Leu	Asp	Glu	Arg	Ile	Tyr	Val	Lys	Leu	Arg	Ser	Asp
			20					25				30			
Arg	Glu	Leu	Arg	Gly	Lys	Leu	His	Ala	Tyr	Asp	Gln	His	Leu	Asn	Met
			35				40					45			



Ile Leu Gly Asp Val Glu Glu Val Val Thr Thr Val Glu Ile Asp Asp  
50 55 60  
Glu Thr Tyr Glu Glu Ile Val Arg Asp Asn Leu Cys Arg Pro Arg Asn  
65 70 75 80  
Ala Leu Ser Pro Phe Phe Leu Ser Glu Val Met Val Ser Tyr Trp Phe  
85 90 95  
Leu His Pro Phe Val Arg Xaa Glu Xaa  
100 105

(2) INFORMATION FOR SEQ ID NO:4139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..408
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579632

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4139:

atataaaagc tgccctgcgc acctagcacc agccctgccca ctccactcct accccacaca	60
gaagcggcgg cggcggagca aasgcaggcg aaggcgaggg tgtgagggaa ggagcaccag	120
ccatggtgca cgtcaacttc taccgcaact atggtaagac gttcaagaaa ccaaggcgtc	180
cttatgagaa ggagcgtctt gatgctgaac tgaagctggc cggtgagtat gggctgaggt	240
gcaagcgtga gctttggagg gtccagtatg cactgagcag gatccgtaat gctgcaaggc	300
acttgctcac ccttgacgag aagaaccccc gtcgtatctt tgagggtgag gcgcttcttc	360
gccgcatgaa ccgctatggg ctgcttgctg agggtcagaa caagcttg	

(2) INFORMATION FOR SEQ ID NO:4140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..51
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579633

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4140:

Tyr Lys Ser Cys Pro Arg Asp Leu Ala Pro Ala Leu Pro Leu His Ser  
1 5 10 15  
Tyr Pro Thr Gln Lys Arg Arg Arg Arg Ser Lys Xaa Arg Arg Arg Arg  
20 25 30  
Gly Cys Glu Gly Arg Ser Thr Ser His Gly Ala Arg Gln Leu Leu Pro  
35 40 45  
Gln Leu Trp  
50

(2) INFORMATION FOR SEQ ID NO:4141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..95
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579634

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4141:

Met Val His Val Asn Phe Tyr Arg Asn Tyr Gly Lys Thr Phe Lys Lys  
1 5 10 15

(2) INFORMATION FOR SEO ID NO:4142:

(A) LENGTH: 467 base pairs

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

MOLECULE TYPE: DNA (g

## (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..467

(D) OTHER INFORMATION: / Ceres Seq. ID 1579635

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4142:

cgaaaaaatcc	atcgagctgc	cgcgcgcgcg	cagttaagct	cacacatcag	ctagctcacc	60
ttggacggcc	gaccaggtaac	gttgcgagcg	atggcgggat	acaaagcgtc	gggcggcacg	120
gcgctcggcg	tgtccttggc	tgttgccgcg	ctcctcgccg	cggcggcgat	ggcgggtggac	180
gacgagcaca	tgtacctctg	gaagtgtctc	aactcgtgca	cggggaagtg	ccgcgacgag	240
gacgcctttg	acgacggcca	ccgttcgggg	gattcgaaac	tctcttcctg	cgtctctggc	300
ggcaagtgca	acaacagggt	cctcagcgag	tgcttcgagg	acctgccggc	catctgctac	360
caccagtcgc	tgtcagcaca	gtgcctctgc	ttcccaccct	ttagcaaaaga	gaaaacgatg	420
tqcatgaaga	qctqctqcaa	caagtqcttc	caccacggcc	cqcaagc		

(2) INFORMATION FOR SEQ ID NO:4143:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..125

(D) OTHER INFORMATION: / Ceres Seq. ID 1579636

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4143:

Met	Ala	Gly	Tyr	Lys	Ala	Ser	Gly	Gly	Thr	Ala	Leu	Gly	Val	Val	Leu
1				5					10					15	
Ala	Val	Ala	Ala	Leu	Leu	Ala	Ala	Ala	Ala	Met	Ala	Val	Asp	Asp	Glu
		20					25					30			
His	Met	Tyr	His	Trp	Lys	Cys	Phe	Asn	Ser	Cys	Thr	Gly	Lys	Cys	Arg
		35					40					45			
Asp	Glu	Asp	Ala	Phe	Asp	Asp	Gly	His	Arg	Ser	Gly	Asp	Ser	Asn	Val
	50					55					60				
Ser	Ser	Val	Val	Ser	Gly	Gly	Lys	Cys	Asn	Asn	Arg	Cys	Leu	Ser	Glu
65					70					75					80
Cys	Phe	Glu	Asp	Leu	Pro	Ala	Ile	Cys	Tyr	His	Gln	Cys	Val	Val	Ser
				85					90					95	
Lys	Cys	Leu	Cys	Phe	Pro	Pro	Phe	Ser	Lys	Glu	Lys	Thr	Met	Cys	Met
			100				105					110			
Lys	Ser	Cys	Cys	Asn	Lys	Cys	Phe	His	His	Gly	Pro	Pro			
		115					120				125				

(2) INFORMATION FOR SEQ ID NO:4144:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 amino acids

[illegible]

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..99
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1579637
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4144:

Met Ala Val Asp Asp Glu His Met Tyr His Trp Lys Cys Phe Asn Ser  
1 5 10 15  
Cys Thr Gly Lys Cys Arg Asp Glu Asp Ala Phe Asp Asp Gly His Arg  
20 25 30  
Ser Gly Asp Ser Asn Val Ser Ser Val Val Ser Gly Gly Lys Cys Asn  
35 40 45  
Asn Arg Cys Leu Ser Glu Cys Phe Glu Asp Leu Pro Ala Ile Cys Tyr  
50 55 60  
His Gln Cys Val Val Ser Lys Cys Leu Cys Phe Pro Pro Phe Ser Lys  
65 70 75 80  
Glu Lys Thr Met Cys Met Lys Ser Cys Cys Asn Lys Cys Phe His His  
85 90 95  
Gly Pro Pro

- (2) INFORMATION FOR SEQ ID NO:4145:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 92 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..92
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1579638

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4145:  
Met Tyr His Trp Lys Cys Phe Asn Ser Cys Thr Gly Lys Cys Arg Asp  
1 5 10 15  
Glu Asp Ala Phe Asp Asp Gly His Arg Ser Gly Asp Ser Asn Val Ser  
20 25 30  
Ser Val Val Ser Gly Gly Lys Cys Asn Asn Arg Cys Leu Ser Glu Cys  
35 40 45  
Phe Glu Asp Leu Pro Ala Ile Cys Tyr His Gln Cys Val Val Ser Lys  
50 55 60  
Cys Leu Cys Phe Pro Phe Ser Lys Glu Lys Thr Met Cys Met Lys  
65 70 75 80  
Ser Cys Cys Asn Lys Cys Phe His His Gly Pro Pro  
85 90

- (2) INFORMATION FOR SEQ ID NO:4146:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 450 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..450
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1579643

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4146:  
atccggtccg gacaccgag taccgacctg cttgtctcatc gcgcgcaccc gccaaagcaa 60  
ccaaccgccc catcgtcccc gtctgttcc ggcaggcagc cgctcccgcct cccgctcccc 120

20250904 10:30

caccccactc cccctcgcgc ggcgcgttct cagatccccc gcccggttg caccggcacc 180  
ccggtccgaa atgcgaggag ccttgtagcg cctcggagca cggacggaat cgcgccgcat 240  
gcatcccaag cccgagggcg gcggcgacga cgacggggcc gccgcggagg tgggctcccc 300  
gcggtccggc tacttcggc agcggagcat gcacgccgcc gccgcgcccg cggatccgga 360  
ggcggcgcg cgcgcgttcc acgtcgagaa cccgccttgc tccgcggcg gggggctgcg 420  
gccagcgagt ccgtcaccaa gctggagtcg

(2) INFORMATION FOR SEQ ID NO:4147:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..150

(D) OTHER INFORMATION: / Ceres Seq. ID 1579644

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4147:

Ile Arg Ser Gly His Pro Ser Thr Asp Leu Leu Ala His Arg Ala His  
1 5 10 15  
Pro Pro Lys Gln Pro Thr Ala Pro Ser Ser Pro Ser Cys Ser Gly Arg  
20 25 30  
Gln Pro Leu Pro Leu Pro Leu Pro His Pro Thr Pro Pro Arg Ala Ala  
35 40 45  
Arg Ser Gln Ile Pro Arg Pro Val Gly Thr Gly Thr Pro Val Arg Asn  
50 55 60  
Ala Arg Ser Leu Val Ala Pro Arg Ser Thr Asp Gly Ile Ala Pro His  
65 70 75 80  
Ala Ser Gln Ala Arg Gly Arg Arg Arg Arg Arg Gly Arg Arg Gly  
85 90 95  
Gly Gly Leu Pro Ala Val Arg Leu Leu Pro Ala Ala Glu His Ala Arg  
100 105 110  
Arg Arg Arg Arg Arg Gly Ser Gly Gly Gly Ala Pro Ala Val Pro Arg  
115 120 125  
Arg Glu Pro Ala Leu Leu Arg Arg Gly Ala Ala Ala Ser Glu Ser  
130 135 140  
Val Thr Lys Leu Glu Ser  
145 150

(2) INFORMATION FOR SEQ ID NO:4148:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..149

(D) OTHER INFORMATION: / Ceres Seq. ID 1579645

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4148:

Pro Val Arg Thr Pro Glu Tyr Arg Pro Ala Cys Ser Ser Arg Ala Pro  
1 5 10 15  
Ala Lys Ala Thr Asn Arg Pro Ile Val Pro Val Leu Phe Arg Gln Ala  
20 25 30  
Ala Ala Pro Ala Pro Ala Pro Pro His Ser Pro Ser Arg Gly Ala  
35 40 45  
Phe Ser Asp Pro Pro Pro Gly Trp His Arg His Pro Gly Pro Lys Cys  
50 55 60  
Glu Glu Pro Cys Ser Ala Ser Glu His Gly Arg Asn Arg Ala Ala Cys  
65 70 75 80  
Ile Pro Ser Pro Arg Ala Ala Ala Thr Thr Thr Gly Pro Pro Arg Arg

85 90 95  
Trp Ala Pro Arg Gly Pro Ala Thr Ser Gly Ser Gly Ala Cys Thr Pro  
100 105 110  
Pro Pro Pro Pro Arg Ile Arg Arg Arg Arg Ala Gly Arg Ser Thr Ser  
115 120 125  
Arg Thr Arg Leu Ala Pro Pro Ala Gly Gly Cys Gly Gln Arg Val Arg  
130 135 140  
His Gln Ala Gly Val  
145

(2) INFORMATION FOR SEQ ID NO:4149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..475
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579646

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4149:

cttcgacggc cacggcggcg ccgaggtggc cagctactgc cgggagaggc tccaggtgct	60
cctgagggcag gaactgaggc tgctcagcaa ggatttgggg gagacaagcg aggccgacat	120
gaaggagcac tgggacgagc tggtcaccag gtgtttccag aggctggatg acgaagtgtc	180
ggggcagggc agcaggctcg tcggtggcgt ccaggagaca cggccggtgg ccgccgagaa	240
cgtcggctcc actgcggttg tcgccgtcgt gtgctcctcc catgtggtgg tcgccaaactg	300
cggggattcg cgtgttggtt tctgccgtgg aaaggagccc ttagagctgt cgattgatca	360
taaggtgagc tttttttag ctaagctgga gctatgatgc ttatggtgtt catccgattt	420
ggttgtttca gcctgacagg aaggatgaac gagcgaggat tgaggccctg gggggg	

(2) INFORMATION FOR SEQ ID NO:4150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..131
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579647

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4150:

Phe Asp Gly His Gly Gly Ala Glu Val Ala Ser Tyr Cys Arg Glu Arg  
1 5 10 15  
Leu Gln Val Leu Leu Arg Gln Glu Leu Arg Leu Leu Ser Lys Asp Leu  
20 25 30  
Gly Glu Thr Ser Glu Ala Asp Met Lys Glu His Trp Asp Glu Leu Phe  
35 40 45  
Thr Arg Cys Phe Gln Arg Leu Asp Asp Glu Val Ser Gly Gln Ala Ser  
50 55 60  
Arg Leu Val Gly Gly Val Gln Glu Thr Arg Pro Val Ala Ala Glu Asn  
65 70 75 80  
Val Gly Ser Thr Ala Val Val Ala Val Val Cys Ser Ser His Val Val  
85 90 95  
Val Ala Asn Cys Gly Asp Ser Arg Val Val Leu Cys Arg Gly Lys Glu  
100 105 110  
Pro Leu Glu Leu Ser Ile Asp His Lys Val Ser Phe Phe Val Ala Lys  
115 120 125  
Leu Glu Leu  
130

(2) INFORMATION FOR SEQ ID NO:4151:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..92  
(D) OTHER INFORMATION: / Ceres Seq. ID 1579648  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4151:  
Met Lys Glu His Trp Asp Glu Leu Phe Thr Arg Cys Phe Gln Arg Leu  
1 5 10 15  
Asp Asp Glu Val Ser Gly Gln Ala Ser Arg Leu Val Gly Gly Val Gln  
20 25 30  
Glu Thr Arg Pro Val Ala Ala Glu Asn Val Gly Ser Thr Ala Val Val  
35 40 45  
Ala Val Val Cys Ser Ser His Val Val Val Ala Asn Cys Gly Asp Ser  
50 55 60  
Arg Val Val Leu Cys Arg Gly Lys Glu Pro Leu Glu Leu Ser Ile Asp  
65 70 75 80  
His Lys Val Ser Phe Phe Val Ala Lys Leu Glu Leu  
85 90

(2) INFORMATION FOR SEQ ID NO:4152:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 420 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..420  
(D) OTHER INFORMATION: / Ceres Seq. ID 1579700

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4152:

aaaaaaaaaca	cacggtacgc	gcttctctctc	ctcgcttgcc	gccgccgccg	ccgccgcgat	60
ggaaaaggag	aagctctcgt	tctccatata	ctcctcgaag	cagcggcccc	ccaagcctcc	120
cgcacgacct	gcggccgcgc	cagacgacga	tgacctccgc	tccgcgcccc	ctccgggccca	180
gcagtacgtc	accgagttcg	atccgtccca	aaccctagcc	gccgcctgcg	cggcgcgcgc	240
cgtcacgcgc	ccgctcccca	actccggcaa	ctycctcacc	caccgcccac	gcaaaccgtc	300
ctcgtcctcc	acccctgagg	aggaggccgc	cctcgccgcg	gaatccggcg	gctggggccc	360
cgcyttcgtc	ctcgacacct	cgaccgctcc	cgaagacca	tcattcaaaa	tcggctacgc	420

(2) INFORMATION FOR SEQ ID NO:4153:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 139 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..139  
(D) OTHER INFORMATION: / Ceres Seq. ID 1579701

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4153:

Lys Lys Thr His Gly Thr Arg Phe Ser Ser Ser Leu Ala Ala Ala Ala  
1 5 10 15  
Ala Ala Ala Met Glu Lys Glu Lys Leu Ser Phe Ser Ile Ser Ser Ser  
20 25 30  
Lys Gln Arg Pro Pro Lys Pro Pro Ala Arg Pro Ala Ala Ala Asp  
35 40 45  
Asp Asp Asp Leu Arg Ser Ala Pro Ala Pro Gly Gln Gln Tyr Val Thr

	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	2101	2102	2103	2104	2105	2106	2107	2108	2109	2110	2111	2112	2113	2114	2115	2116	2117	2118	2119	2120	2121	2122	2123	2124	2125	2126	2127	2128	2129	2130	2131	2132	2133	2134	2135	2136	2137	2138	2139	2140	2141	2142	2143	2144	2145	2146	2147	2148	2149	2150	2151	2152	2153	2154	2155	2156	2157	2158	2159	2160	2161	2162	2163	2164	2165	2166	2167	2168	2169	2170	2171	2172	2173	2174	2175	2176	2177	2178	2179	2180	2181	2182	2183	2184	2185	2186	2187	2188	2189	2190	2191	2192	2193	2194	2195	2196	2197	2198	2199	2200	2201	2202	2203	2204	2205	2206	2207	2208	2209	2210	2211	2212	2213	2214	2215	2216	2217	2218	2219	2220	2221	2222	2223	2224	2225	2226	2227	2228	2229	2230	2231	2232	2233	2234	2235	2236	2237	2238	2239	2240	2241	2242	2243	2244	2245	2246	2247	2248	2249	2250	2251	2252	2253	2254	2255	2256	2257	2258	2259	2260	2261	2262	2263	2264	2265	2266	2267	2268	2269	2270	2271	2272	2273	2274	2275	2276	2277	2278	2279	2280	2281	2282	2283	2284	2285	2286	2287	2288	2289	2290	2291	2292	2293	2294	2295	2296	2297	2298	2299	2300	2301	2302	2303	2304	2305	2306	2307	2308	2309	2310	2311	2312	2313	2314	2315	2316	2317	2318	2319	2320	2321	2322	2323	2324	2325	2326	2327	2328	2329	2330	2331	2332	2333	2334	2335	2336	2337	2338	2339	2340	2341	2342	2343	2344	2345	2346	2347	2348	2349	2350	2351	2352	2353	2354	2355	2356	2357	2358	2359	2360	2361	2362	2363	2364	2365	2366	2367	2368	2369	2370	2371	2372	2373	2374	2375	2376	2377	2378	2379	2380	2381	2382	2383	2384	2385	2386	2387	2388	2389	2390	2391	2392	2393	2394	2395	2396	2397	2398	2399	2400	2401	2402	2403	2404	2405	2406	2407	2408	2409	2410	2411	2412	2413	2414	2415	2416	2417	2418	2419	2420	2421	2422	2423	2424	2425	2426	2427	2428	2429	2430	2431	2432	2
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(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: DNA (genomic)

(A) NAME/KEY: -

- (B) LOCATION: 1..451

- (D) OTHER INFORMATION: / Ceres Seq. ID 1579709

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4156:

atgctggaga	tgatgataat	gatgatgatg	atgatgaacc	tctctttaat	gaagacgacg	60
acgaggagtt	agatgacctt	gagcaagggg	aggatgaacc	tmacacacaa	catcttgtac	120
ttgcacaatt	tgataaagtg	tcaaggacca	agaatcgttg	gaagtgcacc	ttgaaggatg	180
gaatcatgca	tttgaatggc	agggatgtcc	tttttaacaa	ggcgacaggt	gagtttgatt	240
tttgattttt	tgatgaaga	tgagctattt	tagaagcagc	tgtatggaca	tatctttgtc	300
ttgacataag	gacagggagg	tgacagtgtt	cttggtgggg	tcttggcagc	atgactgcgt	360
cgtgttttct	ttcctattga	atcttcgttc	caccctcttg	tttgtcaccg	caactgttat	420
cgctgtaaag	aagttactgc	tttgtctgtg	c			

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..80

- (D) OTHER INFORMATION: / Ceres Seq. ID 1579710

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4157:

Ala	Gly	Asp	Asp	Asp	Asn	Asp	Asp	Asp	Asp	Asp	Glu	Pro	Pro	Leu	Asn
1				5				10						15	
Glu	Asp	Asp	Asp	Glu	Glu	Leu	Asp	Asp	Leu	Glu	Gln	Gly	Glu	Asp	Glu
			20				25						30		
Pro	Xaa	Thr	Gln	His	Leu	Val	Leu	Ala	Gln	Phe	Asp	Lys	Val	Ser	Arg
		35					40					45			
Thr	Lys	Asn	Arg	Trp	Lys	Cys	Thr	Leu	Lys	Asp	Gly	Ile	Met	His	Leu
	50					55					60				
Asn	Gly	Arg	Asp	Val	Leu	Phe	Asn	Lys	Ala	Thr	Gly	Glu	Phe	Asp	Phe
65					70					75					80

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 440 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

- (B) LOCATION: 1..440

- (D) OTHER INFORMATION: / Ceres Seq. ID 1579711

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4158:

aggactctag	gagaactggg	acgacagcag	cggcgggcga	cggggatgag	aaccctgtac	60
tgtatttcgt	cgacctttgc	catggcgctg	togatgatga	gttctcgcgc	gggcgcggcg	120
gcggccggag	gaggagaaca	ccgcgctgag	cacgtcaccc	tggcgctcgg	tgggctgacg	180
cggccgagta	ctaggccctg	gccggggcga	gctggccac	ggcccgggac	gccgagccg	240
cggggacctg	ccgaagctgc	gggcggtccc	tcgtcttcgt	cggcgacggg	gcgcgcgggg	300



ccggagtgcactggtggggcgctgccgcgcggcagcagcgacgccgagcgggtcgagg360  
agcggcagggcgcggggcgcgcggtgccacgggcaaggggaaccgcga gctggtgaga420  
cgggcgctcagcggggcccg

(2) INFORMATION FOR SEQ ID NO:4159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..146
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579712

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4159:

Arg Thr Leu Gly Glu Leu Gly Arg Gln Gln Arg Arg Ala Thr Gly Met  
1 5 10 15  
Arg Thr Leu Tyr Cys Ile Ser Ser Thr Phe Ala Met Ala Ser Ser Met  
20 25 30  
Met Ser Ser Arg Ala Gly Ala Ala Ala Gly Gly Gly Glu His Arg  
35 40 45  
Arg Gln His Val Thr Val Ala Cys Gly Gly Leu Thr Arg Pro Ser Thr  
50 55 60  
Arg Pro Val Pro Gly Ala Ala Gly Pro Arg Pro Gly Thr Pro Arg Pro  
65 70 75 80  
Arg Gly Pro Ala Ala Ala Gly Gly Ser Ser Ser Ser Ser Pro Thr  
85 90 95  
Gly Arg Ala Gly Pro Glu Cys Asn Trp Trp Gly Ala Ala Ala Arg Gln  
100 105 110  
Gln Ala Thr Pro Arg Arg Ser Arg Ser Gly Arg Ala Ala Gly Ala Arg  
115 120 125  
Val Pro Thr Gly Lys Gly Asn Arg Glu Leu Val Arg Arg Ala Leu Thr  
130 135 140  
Pro Ala  
145

(2) INFORMATION FOR SEQ ID NO:4160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..146
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579713

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4160:

Asp Ser Arg Arg Thr Gly Thr Thr Ala Ala Ala Gly Asp Gly Asp Glu  
1 5 10 15  
Asn Pro Val Leu Tyr Phe Val Asp Leu Cys His Gly Val Val Asp Asp  
20 25 30  
Glu Phe Ser Arg Gly Arg Gly Gly Arg Arg Arg Arg Thr Pro Pro  
35 40 45  
Ser Ala Arg His Arg Gly Val Arg Trp Ala Asp Ala Ala Glu Tyr Gln  
50 55 60  
Ala Arg Ala Gly Arg Ser Trp Pro Thr Ala Arg Asp Ala Glu Ala Ala  
65 70 75 80  
Gly Thr Cys Cys Ser Cys Gly Arg Leu Leu Val Phe Val Ala Asp Gly  
85 90 95  
Ala Arg Gly Ala Gly Val Gln Leu Val Gly Arg Cys Arg Ala Ala Ala  
100 105 110

Gly Asp Ala Glu Ala Val Glu Glu Arg Gln Gly Arg Gly Arg Ala Arg  
115 120 125  
Ala His Gly Gln Gly Glu Pro Arg Ala Gly Glu Thr Gly Ala His Ala  
130 135 140  
Gly Pro  
145

(2) INFORMATION FOR SEQ ID NO:4161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..131
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579714

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4161:

Met Arg Thr Leu Tyr Cys Ile Ser Ser Thr Phe Ala Met Ala Ser Ser  
1 5 10 15  
Met Met Ser Ser Arg Ala Gly Ala Ala Ala Ala Gly Gly Gly Glu His  
20 25 30  
Arg Arg Gln His Val Thr Val Ala Cys Gly Gly Leu Thr Arg Pro Ser  
35 40 45  
Thr Arg Pro Val Pro Gly Ala Ala Gly Pro Arg Pro Gly Thr Pro Arg  
50 55 60  
Pro Arg Gly Pro Ala Ala Ala Gly Gly Ser Ser Ser Ser Pro  
65 70 75 80  
Thr Gly Arg Ala Gly Pro Glu Cys Asn Trp Trp Gly Ala Ala Ala Arg  
85 90 95  
Gln Gln Ala Thr Pro Arg Arg Ser Arg Ser Gly Arg Ala Ala Gly Ala  
100 105 110  
Arg Val Pro Thr Gly Lys Gly Asn Arg Glu Leu Val Arg Arg Ala Leu  
115 120 125  
Thr Pro Ala  
130

(2) INFORMATION FOR SEQ ID NO:4162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 434 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..434
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579724

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4162:

ccaattagcc ttgtttaaga ccaacagaaa ggatagcatg tttgctgacc gggtatttga	60
cttgtttgac acgaaacaca atggaattct cgagtttgag gaatttgctc gagccctttc	120
tgtgttccat ccgagtgcac caatcgattt caaaattgat tttgctttca aattgtatga	180
tctcaagcaa carggtttca ttgaaaagca ggaggtcaag caaatggtgg tcgcaacact	240
tgctgaayca ggaatgaatc tttcagatga tattattgaa ggcattattg ataagacatt	300
tgaggaagca gwatacaaaag cacgwtggca aaattgataw ggaggattgg cgcagccttg	360
tcttgaggca tccatctctg ttaaaaaata tgaccctccc atatctccgg gatatcacca	420
caacwtttcm aagc	

(2) INFORMATION FOR SEQ ID NO:4163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..111  
(D) OTHER INFORMATION: / Ceres Seq. ID 1579725

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4163:

Gln	Leu	Ala	Leu	Phe	Lys	Thr	Asn	Arg	Lys	Asp	Ser	Met	Phe	Ala	Asp
1			5						10					15	
Arg	Val	Phe	Asp	Leu	Phe	Asp	Thr	Lys	His	Asn	Gly	Ile	Leu	Glu	Phe
			20					25					30		
Glu	Glu	Phe	Ala	Arg	Ala	Leu	Ser	Val	Phe	His	Pro	Ser	Ala	Pro	Ile
			35				40					45			
Asp	Phe	Lys	Ile	Asp	Phe	Ala	Phe	Lys	Leu	Tyr	Asp	Leu	Lys	Gln	Xaa
			50			55					60				
Gly	Phe	Ile	Glu	Lys	Gln	Glu	Val	Lys	Gln	Met	Val	Val	Ala	Thr	Leu
65					70					75				80	
Ala	Glu	Xaa	Gly	Met	Asn	Leu	Ser	Asp	Asp	Ile	Ile	Glu	Gly	Ile	Ile
				85					90					95	
Asp	Lys	Thr	Phe	Glu	Glu	Ala	Xaa	Tyr	Lys	Ala	Xaa	Trp	Gln	Asn	
			100					105					110		

(2) INFORMATION FOR SEQ ID NO:4164:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 99 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..99  
(D) OTHER INFORMATION: / Ceres Seq. ID 1579726

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4164:

Met	Phe	Ala	Asp	Arg	Val	Phe	Asp	Leu	Phe	Asp	Thr	Lys	His	Asn	Gly
1			5					10					15		
Ile	Leu	Glu	Phe	Glu	Glu	Phe	Ala	Arg	Ala	Leu	Ser	Val	Phe	His	Pro
			20					25				30			
Ser	Ala	Pro	Ile	Asp	Phe	Lys	Ile	Asp	Phe	Ala	Phe	Lys	Leu	Tyr	Asp
			35				40					45			
Leu	Lys	Gln	Xaa	Gly	Phe	Ile	Glu	Lys	Gln	Glu	Val	Lys	Gln	Met	Val
			50			55					60				
Val	Ala	Thr	Leu	Ala	Glu	Xaa	Gly	Met	Asn	Leu	Ser	Asp	Asp	Ile	Ile
65					70					75				80	
Glu	Gly	Ile	Ile	Asp	Lys	Thr	Phe	Glu	Glu	Ala	Xaa	Tyr	Lys	Ala	Xaa
				85					90					95	
Trp	Gln	Asn													

(2) INFORMATION FOR SEQ ID NO:4165:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 58 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..58  
(D) OTHER INFORMATION: / Ceres Seq. ID 1579727

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4165:

Met	Glu	Phe	Ser	Leu	Arg	Asn	Leu	Glu	Pro	Phe	Leu	Cys	Ser
1			5					10				15	

Ile Arg Val His Gln Ser Ile Ser Lys Leu Ile Leu Leu Ser Asn Cys  
20 25 30  
Met Ile Ser Ser Asn Xaa Val Ser Leu Lys Ser Arg Arg Ser Ser Lys  
35 40 45  
Trp Trp Ser Gln His Leu Leu Xaa Gln Glu  
50 55

(2) INFORMATION FOR SEQ ID NO:4166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 516 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..516
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579756

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4166:

aaatggaggc	ggaggcctcc	accgacggag	cagggcagga	caggttgc	ttgc	atctga	60
gttcctgatt	gttgatccc	agtttcttct	gtgagtggaa	tcgcgaggaa	gaaggatgtc		120
gtgctgcgga	ggcaactgcg	ggtgcggcgc	cggctgcaag	tcgcgcagcg	gctgcggagg		180
gtgcaagatg	taccgcgaca	tggcagagca	ggtgaccacc	acccagactg	tcatcatggg		240
tgttgacca	tccaagggcg	ggttcgaggc	ggccgccgga	gctgagaatg	gcgggtgcaa		300
gtgcggcgcc	aactgcacct	gcgacccctg	cacctgcaag	tgagacgacg	gcggcggcga		360
tgacgctgca	gggtctgcag	gccctgatgg	ggtcggaagg	actctttatc	tctctagcta		420
attaataagc	tctagctagt	atataatatt	ctagcagtg	cgtttgctgt	gttttgtycg		480
agtcagttag	acagtcagcc	gcgtgccatg	ggccat				

(2) INFORMATION FOR SEQ ID NO:4167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..75
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579757

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4167:

Met	Ser	Cys	Cys	Gly	Gly	Asn	Cys	Gly	Cys	Gly	Ala	Gly	Cys	Lys	Cys	
1				5				10						15		
Gly	Ser	Gly	Cys	Gly	Gly	Cys	Lys	Met	Tyr	Pro	Asp	Met	Ala	Glu	Gln	
				20				25						30		
Val	Thr	Thr	Thr	Gln	Thr	Val	Ile	Met	Gly	Val	Ala	Pro	Ser	Lys	Gly	
				35				40						45		
Gly	Phe	Glu	Ala	Ala	Ala	Gly	Ala	Glu	Asn	Gly	Gly	Cys	Lys	Cys	Gly	
				50				55						60		
Ala	Asn	Cys	Thr	Cys	Asp	Pro	Cys	Thr	Cys	Lys						
65						70				75						

(2) INFORMATION FOR SEQ ID NO:4168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..51
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579758

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4168:

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Met Tyr Pro Asp Met Ala Glu Gln Val Thr Thr Thr Gln Thr Val Ile  
1 5 10 15  
Met Gly Val Ala Pro Ser Lys Gly Gly Phe Glu Ala Ala Ala Gly Ala  
20 25 30  
Glu Asn Gly Gly Cys Lys Cys Gly Ala Asn Cys Thr Cys Asp Pro Cys  
35 40 45  
Thr Cys Lys  
50

(2) INFORMATION FOR SEQ ID NO:4169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..47
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579759

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4169:

Met Ala Glu Gln Val Thr Thr Thr Gln Thr Val Ile Met Gly Val Ala  
1 5 10 15  
Pro Ser Lys Gly Gly Phe Glu Ala Ala Ala Gly Ala Glu Asn Gly Gly  
20 25 30  
Cys Lys Cys Gly Ala Asn Cys Thr Cys Asp Pro Cys Thr Cys Lys  
35 40 45

(2) INFORMATION FOR SEQ ID NO:4170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..435
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579776

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4170:

atctgattct	gtgatcgaga	tcgaggccga	tcggccaggt	ttcttggtgcg	tgcgctctgc	60
tactgcatgg	cggtagctca	ccttcttctc	caactctctg	ccggagtcaa	tggagctagc	120
aggaacagga	tgctcattcc	agccattctt	tcgattcttc	agcttattca	cctcgagcgc	180
ccggggagcg	gcgggcagga	cttctacgat	gttagcctcg	tcgacggcct	caacgtgccg	240
gtgcgcgtgg	cgccctcggg	cggcggtggc	gactgtcgtc	ccgcggcgtg	cgcgggcgac	300
gtgaacgcga	tgtgccccgc	ggacctccgc	gtcgtcgcct	cgtccggcag	cggcggcgtc	360
gtggcggtaca	agagcgcggtg	cagcgccctac	ggcagcgcg	gctactgctg	caccggccag	420
tacggcacgc	cggag					

(2) INFORMATION FOR SEQ ID NO:4171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..123
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579777

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4171:

Met Ala Val Ala His Leu Leu Leu Gln Leu Ser Ala Gly Val Asn Gly  
1 5 10 15  
Ala Ser Arg Asn Arg Met Leu Ile Pro Ala Ile Leu Ser Ile Leu Gln

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[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4174:

(2) INFORMATION FOR SEQ ID NO:4175:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4175:

(2) INFORMATION FOR SEQ ID NO:4176:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4176:

Met Gln Gln Gln Asp Pro Val His Arg Val Ala Ala Ala Asp Ala Ala  
1 5 10 15  
Ala Val Ala Val Pro Arg Gly Gly Ser Xaa Gly Gly Pro Gly Gly Pro

	20		25		30
Arg Gly Gly Val Arg Gly Arg Arg Gly Ala Ala Val Arg Gly Ala Gly					
	35		40		45
Gly Ala Pro Glu Pro Pro Arg Val Pro Gly Ala Ala Pro Ala Gly Gly					
	50		55		60
Gly Gly Val Arg Val Pro Val Gly Gly Leu Arg Gly Pro His Arg Ala					
	65		70		75
Pro Leu Arg Arg Gly Pro Leu Arg Ala Arg Pro Arg Pro Pro Leu Leu					
	85		90		95
Pro					

(2) INFORMATION FOR SEQ ID NO:4177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..471
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4177:

ggcttggtcg cagttcgtgg cggatggcgt gttcttcgcg gagctgaatg agatgctgac	60
ccgcgagctc gcggaggatg gctactccgg cgtcgagggtc cgcgtcaccc ccatgcgcac	120
cgagatcatc atccgtgccca cccgcactca gaacgttctc ggcgagaagg gccggaggat	180
cagggagctg acttctgttg ttcagaagcg cttcaacttc ccggagggtg gtgttgagct	240
ctacgcagag aaggtgaaca accgtggcct ctgcgccatt gcccaggccg agtcgctccg	300
ctacaagctt cttggtggac tagccgtgag aaggcatgt tatggtgttc tcaggtttgt	360
catggagagt ggtgctaagg gctgtgaggt tattgtaagt ggcaagctca gggctcagcg	420
agctaagtct atgaagttca aggatgggta catgatttct tctggtcatb c	

(2) INFORMATION FOR SEQ ID NO:4178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..156
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579802

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4178:

Ala Trp Ser Gln Phe Val Ala Asp Gly Val Phe Phe Ala Glu Leu Asn	
1	15
Glu Met Leu Thr Arg Glu Leu Ala Glu Asp Gly Tyr Ser Gly Val Glu	
Val Arg Val Thr Pro Met Arg Thr Glu Ile Ile Ile Arg Ala Thr Arg	
Thr Gln Asn Val Leu Gly Glu Lys Gly Arg Arg Ile Arg Glu Leu Thr	
Ser Val Val Gln Lys Arg Phe Asn Phe Pro Glu Gly Gly Val Glu Leu	
65	80
Tyr Ala Glu Lys Val Asn Asn Arg Gly Leu Cys Ala Ile Ala Gln Ala	
Glu Ser Leu Arg Tyr Lys Leu Leu Gly Gly Leu Ala Val Arg Arg Ala	
Cys Tyr Gly Val Leu Arg Phe Val Met Glu Ser Gly Ala Lys Gly Cys	
Glu Val Ile Val Ser Gly Lys Leu Arg Ala Gln Arg Ala Lys Ser Met	
130	140



Lys Phe Lys Asp Gly Tyr Met Ile Ser Ser Gly His  
145 150 155

(2) INFORMATION FOR SEQ ID NO:4179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..139
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579803

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4179:

Met Leu Thr Arg Glu Leu Ala Glu Asp Gly Tyr Ser Gly Val Glu Val  
1 5 10 15  
Arg Val Thr Pro Met Arg Thr Glu Ile Ile Ile Arg Ala Thr Arg Thr  
20 25 30  
Gln Asn Val Leu Gly Glu Lys Gly Arg Arg Ile Arg Glu Leu Thr Ser  
35 40 45  
Val Val Gln Lys Arg Phe Asn Phe Pro Glu Gly Gly Val Glu Leu Tyr  
50 55 60  
Ala Glu Lys Val Asn Asn Arg Gly Leu Cys Ala Ile Ala Gln Ala Glu  
65 70 75 80  
Ser Leu Arg Tyr Lys Leu Leu Gly Gly Leu Ala Val Arg Arg Ala Cys  
85 90 95  
Tyr Gly Val Leu Arg Phe Val Met Glu Ser Gly Ala Lys Gly Cys Glu  
100 105 110  
Val Ile Val Ser Gly Lys Leu Arg Ala Gln Arg Ala Lys Ser Met Lys  
115 120 125  
Phe Lys Asp Gly Tyr Met Ile Ser Ser Gly His  
130 135

(2) INFORMATION FOR SEQ ID NO:4180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..119
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4180:

Met Arg Thr Glu Ile Ile Arg Ala Thr Arg Thr Gln Asn Val Leu  
1 5 10 15  
Gly Glu Lys Gly Arg Arg Ile Arg Glu Leu Thr Ser Val Val Gln Lys  
20 25 30  
Arg Phe Asn Phe Pro Glu Gly Gly Val Glu Leu Tyr Ala Glu Lys Val  
35 40 45  
Asn Asn Arg Gly Leu Cys Ala Ile Ala Gln Ala Glu Ser Leu Arg Tyr  
50 55 60  
Lys Leu Leu Gly Gly Leu Ala Val Arg Arg Ala Cys Tyr Gly Val Leu  
65 70 75 80  
Arg Phe Val Met Glu Ser Gly Ala Lys Gly Cys Glu Val Ile Val Ser  
85 90 95  
Gly Lys Leu Arg Ala Gln Arg Ala Lys Ser Met Lys Phe Lys Asp Gly  
100 105 110  
Tyr Met Ile Ser Ser Gly His  
115

(2) INFORMATION FOR SEQ ID NO:4181:

00000000-00000000

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 529 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..529  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1579820

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4181:

```
agggagagac cctttccatc caagctagcc aaaccctagc caccgtcggg tccaatctgc      60
caacatctcg tccgctgggt ggtggctcgg cctcggcggc atggcctcgt ccgcctacgc      120
ttgggacgcc gcgaggagg cggacatcga cgcctccgca tcgcaggagg agctcatcgt      180
ccgcgcccgc ttcattctccc gtgacaatga ggaggagggg gagggggagg gggaggggga      240
ggaggaggag gaggaggagg tcgagggtgt cagcacgccg cctctcacgc atcaggaccc      300
gcagagtccg ggggaagaag tcatcgccat gtgctccatc ccttcacccc agcctgaccc      360
cacgcctcct cccgctccyg ctccctcccc tcctcgggac agtaagagtc gccgtccgga      420
gcggtgcaaa ttgaagccgc ggaagaaggt ctgcaagagg aaagagtgtc tgcaatgagg      480
aaggtagaaa gagccaaaca agatcaggtc tccgactccg aagccgcag
```

(2) INFORMATION FOR SEQ ID NO:4182:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 143 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..143  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1579821

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4182:

```
Gly Glu Thr Leu Ser Ile Gln Ala Ser Gln Thr Leu Ala Thr Val Gly
1          5          10          15
Ser Asn Leu Pro Thr Ser Arg Pro Leu Val Gly Gly Ser Ala Ser Ala
20          25          30
Ala Trp Pro Arg Pro Pro Thr Leu Gly Thr Pro Arg Arg Arg Thr
35          40          45
Ser Thr Pro Pro His Arg Arg Arg Ser Ser Ser Ser Ala Pro Ala Ser
50          55          60
Ser Pro Val Thr Met Arg Arg Arg Gly Arg Gly Arg Gly Arg Gly Arg
65          70          75          80
Arg Arg Arg Arg Arg Arg Ser Arg Cys Ser Ala Arg Arg Leu Ser Arg
85          90          95
Ile Arg Thr Arg Arg Val Arg Gly Lys Lys Ser Ser Pro Cys Ala Pro
100         105         110
Ser Pro Ser Pro Ser Leu Thr Pro Arg Leu Leu Pro Leu Xaa Leu Pro
115         120         125
Pro Leu Pro Arg Thr Val Arg Val Ala Val Arg Ser Gly Ser Asn
130         135         140
```

(2) INFORMATION FOR SEQ ID NO:4183:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 125 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..125  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1579822

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4183:

Met Ala Ser Ser Ala Tyr Ala Trp Asp Ala Ala Glu Glu Ala Asp Ile  
1 5 10 15  
Asp Ala Ser Ala Ser Gln Glu Glu Leu Ile Val Arg Ala Arg Phe Ile  
20 25 30  
Ser Arg Asp Asn Glu Glu Glu Gly Glu Gly Glu Gly Glu Gly Glu Glu  
35 40 45  
Glu Glu Glu Glu Glu Val Glu Val Phe Ser Thr Pro Pro Leu Thr His  
50 55 60  
Gln Asp Pro Gln Ser Pro Gly Glu Glu Val Ile Ala Met Cys Ser Ile  
65 70 75 80  
Pro Phe Thr Gln Pro Asp Pro Thr Pro Pro Pro Ala Xaa Ala Pro Ser  
85 90 95  
Pro Pro Ser Asp Ser Lys Ser Arg Arg Pro Glu Arg Val Lys Leu Lys  
100 105 110  
Pro Arg Lys Lys Val Cys Lys Arg Lys Glu Cys Leu Gln  
115 120 125

(2) INFORMATION FOR SEQ ID NO:4184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..75
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579823

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4184:

Met Arg Arg Arg Gly Arg Gly Arg Gly Arg Arg Arg Arg Arg Arg  
1 5 10 15  
Arg Arg Ser Arg Cys Ser Ala Arg Arg Leu Ser Arg Ile Arg Thr Arg  
20 25 30  
Arg Val Arg Gly Lys Lys Ser Ser Pro Cys Ala Pro Ser Pro Ser Pro  
35 40 45  
Ser Leu Thr Pro Arg Leu Leu Pro Leu Xaa Leu Pro Pro Leu Pro Arg  
50 55 60  
Thr Val Arg Val Ala Val Arg Ser Gly Ser Asn  
65 70 75

(2) INFORMATION FOR SEQ ID NO:4185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..437
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579828

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4185:

aaggtccaga agcccagaac cagacgagca cggacggatc tcccccaacg cgcgtgcgtc	60
cgcaactagc gtctgcccgc ggcgccttct tccgcacccc ccgacgcggc aaggagcccc	120
ccgccatgag ggtccaccgc gccccgcgga agcgcaccat cgccgtgcaa cgtgcgcc	180
ccgcggcggc gggcgcgctc ggcgggaaga agctgcgcgc cctgccgcac atattcgaca	240
aggtgctgga gctcccgctc gcggccgacg cggacgtgtc cgtcgaggag gacgcggcgc	300
cgctgcgggt cgtcgcgcgc gccgacgagt tctccctcgc gggcgcccgc gcgcacgcgc	360
tcgagatcca cccaggggtc accaaggtcg tcgtccgcgc cctctcctcc tctccctcg	420
gcggcgatgg cgacgac	

(2) INFORMATION FOR SEQ ID NO:4186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..145
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1579829
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4186:

Arg Ser Arg Ser Pro Glu Pro Asp Glu His Gly Arg Ile Ser Pro Asn  
1 5 10 15  
Ala Arg Ala Ser Ala Thr Ser Val Cys Arg Arg Arg Leu Leu Pro His  
20 25 30  
Pro Pro Thr Arg Gln Gly Ala Pro Arg His Glu Gly Pro Pro Gly Pro  
35 40 45  
Ala Glu Ala His His Arg Arg Ala Thr Leu Arg Leu Arg Gly Gly Gly  
50 55 60  
Arg Ala Arg Arg Glu Glu Ala Ala Pro Pro Ala His Ile Arg Gln  
65 70 75 80  
Gly Ala Gly Ala Pro Val Arg Gly Arg Arg Gly Arg Val Arg Arg Gly  
85 90 95  
Gly Arg Gly Gly Ala Ala Val Arg Arg Arg Arg Arg Arg Val Leu Pro  
100 105 110  
Arg Gly Arg Pro Arg Ala Arg Arg Arg Asp Pro Pro Arg Gly His Gln  
115 120 125  
Gly Arg Arg Pro Arg Pro Leu Leu Leu Pro Arg Arg Arg Trp Arg  
130 135 140  
Arg  
145

- (2) INFORMATION FOR SEQ ID NO:4187:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 145 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..145
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1579830
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4187:

Gly Pro Glu Ala Gln Asn Gln Thr Ser Thr Asp Gly Ser Pro Pro Thr  
1 5 10 15  
Arg Val Arg Pro Gln Leu Ala Ser Ala Ala Gly Ala Phe Phe Arg Thr  
20 25 30  
Pro Arg Arg Gly Lys Glu Pro Pro Ala Met Arg Val His Pro Ala Pro  
35 40 45  
Arg Lys Arg Thr Ile Ala Val Gln Arg Cys Ala Ser Ala Ala Ala Gly  
50 55 60  
Ala Leu Gly Gly Lys Lys Leu Arg Arg Leu Pro His Ile Phe Asp Lys  
65 70 75 80  
Val Leu Glu Leu Pro Phe Ala Ala Asp Ala Asp Val Ser Val Glu Glu  
85 90 95  
Asp Ala Ala Ala Leu Arg Phe Val Ala Ala Ala Asp Glu Phe Ser Leu  
100 105 110  
Ala Gly Ala Arg Ala His Ala Val Glu Ile His Pro Gly Val Thr Lys  
115 120 125  
Val Val Val Arg Gly Leu Ser Ser Ser Ser Leu Gly Gly Asp Gly Asp  
130 135 140  
Asp

002104-15553500

145

(2) INFORMATION FOR SEQ ID NO:4188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579831

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4188:

Met Arg Val His Pro Ala Pro Arg Lys Arg Thr Ile Ala Val Gln Arg  
1 5 10 15  
Cys Ala Ser Ala Ala Ala Gly Ala Leu Gly Gly Lys Lys Leu Arg Arg  
20 25 30  
Leu Pro His Ile Phe Asp Lys Val Leu Glu Leu Pro Phe Ala Ala Asp  
35 40 45  
Ala Asp Val Ser Val Glu Glu Asp Ala Ala Ala Leu Arg Phe Val Ala  
50 55 60  
Ala Ala Asp Glu Phe Ser Leu Ala Gly Ala Arg Ala His Ala Val Glu  
65 70 75 80  
Ile His Pro Gly Val Thr Lys Val Val Val Arg Gly Leu Ser Ser Ser  
85 90 95  
Ser Leu Gly Gly Asp Gly Asp Asp  
100

(2) INFORMATION FOR SEQ ID NO:4189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..425
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579836

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4189:

attcctcttc cagctccagc tatttccacc gcacattgtc cacgtctgcc attggcccat 60  
tgccgggttc tctcgtcaag ccctagctcc aaccaaccg tttccatggg agccatacga 120  
gttgcaagcc ttctactcct cgtggggta atctggctgt cgcgggcgat gttcggcgcg 180  
gaggccgccg gcacgacggt gttcacgctg cacaacaact gacccacac ggtctggccg 240  
gccacactgt ccgggaacag cgcggcggcc gtcggggcg ggggcttcga gctgtcgccc 300  
ggcgccaccg tctcgttccc ggcgccggcg ggctggtcg gccgcctgtg ggcgcgcacg 360  
ggctgcgtcg cgtcgtcgtc gtccccgcc ggccgcctct cgtgcgcacg ggcgactgca 420  
gcggc

(2) INFORMATION FOR SEQ ID NO:4190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..141
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579837

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4190:

Ile Pro Leu Pro Ala Pro Ala Ile Ser Thr Ala His Cys Pro Arg Leu  
1 5 10 15

Pro Leu Ala His Cys Arg Phe Leu Ser Ser Ser Pro Ser Ser Asn Gln  
20 25 30  
Pro Val Ser Met Gly Ala Ile Arg Val Ala Ser Leu Leu Leu Leu Ala  
35 40 45  
Gly Val Ile Trp Leu Ser Arg Ala Met Phe Gly Ala Glu Ala Ala Gly  
50 55 60  
Thr Thr Val Phe Thr Leu His Asn Asn Cys Thr His Thr Val Trp Pro  
65 70 75 80  
Ala Thr Leu Ser Gly Asn Ser Ala Ala Val Gly Gly Gly Gly Phe  
85 90 95  
Glu Leu Ser Pro Gly Ala Thr Val Ser Phe Pro Ala Pro Ala Gly Trp  
100 105 110  
Ser Gly Arg Leu Trp Ala Arg Thr Gly Cys Val Ala Ser Ser Ser Ser  
115 120 125  
Pro Ala Gly Arg Leu Ser Cys Ala Arg Ala Thr Ala Ala  
130 135 140

(2) INFORMATION FOR SEQ ID NO:4191:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 106 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..106

(D) OTHER INFORMATION: / Ceres Seq. ID 1579838

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4191:

Met Gly Ala Ile Arg Val Ala Ser Leu Leu Leu Ala Gly Val Ile  
1 5 10 15  
Trp Leu Ser Arg Ala Met Phe Gly Ala Glu Ala Ala Gly Thr Thr Val  
20 25 30  
Phe Thr Leu His Asn Asn Cys Thr His Thr Val Trp Pro Ala Thr Leu  
35 40 45  
Ser Gly Asn Ser Ala Ala Val Gly Gly Gly Gly Phe Glu Leu Ser  
50 55 60  
Pro Gly Ala Thr Val Ser Phe Pro Ala Pro Ala Gly Trp Ser Gly Arg  
65 70 75 80  
Leu Trp Ala Arg Thr Gly Cys Val Ala Ser Ser Ser Ser Pro Ala Gly  
85 90 95  
Arg Leu Ser Cys Ala Arg Ala Thr Ala Ala  
100 105

(2) INFORMATION FOR SEQ ID NO:4192:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 85 aminoacids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..85

(D) OTHER INFORMATION: / Ceres Seq. ID 1579839

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4192:

Met Phe Gly Ala Glu Ala Ala Gly Thr Thr Val Phe Thr Leu His Asn  
1 5 10 15  
Asn Cys Thr His Thr Val Trp Pro Ala Thr Leu Ser Gly Asn Ser Ala  
20 25 30  
Ala Ala Val Gly Gly Gly Gly Phe Glu Leu Ser Pro Gly Ala Thr Val  
35 40 45  
Ser Phe Pro Ala Pro Ala Gly Trp Ser Gly Arg Leu Trp Ala Arg Thr

50 55 60  
Gly Cys Val Ala Ser Ser Ser Ser Pro Ala Gly Arg Leu Ser Cys Ala  
65 70 75 80  
Arg Ala Thr Ala Ala  
85

(2) INFORMATION FOR SEQ ID NO:4193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..406
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579865

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4193:

aacaaatagt agccatggcg atgatggcgt tggctattgg gtccgatcag atatctactc	60
aagctaggag ggacagtatc attagtggac tgaacaacct ttcaagcaat gtcagcgaag	120
ttctcaagct agatgctgga atgaaggagc tcgcctcttc gctgatcgac tcagagtgcg	180
tcctcgtgtt cggaaggggt tacaactacg ccaccgcgct ggagggcgcc ctgaagggtca	240
aggaggtggc gctgatgcac agcgaaggca tgctcgtctg cgagatgaag cacggaccgc	300
tggccctcgt ggacgagaac ctccccatca ttgtcattgc gactcgcgac gcgtgcttca	360
gcaagcagca gtcggtgatc cagcagctcc tctcgcgtag ggggcg	

(2) INFORMATION FOR SEQ ID NO:4194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..134
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579866

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4194:

Gln Ile Val Ala Met Ala Met Met Ala Leu Ala Ile Gly Ser Asp Gln	
1 5 10 15	
Ile Ser Thr Gln Ala Arg Arg Asp Ser Ile Ile Ser Gly Leu Asn Asn	
20 25 30	
Leu Ser Ser Asn Val Ser Glu Val Leu Lys Leu Asp Ala Gly Met Lys	
35 40 45	
Glu Leu Ala Ser Ser Leu Ile Asp Ser Glu Ser Leu Leu Val Phe Gly	
50 55 60	
Arg Gly Tyr Asn Tyr Ala Thr Ala Leu Glu Gly Ala Leu Lys Val Lys	
65 70 75 80	
Glu Val Ala Leu Met His Ser Glu Gly Met Leu Ala Gly Glu Met Lys	
85 90 95	
His Gly Pro Leu Ala Leu Val Asp Glu Asn Leu Pro Ile Ile Val Ile	
100 105 110	
Ala Thr Arg Asp Ala Cys Phe Ser Lys Gln Gln Ser Val Ile Gln Gln	
115 120 125	
Leu Leu Ser Arg Arg Gly	
130	

(2) INFORMATION FOR SEQ ID NO:4195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..130

(D) OTHER INFORMATION: / Ceres Seq. ID 1579867

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4195:

Met Ala Met Met Ala Leu Ala Ile Gly Ser Asp Gln Ile Ser Thr Gln  
1 5 10 15  
Ala Arg Arg Asp Ser Ile Ile Ser Gly Leu Asn Asn Leu Ser Ser Asn  
20 25 30  
Val Ser Glu Val Leu Lys Leu Asp Ala Gly Met Lys Glu Leu Ala Ser  
35 40 45  
Ser Leu Ile Asp Ser Glu Ser Leu Leu Val Phe Gly Arg Gly Tyr Asn  
50 55 60  
Tyr Ala Thr Ala Leu Glu Gly Ala Leu Lys Val Lys Glu Val Ala Leu  
65 70 75 80  
Met His Ser Glu Gly Met Leu Ala Gly Glu Met Lys His Gly Pro Leu  
85 90 95  
Ala Leu Val Asp Glu Asn Leu Pro Ile Ile Val Ile Ala Thr Arg Asp  
100 105 110  
Ala Cys Phe Ser Lys Gln Gln Ser Val Ile Gln Gln Leu Leu Ser Arg  
115 120 125  
Arg Gly  
130

(2) INFORMATION FOR SEQ ID NO:4196:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..128

(D) OTHER INFORMATION: / Ceres Seq. ID 1579868

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4196:

Met Met Ala Leu Ala Ile Gly Ser Asp Gln Ile Ser Thr Gln Ala Arg  
1 5 10 15  
Arg Asp Ser Ile Ile Ser Gly Leu Asn Asn Leu Ser Ser Asn Val Ser  
20 25 30  
Glu Val Leu Lys Leu Asp Ala Gly Met Lys Glu Leu Ala Ser Ser Leu  
35 40 45  
Ile Asp Ser Glu Ser Leu Leu Val Phe Gly Arg Gly Tyr Asn Tyr Ala  
50 55 60  
Thr Ala Leu Glu Gly Ala Leu Lys Val Lys Glu Val Ala Leu Met His  
65 70 75 80  
Ser Glu Gly Met Leu Ala Gly Glu Met Lys His Gly Pro Leu Ala Leu  
85 90 95  
Val Asp Glu Asn Leu Pro Ile Ile Val Ile Ala Thr Arg Asp Ala Cys  
100 105 110  
Phe Ser Lys Gln Gln Ser Val Ile Gln Gln Leu Leu Ser Arg Arg Gly  
115 120 125

(2) INFORMATION FOR SEQ ID NO:4197:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 489 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:



- (A) NAME/KEY: -  
(B) LOCATION: 1..489  
(D) OTHER INFORMATION: / Ceres Seq. ID 1579873

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4197:

aaggccaggg	atgacgaagg	acaagagaag	aaaaagccaa	agaagaaaaa	agatccgaat	60
gctccgaaac	gagccatgac	cccgttcacg	tattttctcaa	tggctgagcg	aggaaacatg	120
aagagcagca	acccagatgt	gcctacgact	gagatcgcaa	agaagcttgg	ggagatgtgg	180
caaaagatgt	caggcgaaga	gaaacagcct	tacatccagc	aggcccaggt	cgacaagaaa	240
cgttatgaaa	aagaatccgc	tgtctatcgc	ggtgaagcta	cagtcgatgt	ggattctggg	300
aacgagtcct	actagagatc	caagctcttg	ggctggcatg	gtggcacggg	atgaaagtct	360
agtgccatgt	gtgctattgt	tatgtcagca	actgttgcca	acaacattgc	tgacagtaaa	420
gagagtttct	ctcgcagcgt	acctctgcag	ggcaaaaaga	tgtacgagtg	tagtctagtg	480
attttgtgt						

(2) INFORMATION FOR SEQ ID NO:4198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..104  
(D) OTHER INFORMATION: / Ceres Seq. ID 1579874

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4198:

Lys	Ala	Arg	Asp	Asp	Glu	Gly	Gln	Glu	Lys	Lys	Lys	Pro	Lys	Lys	Lys
1			5					10						15	
Lys	Asp	Pro	Asn	Ala	Pro	Lys	Arg	Ala	Met	Thr	Pro	Phe	Met	Tyr	Phe
			20				25					30			
Ser	Met	Ala	Glu	Arg	Gly	Asn	Met	Lys	Ser	Ser	Asn	Pro	Asp	Leu	Pro
		35				40					45				
Thr	Thr	Glu	Ile	Ala	Lys	Lys	Leu	Gly	Glu	Met	Trp	Gln	Lys	Met	Ser
	50					55				60					
Gly	Glu	Glu	Lys	Gln	Pro	Tyr	Ile	Gln	Gln	Ala	Gln	Val	Asp	Lys	Lys
65				70				75						80	
Arg	Tyr	Glu	Lys	Glu	Ser	Ala	Val	Tyr	Arg	Gly	Glu	Ala	Thr	Val	Asp
			85					90						95	
Val	Asp	Ser	Gly	Asn	Glu	Ser	Asp								
			100												

(2) INFORMATION FOR SEQ ID NO:4199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..79  
(D) OTHER INFORMATION: / Ceres Seq. ID 1579875

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4199:

Met	Thr	Pro	Phe	Met	Tyr	Phe	Ser	Met	Ala	Glu	Arg	Gly	Asn	Met	Lys
1			5					10						15	
Ser	Ser	Asn	Pro	Asp	Leu	Pro	Thr	Thr	Glu	Ile	Ala	Lys	Lys	Leu	Gly
		20					25					30			
Glu	Met	Trp	Gln	Lys	Met	Ser	Gly	Glu	Glu	Lys	Gln	Pro	Tyr	Ile	Gln
	35				40						45				
Gln	Ala	Gln	Val	Asp	Lys	Lys	Arg	Tyr	Glu	Lys	Glu	Ser	Ala	Val	Tyr
	50				55				60						
Arg	Gly	Glu	Ala	Thr	Val	Asp	Val	Asp	Ser	Gly	Asn	Glu	Ser	Asp	
65					70				75						

(2) INFORMATION FOR SEQ ID NO:4200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..77
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579876

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4200:

```
Met Lys Lys Asn Pro Leu Ser Ile Ala Val Lys Leu Gln Ser Met Trp
1           5           10           15
Ile Leu Gly Thr Ser Leu Thr Arg Asp Pro Ser Ser Trp Ala Gly Met
          20          25          30
Val Ala Arg Asp Glu Ser Leu Val Pro Cys Val Leu Leu Leu Cys Gln
          35          40          45
Gln Leu Leu Pro Thr Thr Leu Leu Thr Val Lys Arg Val Ser Leu Ala
          50          55          60
Ala Tyr Leu Cys Arg Ala Lys Glu Cys Thr Ser Val Val
65          70          75
```

(2) INFORMATION FOR SEQ ID NO:4201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..356
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579877

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4201:

```
attattagga agaacactgt tttgtctccg gcccgctcgca gcccactgc cgtgcgcgcc      60
accctgccgg cgcacccggc cccgccagcg cgttcgaggc cgacgcgcgc cgccacctgc      120
cgcgtcaacg tccggccatt cctgccccct caccattctg ccgcctccac cgcagcagcc      180
gcggcgatgc gaccgcgcatc ctctctctcc cgcttctcgg ccacaacatc tccgtctcgc      240
tgccgacctg aacaacgagg cacactccat tgttggccat gcttgatctc ctcacctcgc      300
tgcagtgctg ccgtggaagg gaggccagtg cggaacaac ccagactgcg agcgcc
```

(2) INFORMATION FOR SEQ ID NO:4202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..118
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579878

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4202:

```
Ile Ile Arg Lys Asn Thr Val Leu Ser Pro Ala Arg Arg Ser Pro Thr
1           5           10           15
Ala Val Arg Ala Thr Leu Pro Ala His Pro Ala Pro Pro Ala Arg Ser
          20          25          30
Arg Pro Thr Arg Ala Ala Thr Cys Arg Val Thr Leu Arg Pro Phe Leu
          35          40          45
Pro Pro His His Ser Ala Ala Ser Thr Ala Ala Ala Ala Met Arg
          50          55          60
Pro Ala Ser Ser Ser Ser Arg Phe Ser Ala Thr Thr Ser Pro Ser Arg
```

(2) INFORMATION FOR SEQ ID NO:4203:

(A) LENGTH: 94 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

(ix) FEATURE:

(A) NAM

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEO ID NO:4203:

## Leu Gly Arg Thr Leu Phe Cys Leu Arg Pro Val

(2) INFORMATION FOR SEQ ID NO:4204:

(A) LENGTH: 476 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

MOLECULE TYPE: DNA (g

(ix) FEATURE:

(A) NAM

(B) LOCATION: 1

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:4204:

ctgtcat tgctgcaacg aactttcctg agtcgctaga ta

ggcgtttttga	ccgtcatatt	gttgttccca	accagatgt	tgaaggtcga	cgccaaattc	120
tagaatgcc	atatgtcaaa	gatcttgaaa	ggtgatgatg	tggacttaat	gatcattgct	180
agaggaacac	cgggattctc	tggtgcagac	cttgctaact	tggtaaatgt	tgctgctctt	240
aaggctgcc	tggatggtgc	aaaagctgtc	acaatggatg	atcttgagta	tgcaaaggac	300
cgaatcatga	tgggtagtga	gcggaagtcg	gcagttatct	ctgacgaatg	caggaagctg	360
acagcatacc	atgagggagg	gcattgccct	gttgcaatcc	acacagaagg	agctcaccct	420
gtccacaagg	ctaccatcgt	acctaggggg	atggccctag	gaatggtggc	ccaact	

(2) INFORMATION FOR SEQ ID NO:4205:

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptid

(ix) FEATURE:

(A) NAM

(B) LOCATION: 1..114

[illegible]

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4205:

(2) INFORMATION FOR SEQ ID NO:4206:

(A) LENGTH: 102 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..102

(D) OTHER INFORMATION: / Ceres Seq. ID 1579906

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4206:

(2) INFORMATION FOR SEQ ID NO:4207:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..75

(D) OTHER INFORMATION: / Ceres Seq. ID 1579907

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4207:

Met	Asp	Gly	Ala	Lys	Ala	Val	Thr	Met	Asp	Asp	Leu	Glu	Tyr	Ala	Lys
1				5					10					15	
Asp	Arg	Ile	Met	Met	Gly	Ser	Glu	Arg	Lys	Ser	Ala	Val	Ile	Ser	Asp
			20					25					30		
Glu	Cys	Arg	Lys	Leu	Thr	Ala	Tyr	His	Glu	Gly	Gly	His	Ala	Leu	Val

(2) INFORMATION FOR SEQ ID NO:4208:

(A) LENGTH: 439 base pairs

(C) STRANDEDNESS: sing

(D) TOPOLOGY: linear

MOLECULE TYPE: DNA (q

(A) NAME

(B) LOCATION: 1

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:4208:

agtcacctca	aatcccttcg	atccaatctc	caaacyctag	gcaatccaac	atcaaagtat	120
tagctgcccc	cttcgtcaaa	ccgcggcggc	gcggccatgg	cccacggcgg	cggcgcgggg	180
aaggcgaagg	tgacgcgcga	cctggcggtg	gacggcgagg	gcacgcgcac	gctcaaccgc	240
actgtgctgc	agcgccctcg	cccggccggt	gaggatattc	tcataccgcg	ggctcacgtc	300
acgctgtacg	actttgacac	cgatgtcaac	cagtggagac	ggaaggacgt	ggaggggtcg	360
ctcttcctcg	tcaagaggaa	tgctcaacct	agattccagt	tcatggtcat	gaaccgcagg	420
aatacagata	atctagttg					

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 89 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..89

(D) OTHER INFORMATION: / Ceres Seq. ID 1579912

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 94 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..94

(D) OTHER INFORMATION: / Ceres Seq. ID 1579913

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4210:

Variable	Mean	SD	Min	Max
Age	34.5	10.2	22	55
Gender	0.5	0.5	0	1
Marital status	0.6	0.5	0	1
Education	12.5	1.5	9	16
Income	1500	500	500	3000
Health status	0.8	0.2	0	1
Smoking status	0.3	0.5	0	1
Alcohol consumption	0.2	0.4	0	1
Exercise frequency	0.5	0.5	0	1
Stress level	0.7	0.3	0	1
Sleep quality	0.6	0.4	0	1
Work satisfaction	0.5	0.5	0	1
Life satisfaction	0.6	0.4	0	1
Depression score	0.3	0.5	0	1
Anxiety score	0.2	0.4	0	1
Loneliness score	0.4	0.5	0	1
Self-esteem score	0.5	0.5	0	1
Resilience score	0.6	0.4	0	1
Optimism score	0.7	0.3	0	1
Gratitude score	0.8	0.2	0	1
Forgiveness score	0.9	0.1	0	1
Compassion score	0.8	0.2	0	1
Kindness score	0.9	0.1	0	1
Generosity score	0.8	0.2	0	1
Patience score	0.7	0.3	0	1
Humility score	0.6	0.4	0	1
Modesty score	0.5	0.5	0	1
Shyness score	0.4	0.5	0	1
Introversion score	0.3	0.5	0	1
Extroversion score	0.7	0.3	0	1
Social skills score	0.6	0.4	0	1
Empathy score	0.8	0.2	0	1
Emotional stability score	0.7	0.3	0	1
Neuroticism score	0.3	0.5	0	1
Conscientiousness score	0.6	0.4	0	1
Agreeableness score	0.7	0.3	0	1
Openness score	0.5	0.5	0	1
Self-efficacy score	0.6	0.4	0	1
Self-regulation score	0.7	0.3	0	1
Self-motivation score	0.8	0.2	0	1
Self-discipline score	0.9	0.1	0	1
Self-control score	0.8	0.2	0	1
Self-awareness score	0.7	0.3	0	1
Self-reflection score	0.6	0.4	0	1
Self-improvement score	0.8	0.2	0	1
Self-acceptance score	0.9	0.1	0	1
Self-compassion score	0.8	0.2	0	1
Self-kindness score	0.9	0.1	0	1
Self-love score	0.8	0.2	0	1
Self-respect score	0.9	0.1	0	1
Self-worth score	0.8	0.2	0	1
Self-esteem score	0.7	0.3	0	1
Self-confidence score	0.6	0.4	0	1
Self-belief score	0.5	0.5	0	1
Self-trust score	0.4	0.5	0	1
Self-respect score	0.3	0.5	0	1
Self-love score	0.2	0.4	0	1
Self-kindness score	0.1	0.3	0	1
Self-compassion score	0.0	0.2	0	1
Self-awareness score	0.0	0.1	0	1
Self-reflection score	0.0	0.0	0	1
Self-improvement score	0.0	0.0	0	1
Self-acceptance score	0.0	0.0	0	1
Self-compassion score	0.0	0.0	0	1
Self-kindness score	0.0	0.0	0	1
Self-love score	0.0	0.0	0	1
Self-respect score	0.0	0.0	0	1
Self-worth score	0.0	0.0	0	1
Self-esteem score	0.0	0.0	0	1
Self-confidence score	0.0	0.0	0	1
Self-belief score	0.0	0.0	0	1
Self-trust score	0.0	0.0	0	1
Self-respect score	0.0	0.0	0	1
Self-love score	0.0	0.0	0	1
Self-kindness score	0.0	0.0	0	1
Self-compassion score	0.0	0.0	0	1
Self-awareness score	0.0	0.0	0	1
Self-reflection score	0.0	0.0	0	1
Self-improvement score	0.0	0.0	0	1
Self-acceptance score	0.0	0.0	0	1
Self-compassion score	0.0	0.0	0	1
Self-kindness score	0.0	0.0	0	1
Self-love score	0.0	0.0	0	

Met Ala His Gly Gly Gly Ala Gly Lys Ala Lys Val Thr Pro Asn Leu  
1 5 10 15  
Ala Val Asp Gly Glu Gly Thr Arg Thr Leu Asn Arg Thr Val Leu Gln  
20 25 30  
Arg Leu Asp Pro Ala Val Glu Asp Ile Leu Ile Thr Ala Ala His Val  
35 40 45  
Thr Leu Tyr Asp Phe Asp Thr Asp Val Asn Gln Trp Arg Arg Lys Asp  
50 55 60  
Val Glu Gly Ser Leu Phe Val Val Lys Arg Asn Ala Gln Pro Arg Phe  
65 70 75 80  
Gln Phe Met Val Met Asn Arg Arg Asn Thr Asp Asn Leu Val  
85 90

(2) INFORMATION FOR SEQ ID NO:4211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..496
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579922

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4211:

aaggccctct	gtctgtgtgc	gagcgcaaga	gaaagggagt	cagagagaga	gagagagga	60
ggagaccttg	cagaggagcg	aagcaagcaa	ggtgggaaag	aagcagcagc	aagggcggcg	120
ggctgccgga	aggggaacat	gtccctcct	catctcacag	agaatggcgc	ggtgatgatt	180
cagtttgcc	atcagatgcc	tgattacgac	tccccggcta	cccagtcaac	cagtgaacg	240
agccatcaag	aagcgtctgg	aatgagcgaa	gggagcctca	acgagcataa	taatgaccat	300
tcaggcaacc	ttgatgggta	ctogaagagt	gacgaaaaca	agatgatgtc	agcgttatcc	360
ctgggcaatc	cggaaacagc	ttacgcacat	aatccgaagc	ctgaccgtac	tcagtccttc	420
gccatatcat	acccatatgc	cgatccatac	tacgggtggcg	cggtggcagc	agcttatggc	480
ccgcatgcta	tcatgc					

(2) INFORMATION FOR SEQ ID NO:4212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..165
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579923

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4212:

Lys Ala Leu Cys Leu Cys Ala Ser Ala Arg Glu Arg Glu Ser Glu Arg  
1 5 10 15  
Glu Arg Glu Gly Gly Asp Leu Ala Glu Glu Arg Ser Lys Gln Gly Gly  
20 25 30  
Lys Glu Ala Ala Ala Arg Ala Ala Gly Cys Arg Lys Gly Asn Met Leu  
35 40 45  
Pro Pro His Leu Thr Glu Asn Gly Ala Val Met Ile Gln Phe Gly His  
50 55 60  
Gln Met Pro Asp Tyr Asp Ser Pro Ala Thr Gln Ser Thr Ser Glu Thr  
65 70 75 80  
Ser His Gln Glu Ala Ser Gly Met Ser Glu Gly Ser Leu Asn Glu His  
85 90 95  
Asn Asn Asp His Ser Gly Asn Leu Asp Gly Tyr Ser Lys Ser Asp Glu  
100 105 110  
Asn Lys Met Met Ser Ala Leu Ser Leu Gly Asn Pro Glu Thr Ala Tyr  
115 120 125

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Ala His Asn Pro Lys Pro Asp Arg Thr Gln Ser Phe Ala Ile Ser Tyr  
130 135 140  
Pro Tyr Ala Asp Pro Tyr Tyr Gly Gly Ala Val Ala Ala Ala Tyr Gly  
145 150 155 160  
Pro His Ala Ile Met  
165

(2) INFORMATION FOR SEQ ID NO:4213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..119

(D) OTHER INFORMATION: / Ceres Seq. ID 1579924

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4213:

Met Leu Pro Pro His Leu Thr Glu Asn Gly Ala Val Met Ile Gln Phe  
1 5 10 15  
Gly His Gln Met Pro Asp Tyr Asp Ser Pro Ala Thr Gln Ser Thr Ser  
20 25 30  
Glu Thr Ser His Gln Glu Ala Ser Gly Met Ser Glu Gly Ser Leu Asn  
35 40 45  
Glu His Asn Asn Asp His Ser Gly Asn Leu Asp Gly Tyr Ser Lys Ser  
50 55 60  
Asp Glu Asn Lys Met Met Ser Ala Leu Ser Leu Gly Asn Pro Glu Thr  
65 70 75 80  
Ala Tyr Ala His Asn Pro Lys Pro Asp Arg Thr Gln Ser Phe Ala Ile  
85 90 95  
Ser Tyr Pro Tyr Ala Asp Pro Tyr Tyr Gly Gly Ala Val Ala Ala Ala  
100 105 110  
Tyr Gly Pro His Ala Ile Met  
115

(2) INFORMATION FOR SEQ ID NO:4214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..107

(D) OTHER INFORMATION: / Ceres Seq. ID 1579925

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4214:

Met Ile Gln Phe Gly His Gln Met Pro Asp Tyr Asp Ser Pro Ala Thr  
1 5 10 15  
Gln Ser Thr Ser Glu Thr Ser His Gln Glu Ala Ser Gly Met Ser Glu  
20 25 30  
Gly Ser Leu Asn Glu His Asn Asn Asp His Ser Gly Asn Leu Asp Gly  
35 40 45  
Tyr Ser Lys Ser Asp Glu Asn Lys Met Met Ser Ala Leu Ser Leu Gly  
50 55 60  
Asn Pro Glu Thr Ala Tyr Ala His Asn Pro Lys Pro Asp Arg Thr Gln  
65 70 75 80  
Ser Phe Ala Ile Ser Tyr Pro Tyr Ala Asp Pro Tyr Tyr Gly Gly Ala  
85 90 95  
Val Ala Ala Ala Tyr Gly Pro His Ala Ile Met  
100 105

(2) INFORMATION FOR SEQ ID NO:4215:

00000000-00000000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4215:

(2) INFORMATION FOR SEQ ID NO:4216:

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4216:

(2) INFORMATION FOR SEQ ID NO:4217:

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4217:

ctaataaacc	gtgccctcc	gtcccaaccg	tccgcgcct	cctcccttt	ccgtccgcc	60
aagacctcc	tcctacccc	actacccag	ctccctcga	gccagaagc	accgcgcga	120
ccatgcggcc	accgagagg	cgcggcggc	gcggcggtc	ggcggaggtg	gaggccagg	180
cggcggcgg	ggccggttc	gcggcggagg	ccgtggtgg	cgttcggcg	gcgggttcg	240



cgacgagggc cgcgccgcag aggttcgtcg aggtgtcg

(2) INFORMATION FOR SEQ ID NO:4218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..92

(D) OTHER INFORMATION: / Ceres Seq. ID 1579932

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4218:

Leu	Ile	Asn	Arg	Ala	Pro	Pro	Ser	Gln	Pro	Ser	Ala	Ala	Ser	Leu	Pro
1				5					10					15	
Phe	Arg	Ser	Ala	Lys	Thr	Leu	Leu	Leu	Thr	Pro	Leu	Thr	Gln	Leu	Pro
			20					25					30		
Ser	Ser	Pro	Glu	Ala	Pro	Arg	Ala	Pro	Cys	Gly	His	Arg	Glu	Gly	Ala
		35					40					45			
Ala	Ala	Ala	Ala	Val	Arg	Arg	Arg	Trp	Arg	Pro	Arg	Arg	Arg	Arg	Trp
		50				55					60				
Pro	Val	Arg	Arg	Arg	Arg	Pro	Trp	Trp	Pro	Val	Arg	Arg	Arg	Val	Pro
65					70					75					80
Arg	Arg	Gly	Pro	Ala	Arg	Arg	Gly	Ser	Ser	Arg	Cys				
				85					90						

(2) INFORMATION FOR SEQ ID NO:4219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..92

(D) OTHER INFORMATION: / Ceres Seq. ID 1579933

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4219:

Asn	Lys	Pro	Cys	Pro	Ser	Val	Pro	Thr	Val	Arg	Arg	Leu	Pro	Pro	Phe
1				5					10					15	
Pro	Leu	Arg	Gln	Asp	Pro	Pro	Pro	His	Pro	Thr	His	Pro	Ala	Pro	Leu
			20					25					30		
Glu	Pro	Arg	Ser	Thr	Ala	Arg	Thr	Met	Arg	Pro	Pro	Arg	Gly	Arg	Gly
		35					40					45			
Gly	Gly	Gly	Gly	Ser	Ala	Glu	Val	Glu	Ala	Glu	Ala	Ala	Ala	Val	Ala
		50				55					60				
Gly	Ser	Ala	Ala	Glu	Ala	Val	Val	Ala	Gly	Ser	Ala	Ala	Gly	Ser	Ala
65				70					75						80
Thr	Arg	Ala	Arg	Pro	Gln	Arg	Phe	Val	Glu	Val	Ser				
				85					90						

(2) INFORMATION FOR SEQ ID NO:4220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..52

(D) OTHER INFORMATION: / Ceres Seq. ID 1579934

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4220:

Met Arg Pro Pro Arg Gly Arg Gly Gly Gly Gly Gly Ser Ala Glu Val  
1 5 10 15  
Glu Ala Glu Ala Ala Val Ala Gly Ser Ala Ala Glu Ala Val Val  
20 25 30  
Ala Gly Ser Ala Ala Gly Ser Ala Thr Arg Ala Arg Pro Gln Arg Phe  
35 40 45  
Val Glu Val Ser  
50

(2) INFORMATION FOR SEQ ID NO:4221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..459
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579953

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4221:

aaaacgctga tcggagcaac gaagcccgcga gccatgccga cggcgacggc cacggcagct	60
cctcgccaag cggcgctctt cctgcccctg ctgctgctcc tgctcggcct ccacgccacg	120
tccgcgcgcg ccgcgcgcgc gggcgctgcc gtggacgcgc agctcacgtc caccaagcgc	180
tccccggtcc cgaagaagcc cagcgtgaag ccgcccggcc ccggcgccgc gagcccgacc	240
ttcccggtct tcggcatccc cgggatgggc gggttcggca tccccgggat gggcgccggc	300
gggtggggcg ggcgctacgg cgggcccgcc ggcggtacg cccgcggcgc cgtggtggcg	360
cccacgctga cgtgctccga gaagggggcc tgctacagga agaaggtcac ctgccccaa	420
aagtgtttct cctcgtagag cggcgcgcca aggggtacg	

(2) INFORMATION FOR SEQ ID NO:4222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..153
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579954

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4222:

Lys Thr Leu Ile Gly Ala Thr Lys Pro Ala Ala Met Pro Thr Ala Thr  
1 5 10 15  
Ala Thr Ala Ala Pro Arg His Ala Ala Leu Phe Leu Pro Leu Leu Leu  
20 25 30  
Leu Leu Leu Gly Leu His Ala Thr Ser Ala Ala Ala Ala Arg Ala Gly  
35 40 45  
Val Ala Val Asp Ala Glu Leu Thr Ser Thr Lys Pro Ser Pro Val Pro  
50 55 60  
Lys Lys Pro Ser Val Lys Pro Pro Gly Pro Gly Ala Ala Ser Pro Thr  
65 70 75 80  
Phe Pro Gly Phe Gly Ile Pro Gly Met Gly Gly Phe Gly Ile Pro Gly  
85 90 95  
Met Gly Ala Gly Gly Trp Gly Gly Gly Tyr Gly Gly Pro Ala Gly Gly  
100 105 110  
Tyr Ala Arg Gly Gly Val Val Ala Pro Thr Val Thr Cys Ser Glu Lys  
115 120 125  
Gly Pro Cys Tyr Arg Lys Lys Val Thr Cys Pro Lys Lys Cys Phe Ser  
130 135 140  
Ser Tyr Ser Gly Ala Ala Arg Gly Thr  
145 150

(2) INFORMATION FOR SEQ ID NO:4223:

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- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 152 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..152  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1579955  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4223:

Asn Ala Asp Arg Ser Asn Glu Ala Arg Ser His Ala Asp Gly Asp Gly  
1                  5                  10                  15  
His Gly Ser Ser Ser Pro Arg Gly Ala Leu Pro Ala Pro Ala Ala Ala  
                  20                  25                  30  
Pro Ala Arg Pro Pro Arg His Val Arg Arg Arg Arg Ala Arg Gly Arg  
                  35                  40                  45  
Arg Arg Gly Arg Arg Ala His Val His Gln Ala Val Pro Gly Pro Glu  
50                  55                  60  
Glu Ala Gln Arg Glu Ala Ala Arg Pro Arg Arg Glu Pro Asp Leu  
65                  70                  75                  80  
Pro Gly Leu Arg His Pro Arg Asp Gly Arg Val Arg His Pro Arg Asp  
                  85                  90                  95  
Gly Arg Arg Arg Val Gly Arg Arg Leu Arg Arg Ala Arg Arg Arg Val  
                  100                  105                  110  
Arg Pro Arg Arg Arg Gly Gly Ala His Arg Asp Val Leu Arg Glu Gly  
                  115                  120                  125  
Ala Leu Leu Gln Glu Glu Gly His Leu Pro Gln Glu Val Leu Leu Leu  
130                  135                  140  
Val Gln Arg Arg Gly Lys Gly Tyr  
145                  150

(2) INFORMATION FOR SEQ ID NO:4224:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 142 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..142  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1579956  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4224:

Met Pro Thr Ala Thr Ala Thr Ala Ala Pro Arg His Ala Ala Leu Phe  
1                  5                  10                  15  
Leu Pro Leu Leu Leu Leu Leu Leu Gly Leu His Ala Thr Ser Ala Ala  
                  20                  25                  30  
Ala Ala Arg Ala Gly Val Ala Val Asp Ala Glu Leu Thr Ser Thr Lys  
                  35                  40                  45  
Pro Ser Pro Val Pro Lys Lys Pro Ser Val Lys Pro Pro Gly Pro Gly  
50                  55                  60  
Ala Ala Ser Pro Thr Phe Pro Gly Phe Gly Ile Pro Gly Met Gly Gly  
65                  70                  75                  80  
Phe Gly Ile Pro Gly Met Gly Ala Gly Gly Trp Gly Gly Gly Tyr Gly  
                  85                  90                  95  
Gly Pro Ala Gly Gly Tyr Ala Arg Gly Gly Val Val Ala Pro Thr Val  
                  100                  105                  110  
Thr Cys Ser Glu Lys Gly Pro Cys Tyr Arg Lys Lys Val Thr Cys Pro  
115                  120                  125  
Lys Lys Cys Phe Ser Ser Tyr Ser Gly Ala Ala Arg Gly Thr  
130                  135                  140

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 524 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..524  
(D) OTHER INFORMATION: / Ceres Seq. ID 1579968

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4225:

tttttagcacc	acctctcatg	actaynacat	ttcttttcggg	aaagtagaaa	aaaatctatt	60
acccatgagg	ccatgatact	ttccacttgg	acgaagcgaa	attgttaatt	cctcccttcc	120
agtatatagc	tcgtctgctc	acactcggag	ctcgtaacaa	agtcatcact	catcacatga	180
gcttgcttgt	gactgccagc	tttgcccagt	gttcatcgcc	catggaagag	cgggcactgt	240
tcccggtgtc	cgattccagc	accacctgca	gcagctctgg	ctgtaccggc	cccaactccc	300
ctgtctcgtc	gtcgcagtat	ttggaacgaca	ccagcgcagg	cgccggcagc	tcgagcagcc	360
ggaagcggcc	gcgcgcggag	ctgaagcatc	caacgtaccg	cggcgctgcg	atgcgtgcgt	420
ggggcaagtg	ggtgtccgag	atccgggagc	cccgcaagaa	gtcgcgcatc	tggctggggca	480
ccttcgacac	tcccccgaqa	tggccgcgcg	cgcgcacgac	gtcgcgcgcg		

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..116  
(D) OTHER INFORMATION: / Ceres Seq. ID 1579969

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4226:

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..101  
(D) OTHER INFORMATION: / Ceres Seq. ID 1579970

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4227:

Met Glu Glu Arg Ala Leu Phe Pro Val Ser Asp Ser Ser Thr Thr Cys  
1 5 10 15  
Ser Ser Ser Gly Cys Thr Gly Pro Asn Ser Pro Val Ser Ser Ser Gln  
20 25 30  
Tyr Leu Asp Asp Thr Ser Asp Gly Ala Gly Ser Ser Ser Ser Arg Lys  
35 40 45  
Arg Pro Arg Arg Glu Leu Lys His Pro Thr Tyr Arg Gly Val Arg Met  
50 55 60  
Arg Ala Trp Gly Lys Trp Val Ser Glu Ile Arg Glu Pro Arg Lys Lys  
65 70 75 80  
Ser Arg Ile Trp Leu Gly Thr Phe Asp Thr Pro Xaa Arg Trp Pro Arg  
85 90 95  
Ala Arg Met Thr Ser  
100

(2) INFORMATION FOR SEQ ID NO:4228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..513
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579975

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4228:

acttcacccc tctcaatctc gtcctacact ctctcccacc ttcaattcac ctgctctctc	60
tggttctcgag ctagctcaca tcagggggag gaagaggaac cagcacctgc ctcgccatgt	120
cgctctccat ggtgtccaag aacgcgccgc cgccggccgg gtacggcgac ggcgaaggca	180
gcgtgctcga ggccgcgccg gtgacgagct gcctgtacct gcgccccggg gcggggggcg	240
tggacagga cgccgtgctg cgccgcatcc gccaccggag gcgccacgac cgctccacg	300
acacgctgcg ctccatggtg caggcgccgc cgcggtcggc tgagccggac ggcattggacg	360
gcgcagaacg gcacctcccg tggccgctcg acgacgcctt ctggcgccct tagcttttgt	420
aatatagaat tagtctcttg tgcagattaa gsaaatgcac atggaacatg gtccagttcg	480
cctctctcttg tgtagactgt gaataacaga tgc	

(2) INFORMATION FOR SEQ ID NO:4229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..113
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579976

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4229:

Leu His Pro Ser Gln Ser Arg Ser Ser Leu Ser Pro Thr Phe Thr Ser  
1 5 10 15  
Pro Ala Leu Ser Val Leu Glu Leu Ala His Ile Arg Gly Arg Lys Arg  
20 25 30  
Asn Gln His Leu Pro Arg His Val Val Leu His Gly Val Gln Glu Arg  
35 40 45  
Ala Ala Ala Gly Arg Val Arg Arg Arg Arg Gln Arg Arg Arg Gly  
50 55 60  
Arg Ala Gly Asp Glu Leu Pro Val Pro Ala Pro Arg Gly Gly Gly Ala  
65 70 75 80  
Gly Gln Gly Arg Arg Ala Ala Pro His Pro Pro Pro Glu Ala Pro Arg  
85 90 95  
Pro Pro Pro Arg His Ala Ala Leu His Gly Ala Gly Ala Ala Val  
100 105 110

(2) INFORMATION FOR SEQ ID NO:4230:

- [illegible]

- (2) INFORMATION FOR SEQ ID NO:4231:

- |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Ser | Lys | Asn | Ala | Pro | Pro | Pro | Ala | Gly | Tyr | Gly | Asp | Gly | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Ser | Val | Val | Glu | Ala | Ala | Pro | Val | Thr | Ser | Cys | Leu | Tyr | Leu | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Gly | Ala | Gly | Ala | Leu | Asp | Arg | Asp | Ala | Val | Leu | Arg | Arg | Ile | Arg |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| His | Arg | Arg | Arg | His | Asp | Arg | Leu | His | Asp | Thr | Leu | Arg | Ser | Met | Val |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gln | Ala | Pro | Pro | Arg | Ser | Ala | Glu | Pro | Asp | Gly | Met | Asp | Gly | Ala | Glu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Arg | His | Leu | Pro | Trp | Pro | Leu | Asp | Asp | Ala | Phe | Ser | Ala | Pro |     |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     |     |

- (2) INFORMATION FOR SEQ ID NO:4232:

- [illegible]

(B) LOCATION: 1..481

(D) OTHER INFORMATION: / Ceres Seq. ID 1579979

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4232:

ctctccacgc	ccgcgcaccg	ccgctccgcc	actccacact	tctactcacc	gccgccaccg	60
ctcggctccg	cccgtgcgca	gcgccagcga	ccaagccccg	ccgccgctcc	ctcgtcctcg	120
tccgcgcctc	cagctcggac	cctccgcagc	agcagctcaa	cctctccgtg	ctccgcttca	180
ccctcgggat	tccggggctg	gacgaatcgt	acctcccccg	gtggataggc	ctcggtttgc	240
gcgcgctcgt	cgtgctcaac	cacctcctct	ctgcgtcccc	gacgcccgcg	cagctcaggt	300
ccgaggctgt	ggggctgtgc	ctggccgcgt	tctcggcgac	gctgccgttc	ctggggaggt	360
tccttgaggg	cgctgatgct	gccagccgag	tgccgttgcc	cgaggggagc	atccaagtat	420
tcgtcatgtc	tgagaacctg	tcagctgtgc	agaaggagga	catggcgtgg	gcgtcgtacg	480
t						

(2) INFORMATION FOR SEQ ID NO:4233:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 121 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..121

(D) OTHER INFORMATION: / Ceres Seq. ID 1579980

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4233:

Ser	Pro	Arg	Pro	Arg	Thr	Ala	Ala	Pro	Pro	Leu	Pro	Pro	Ser	Thr	His
1				5					10					15	
Arg	Arg	His	Arg	Ser	Ala	Pro	Pro	Val	Arg	Ser	Ala	Ser	Asp	Gln	Ala
			20					25					30		
Pro	Pro	Pro	Leu	Pro	Arg	Pro	Arg	Pro	Arg	Leu	Gln	Leu	Gly	Pro	Ser
			35				40						45		
Ala	Ala	Ala	Ala	Gln	Pro	Leu	Arg	Ala	Pro	Leu	His	Pro	Arg	Asp	Ser
			50				55				60				
Gly	Ala	Gly	Arg	Ile	Val	Pro	Pro	Pro	Val	Asp	Arg	Pro	Arg	Phe	Arg
65				70					75					80	
Arg	Ala	Arg	Arg	Ala	Gln	Pro	Pro	Pro	Leu	Cys	Val	Pro	Asp	Ala	Arg
				85				90					95		
Ala	Ala	Gln	Val	Arg	Gly	Cys	Gly	Ala	Val	Pro	Gly	Arg	Val	Leu	Gly
			100					105					110		
Asp	Ala	Ala	Val	Pro	Gly	Glu	Val	Pro							
			115				120								

(2) INFORMATION FOR SEQ ID NO:4234:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..159

(D) OTHER INFORMATION: / Ceres Seq. ID 1579981

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4234:

Leu	His	Ala	Arg	Ala	Pro	Pro	Leu	Arg	His	Ser	His	Leu	Leu	Leu	Thr
1				5					10					15	
Ala	Ala	Thr	Ala	Arg	Leu	Arg	Pro	Cys	Ala	Ala	Pro	Ala	Thr	Lys	Pro
			20					25					30		
Arg	Arg	Arg	Ser	Leu	Val	Leu	Val	Arg	Ala	Ser	Ser	Ser	Asp	Pro	Pro
			35				40					45			
Gln	Gln	Gln	Leu	Asn	Leu	Ser	Val	Leu	Arg	Phe	Thr	Leu	Gly	Ile	Pro
			50				55				60				
Gly	Leu	Asp	Glu	Ser	Tyr	Leu	Pro	Arg	Trp	Ile	Gly	Leu	Gly	Phe	Gly

(2) INFORMATION FOR SEO ID NO:4235:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4235:

(2) INFORMATION FOR SEQ ID NO:4236:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4236:

[illegible]



130	135	140
Asp Val Arg Ala Ser Ile Gly Ala Gly Phe Ile Tyr Pro Leu Val Gly		
145	150	155
		160

(2) INFORMATION FOR SEQ ID NO:4237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..139
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579988

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4237:

Met Lys Ala Val His Ser Ala Ala Met Ala Ala Gly Ala Phe Asp Ala  
1 5 10 15  
Val Val Cys Thr His His Ala His Gly Gly Lys Gly Ala Val Glu Leu  
20 25 30  
Gly Leu Ala Val Gln Arg Ala Cys Glu Ser Gln Ala Glu Pro Leu Lys  
35 40 45  
Phe Leu Tyr Pro Leu Glu Ser Ser Ile Lys Glu Lys Ile Glu Ser Ile  
50 55 60  
Ala Lys Phe Tyr Gly Ala Ser Gly Val Glu Tyr Ser Glu Gln Ala Glu  
65 70 75 80  
Lys Gln Ile Glu Met Tyr Thr Lys Gln Gly Phe Ser Ser Leu Pro Ile  
85 90 95  
Cys Met Ala Lys Thr Gln Tyr Ser Phe Ser His Val Pro Ser Met Lys  
100 105 110  
Gly Ala Pro Thr Gly Phe Val Leu Pro Ile Arg Asp Val Arg Ala Ser  
115 120 125  
Ile Gly Ala Gly Phe Ile Tyr Pro Leu Val Gly  
130 135

(2) INFORMATION FOR SEQ ID NO:4238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..131
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579989

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4238:

Met Ala Ala Gly Ala Phe Asp Ala Val Val Cys Thr His His Ala His  
1 5 10 15  
Gly Gly Lys Gly Ala Val Glu Leu Gly Leu Ala Val Gln Arg Ala Cys  
20 25 30  
Glu Ser Gln Ala Glu Pro Leu Lys Phe Leu Tyr Pro Leu Glu Ser Ser  
35 40 45  
Ile Lys Glu Lys Ile Glu Ser Ile Ala Lys Phe Tyr Gly Ala Ser Gly  
50 55 60  
Val Glu Tyr Ser Glu Gln Ala Glu Lys Gln Ile Glu Met Tyr Thr Lys  
65 70 75 80  
Gln Gly Phe Ser Ser Leu Pro Ile Cys Met Ala Lys Thr Gln Tyr Ser  
85 90 95  
Phe Ser His Val Pro Ser Met Lys Gly Ala Pro Thr Gly Phe Val Leu  
100 105 110

Pro Ile Arg Asp Val Arg Ala Ser Ile Gly Ala Gly Phe Ile Tyr Pro  
115 120 125  
Leu Val Gly  
130

(2) INFORMATION FOR SEQ ID NO:4239:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..433
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579994

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4239:

acaatttgat tttgaccgct cgcctgcctg gccgcctcct agtcgtaatc ccgccccgcc	60
gcctcccccct ctccggcctt ctccgctccg cgcgggcgcc atgtcgggtga cgctgcacac	120
gaacctgggc gacatcaagt gcgaggtgtt ctgcgaccag gtgccgcgca cggcggagaa	180
cttcttggcg ctctgcgga gccgctacta cgacggcacc gtgttccacc gcaacatcaa	240
gggcttcatg gtccagggcg gcgacccac cggcaccggc aaggcggggt cgtccatctg	300
ggcgccaag ttcgcgacg agttgaggga gtcgctcaag cacaacgcgc gcgggatcat	360
gtcgatggcc aacagcgggc ccaacaccaa cggcagccag ttcttcatca cctacgcca	420
gcagccgcac etc	

(2) INFORMATION FOR SEQ ID NO:4240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..144
- (D) OTHER INFORMATION: / Ceres Seq. ID 1579995

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4240:

Gln Phe Asp Phe Asp Pro Ser Pro Ala Trp Pro Pro Pro Ser Arg Asn	
1 5 10 15	
Pro Ala Pro Pro Pro Pro Pro Leu Arg Pro Ser Pro Leu Arg Ala Gly	
20 25 30	
Ala Met Ser Val Thr Leu His Thr Asn Leu Gly Asp Ile Lys Cys Glu	
35 40 45	
Val Phe Cys Asp Gln Val Pro Arg Thr Ala Glu Asn Phe Leu Ala Leu	
50 55 60	
Cys Gly Ser Gly Tyr Tyr Asp Gly Thr Val Phe His Arg Asn Ile Lys	
65 70 75 80	
Gly Phe Met Val Gln Gly Gly Asp Pro Thr Gly Thr Gly Lys Gly Gly	
85 90 95	
Ser Ser Ile Trp Gly Ala Lys Phe Ala Asp Glu Leu Arg Glu Ser Leu	
100 105 110	
Lys His Asn Ala Arg Gly Ile Met Ser Met Ala Asn Ser Gly Pro Asn	
115 120 125	
Thr Asn Gly Ser Gln Phe Phe Ile Thr Tyr Ala Lys Gln Pro His Leu	
130 135 140	

(2) INFORMATION FOR SEQ ID NO:4241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..111  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1579996  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4241:  
Met Ser Val Thr Leu His Thr Asn Leu Gly Asp Ile Lys Cys Glu Val  
1                  5                  10                  15  
Phe Cys Asp Gln Val Pro Arg Thr Ala Glu Asn Phe Leu Ala Leu Cys  
                  20                  25                  30  
Gly Ser Gly Tyr Tyr Asp Gly Thr Val Phe His Arg Asn Ile Lys Gly  
                  35                  40                  45  
Phe Met Val Gln Gly Gly Asp Pro Thr Gly Thr Gly Lys Gly Gly Ser  
                  50                  55                  60  
Ser Ile Trp Gly Ala Lys Phe Ala Asp Glu Leu Arg Glu Ser Leu Lys  
65                  70                  75                  80  
His Asn Ala Arg Gly Ile Met Ser Met Ala Asn Ser Gly Pro Asn Thr  
                  85                  90                  95  
Asn Gly Ser Gln Phe Phe Ile Thr Tyr Ala Lys Gln Pro His Leu  
                  100                  105                  110

(2) INFORMATION FOR SEQ ID NO:4242:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 291 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:

    (A) NAME/KEY: -  
    (B) LOCATION: 1..291  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1580028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4242:

acctggccgc caccttcctt ctacctcgtc ccctgcttc cctgaccgag cagcgcccag 60  
gcaaccgcat agcaccgcgt gacctgacc gccaggagcc cgaccggccg aagccccacc 120  
gccaggacgc cagccgcgcc acccgaccg aagccgccc cgctccctgca cagcagcgc 180  
caccgaggac cgacgccagg actcgaccgc gaccaggt accgtcgcca cgtcgcgcca 240  
ggccgagccc tgcattccgc ccgagcgacc gcgccaggaa cccgacacc g

(2) INFORMATION FOR SEQ ID NO:4243:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 96 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..96  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1580029

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4243:

Leu Ala Ala Thr Phe Leu Leu Pro Arg Pro Pro Ala Ser Leu Thr Glu  
1                  5                  10                  15  
Gln Arg Pro Gly Asn Arg Ile Ala Pro Arg Asp Pro Asp Arg Gln Glu  
                  20                  25                  30  
Pro Asp Arg Pro Lys Pro His Arg Gln Asp Ala Ser Arg Ala Thr Arg  
                  35                  40                  45  
Pro Glu Ala Ala Arg Val Pro Ala His Asp Ala Pro Pro Arg Thr Asp  
                  50                  55                  60  
Ala Arg Thr Arg Pro Arg Pro Arg Leu Pro Ser Pro Arg Arg Ala Arg  
65                  70                  75                  80  
Pro Ser Pro Ala Ser Ala Pro Ser Asp Arg Ala Arg Asn Pro Thr Pro

00000000-00000000

85

90

95

(2) INFORMATION FOR SEQ ID NO:4244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..302
- (D) OTHER INFORMATION: / Ceres Seq. ID 1580030

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4244:

attttttccc ttgcgcatga cgccgcccgc gccgcctccg tgcctcgcct gcctcctcac	60
cctcctcctc ctgcgcccgc cggcgccgcy accggccggc gccatctgcg tcccgcgcaa	120
tcccgggtggc cacagcaagc caggagcgcc ggccaagccc gcgccaccga aactaaagcc	180
cctcacgccc gggcgccgcy cgccgcccga gccgacgccc atggcccccg gcgccgacat	240
cgtgcggagc ctgtgcctga agaccgacta ccccgacctg tgcattgctg ccatcgcgaa	300

gc

(2) INFORMATION FOR SEQ ID NO:4245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..100
- (D) OTHER INFORMATION: / Ceres Seq. ID 1580031

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4245:

Ile Ser Ser Leu Arg His Asp Ala Ala Ala Ala Ser Val Pro Arg	
1 5 10 15	
Leu Pro Pro His Pro Pro Pro Pro Arg Arg Arg Gly Gly Xaa Thr Gly	
20 25 30	
Arg Arg His Leu Arg Pro Ala Gln Ser Arg Trp Pro Gln Gln Ala Arg	
35 40 45	
Ser Ala Gly Gln Ala Arg Ala Thr Glu Thr Lys Ala Pro His Ala Arg	
50 55 60	
Gly Ala Gly Ala Ala Glu Ala Asp Ala Asp Gly Pro Gly Arg Arg His	
65 70 75 80	
Arg Ala Glu Pro Val Pro Glu Asp Arg Leu Pro Arg Pro Val His Val	
85 90 95	
Gly His Arg Glu	
100	

(2) INFORMATION FOR SEQ ID NO:4246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..100
- (D) OTHER INFORMATION: / Ceres Seq. ID 1580032

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4246:

Phe Leu Pro Phe Ala Met Thr Pro Pro Pro Pro Pro Cys Leu Ala	
1 5 10 15	

Cys Leu Leu Thr Leu Leu Leu Leu Ala Ala Ala Ala Xaa Pro Ala  
20 25 30  
Gly Ala Ile Cys Val Pro Arg Asn Pro Gly Gly His Ser Lys Pro Gly  
35 40 45  
Ala Pro Ala Lys Pro Ala Pro Pro Lys Leu Lys Pro Leu Thr Pro Ala  
50 55 60  
Ala Pro Ala Pro Pro Lys Pro Thr Pro Met Ala Pro Gly Ala Asp Ile  
65 70 75 80  
Val Arg Ser Leu Cys Leu Lys Thr Asp Tyr Pro Asp Leu Cys Met Ser  
85 90 95  
Ala Ile Ala Lys  
100

(2) INFORMATION FOR SEQ ID NO:4247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..95
- (D) OTHER INFORMATION: / Ceres Seq. ID 1580033

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4247:

Met Thr Pro Pro Pro Pro Pro Pro Cys Leu Ala Cys Leu Leu Thr Leu  
1 5 10 15  
Leu Leu Leu Ala Ala Ala Ala Ala Xaa Pro Ala Gly Ala Ile Cys Val  
20 25 30  
Pro Arg Asn Pro Gly Gly His Ser Lys Pro Gly Ala Pro Ala Lys Pro  
35 40 45  
Ala Pro Pro Lys Leu Lys Pro Leu Thr Pro Ala Ala Pro Ala Pro Pro  
50 55 60  
Lys Pro Thr Pro Met Ala Pro Gly Ala Asp Ile Val Arg Ser Leu Cys  
65 70 75 80  
Leu Lys Thr Asp Tyr Pro Asp Leu Cys Met Ser Ala Ile Ala Lys  
85 90 95

(2) INFORMATION FOR SEQ ID NO:4248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 416 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..416
- (D) OTHER INFORMATION: / Ceres Seq. ID 1580051

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4248:

cgcgccctcct	ctcgccctcg	ctccgcgcgc	gccgcgcgc	cgccgcatca	agcaccgcgc	60
ccgccgtcgc	ctgaggtaga	caccaatccg	ccgccatggg	gcgtatgcac	agccgcggga	120
agggtatctc	atcgctggcg	ctgcctgaca	agaggacgcc	tcctcccttg	tcaagatcct	180
ccgcatcctc	aaggcccatg	ggctggcacc	agaaatcccc	gaggacctgt	acttcctcat	240
caagaaggcg	gtggcgataa	ggaagcacct	tgagaggaac	aggaaggaca	aagactctaa	300
attcaggctc	attcttggtg	agagcaggat	ccaccgcctt	gcccgtact	acaagcgcac	360
aaagaagctt	ccaccacac	ggaagtatga	gtcaaccaca	gcgagcactc	tggtgg	

(2) INFORMATION FOR SEQ ID NO:4249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..90
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1580052

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4249:

Arg Ala Ser Ser Arg Pro Arg Ser Ala Ala Ala Ala Ala Pro Pro His  
1 5 10 15  
Gln Ala Pro Ala Pro Pro Ser Pro Glu Val Asp Thr Asn Pro Pro Pro  
20 25 30  
Trp Gly Val Cys Thr Ala Ala Gly Arg Val Ser His Arg Arg Arg Cys  
35 40 45  
Arg Thr Arg Gly Arg Leu Leu Pro Cys Gln Asp Pro Pro His Pro Gln  
50 55 60  
Gly Pro Trp Ala Gly Thr Arg Asn Pro Arg Gly Pro Val Leu Pro His  
65 70 75 80  
Gln Glu Gly Gly Gly Asp Lys Glu Ala Pro  
85 90

(2) INFORMATION FOR SEQ ID NO:4250:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 54 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..54
- (D) OTHER INFORMATION: / Ceres Seq. ID 1580053

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4250:

Met Gly Arg Met His Ser Arg Gly Lys Gly Ile Ser Ser Ser Ala Leu  
1 5 10 15  
Pro Tyr Lys Arg Thr Pro Pro Pro Leu Ser Arg Ser Ser Ala Ser Ser  
20 25 30  
Arg Pro Met Gly Trp His Gln Lys Ser Pro Arg Thr Cys Thr Ser Ser  
35 40 45  
Ser Arg Arg Arg Trp Arg  
50

(2) INFORMATION FOR SEQ ID NO:4251:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 51 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..51
- (D) OTHER INFORMATION: / Ceres Seq. ID 1580054

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4251:

Met His Ser Arg Gly Lys Gly Ile Ser Ser Ser Ala Leu Pro Tyr Lys  
1 5 10 15  
Arg Thr Pro Pro Pro Leu Ser Arg Ser Ser Ala Ser Ser Arg Pro Met  
20 25 30  
Gly Trp His Gln Lys Ser Pro Arg Thr Cys Thr Ser Ser Ser Arg Arg  
35 40 45  
Arg Trp Arg  
50

(2) INFORMATION FOR SEQ ID NO:4252:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 290 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..290
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1580058
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4252:

```
atatatagat tatagagagg caaacaacc tcgcccactc caacacgtga caccgcgcgc      60
cgcgctccg ccgcacgccc ccactctctc accgccaccg ccgagatggc cgctgctcc      120
cacctgcgc ccgcgggtgg ctcttccctt gccgcgcgcg cagtgggtcg ttccccggcg      180
cattctcag ccgcgcgcgc ctctgcgcgc ctccggtcga cgctgcgttt ctgcagcgcc      240
ggcctgtcgg ttaagggaag cagggcgact ttcccgtagg tcgcccgcgc
```

(2) INFORMATION FOR SEQ ID NO:4253:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 96 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..96
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1580059
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4253:

```
Tyr Ile Asp Tyr Arg Glu Ala Asn Lys Pro Arg Pro Leu Gln His Val
1      5      10      15
Thr Pro Arg Gly Ala Pro Pro Pro His Ala Pro Thr Leu Ser Pro Pro
20     25     30
Pro Pro Arg Trp Pro Pro Ala Pro Thr Ser Pro Pro Arg Val Ala Leu
35     40     45
Pro Leu Pro Pro Pro Gln Trp Phe Val Pro Arg Arg Ile Pro Gln Pro
50     55     60
Pro Pro Pro Ser Arg Ala Ser Gly Arg Arg Cys Val Ser Arg Ala Pro
65     70     75     80
Ala Cys Arg Leu Arg Glu Ala Gly Arg Leu Ser Arg Gly Ser Pro Pro
85     90     95
```

(2) INFORMATION FOR SEQ ID NO:4254:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 61 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..61
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1580060
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4254:

```
Met Ala Ala Cys Ser His Leu Ala Ala Gly Gly Ser Ser Pro Ala
1      5      10      15
Ala Ala Ala Val Val Arg Ser Pro Ala His Ser Ser Ala Ala Ala Ala
20     25     30
Phe Ala Arg Leu Arg Ser Thr Leu Arg Phe Ser Ser Ala Gly Leu Ser
35     40     45
Val Lys Gly Ser Arg Ala Thr Phe Pro Trp Val Ala Ala
50     55     60
```

(2) INFORMATION FOR SEQ ID NO:4255:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4255:

(2) INFORMATION FOR SEQ ID NO:4256:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4256:

(2) INFORMATION FOR SEO ID NO:4257:

```

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 107 amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS:
    (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
    (A) NAME/KEY: peptide
    (B) LOCATION: 1..107

```



(D) OTHER INFORMATION: / Ceres Seq. ID 1580063

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4257:

Met Glu Ser Pro Asp Gln Ala Ala Ala Ala Arg Gln Asp  
1 5 10 15  
Lys Glu Gln Arg Asp Tyr Arg Leu Ile Ala Lys Ala Val Asp Glu Ala  
20 25 30  
Tyr Arg Ala Val Glu Cys Asp Gly Gly Gly Tyr Pro Phe Gly Ala Val  
35 40 45  
Val Val His Gly Gly Gly Asp Asp Glu Val Val Ser Ser Ser His Asn  
50 55 60  
Ser Val Arg Lys Asp Ala Asp Pro Ser Ala His Ala Glu Val Thr Ala  
65 70 75 80  
Ile Arg Gln Ala Cys Lys Lys Leu Gly Lys Thr Ser Leu Ala Gly Cys  
85 90 95  
Glu Ile Tyr Thr Ser Cys Glu Pro Cys Arg Cys  
100 105

(2) INFORMATION FOR SEQ ID NO:4258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..242
- (D) OTHER INFORMATION: / Ceres Seq. ID 1580068

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4258:

tcacgacgtg cgcctctggg acctggacgc cgarggggtc gcgacgtgct gctcgccctac 60  
gcggarccgc tkcggcaact cggggarcac cctgcgggtgc agtatgttca ggtgtttaag 120  
aaccatgggg catctgctgg agcttcgatg cgcattcac acagccaaat gttgggaact 180  
ccctttgtcc ctccctctgt tacaactcgg cttaactgca tgaaggagat ttttgacaga 240  
tc

(2) INFORMATION FOR SEQ ID NO:4259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..80
- (D) OTHER INFORMATION: / Ceres Seq. ID 1580069

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4259:

Ser Arg Arg Ala Pro Leu Gly Pro Gly Arg Arg Xaa Gly Arg Asp Val  
1 5 10 15  
Leu Leu Ala Tyr Ala Xaa Arg Xaa Arg Gln Leu Gly Xaa His Pro Ala  
20 25 30  
Val Gln Tyr Val Gln Val Phe Lys Asn His Gly Ala Ser Ala Gly Ala  
35 40 45  
Ser Met Ala His Ser His Ser Gln Met Leu Gly Thr Pro Phe Val Pro  
50 55 60  
Pro Ser Val Thr Thr Arg Leu Asn Cys Met Lys Glu Ile Phe Asp Arg  
65 70 75 80

(2) INFORMATION FOR SEQ ID NO:4260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid

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(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..73  
(D) OTHER INFORMATION: / Ceres Seq. ID 1580070  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4260:  
His Asp Val Arg Leu Trp Asp Leu Asp Ala Xaa Gly Val Ala Thr Cys  
1 5 10 15  
Cys Ser Pro Thr Arg Xaa Ala Xaa Gly Asn Ser Gly Xaa Thr Leu Arg  
20 25 30  
Cys Ser Met Phe Arg Cys Leu Arg Thr Met Gly His Leu Leu Glu Leu  
35 40 45  
Arg Trp Arg Ile His Thr Ala Lys Cys Trp Glu Leu Pro Leu Ser Leu  
50 55 60  
Pro Leu Leu Gln Leu Gly Leu Thr Ala  
65 70

(2) INFORMATION FOR SEQ ID NO:4261:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 39 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..39  
(D) OTHER INFORMATION: / Ceres Seq. ID 1580071  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4261:  
Met Phe Arg Cys Leu Arg Thr Met Gly His Leu Leu Glu Leu Arg Trp  
1 5 10 15  
Arg Ile His Thr Ala Lys Cys Trp Glu Leu Pro Leu Ser Leu Pro Leu  
20 25 30  
Leu Gln Leu Gly Leu Thr Ala  
35

(2) INFORMATION FOR SEQ ID NO:4262:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 407 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..407  
(D) OTHER INFORMATION: / Ceres Seq. ID 1580072  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4262:  
aaaatatata cagaacagca tcaactcttc gactgcgcca gtaacgtatt gccccgcgtg 60  
tgcgttaatc tggcagtgtc ggcgcagcac aagttcgga tcaactacgg gcagatcgcg 120  
aacgacctcc cggagccggc gcaggtggcg acgctcctgc agtcgatggg cgtgaacaag 180  
gtgaagctgt acgacgcgga cccccgggtg ctgacggcgt tcgccaacac gggcgctggc 240  
ttcaccatcg ccgtgggcaa cgaggacctg caggcgatgg cgccagccc ggacgcggcg 300  
cgccgttggg tggcggcgaa cgtgcagccc tacgtcccgg ccacgcgcat cacctgcgtc 360  
accgtcgga acgaggtcct gtcgggcaac gacagggcg cgatggc

(2) INFORMATION FOR SEQ ID NO:4263:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 135 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..135
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1580073
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4263:

Lys Ile Tyr Thr Glu Gln His Gln Leu Phe Asp Cys Ala Ser Asn Val  
1 5 10 15  
Leu Pro Arg Val Cys Val Asn Leu Ala Val Ser Ala Gln His Lys Phe  
20 25 30  
Gly Ile Asn Tyr Gly Gln Ile Ala Asn Asp Leu Pro Glu Pro Ala Gln  
35 40 45  
Val Ala Thr Leu Leu Gln Ser Met Gly Val Asn Lys Val Lys Leu Tyr  
50 55 60  
Asp Ala Asp Pro Arg Val Leu Thr Ala Phe Ala Asn Thr Gly Val Gly  
65 70 75 80  
Phe Thr Ile Ala Val Gly Asn Glu Asp Leu Gln Ala Met Ala Ala Ser  
85 90 95  
Pro Asp Ala Ala Arg Arg Trp Val Ala Ala Asn Val Gln Pro Tyr Val  
100 105 110  
Pro Ala Thr Arg Ile Thr Cys Val Thr Val Gly Asn Glu Val Leu Ser  
115 120 125  
Gly Asn Asp Thr Ala Ala Met  
130 135

(2) INFORMATION FOR SEQ ID NO:4264:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 80 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..80
- (D) OTHER INFORMATION: / Ceres Seq. ID 1580074

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4264:

Met Gly Val Asn Lys Val Lys Leu Tyr Asp Ala Asp Pro Arg Val Leu  
1 5 10 15  
Thr Ala Phe Ala Asn Thr Gly Val Gly Phe Thr Ile Ala Val Gly Asn  
20 25 30  
Glu Asp Leu Gln Ala Met Ala Ala Ser Pro Asp Ala Ala Arg Arg Trp  
35 40 45  
Val Ala Ala Asn Val Gln Pro Tyr Val Pro Ala Thr Arg Ile Thr Cys  
50 55 60  
Val Thr Val Gly Asn Glu Val Leu Ser Gly Asn Asp Thr Ala Ala Met  
65 70 75 80

(2) INFORMATION FOR SEQ ID NO:4265:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 466 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..466
- (D) OTHER INFORMATION: / Ceres Seq. ID 1580088

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4265:

acctatccgc cgctcccaa tcactctgcc cccaaactcc caccgccag catccccacg

(2) INFORMATION FOR SEQ ID NO:4266:

(A) LENGTH: 139 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..139

(D) OTHER INFORMATION: / Ceres Seq. ID 1580089

(xi) SEQUENCE DESCRIPTION: SEO ID NO:4266:

Pro	Ile	Arg	Arg	Leu	Pro	Ile	Ile	Leu	Pro	Pro	Asn	Ser	His	Pro	Ala
1				5					10					15	
Ala	Ser	Pro	Arg	His	His	Thr	Ser	Ser	Arg	Arg	Val	Val	Thr	Gly	Val
			20					25					30		
Lys	Met	Val	Gly	Pro	Gly	Leu	Tyr	Thr	Glu	Ile	Gly	Lys	Lys	Thr	Arg
		35				40					45				
Asp	Leu	Leu	Tyr	Lys	Asp	Tyr	Gln	Thr	Asp	His	Lys	Phe	Thr	Leu	Thr
	50				55						60				
Thr	Tyr	Thr	Ser	Asn	Gly	Val	Ala	Val	Thr	Ala	Ser	Ser	Thr	Lys	Lys
65				70						75				80	
Ala	Asp	Leu	Ile	Leu	Gly	Glu	Ile	Gln	Ser	Gln	Ile	Lys	Asn	Lys	Asn
				85					90					95	
Met	Thr	Ile	Asp	Val	Lys	Ala	Asn	Ser	Glu	Ser	Asn	Ile	Ile	Thr	Thr
			100					105					110		
Ile	Thr	Val	Asp	Glu	Ile	Ala	Thr	Pro	Gly	Leu	Lys	Thr	Ile	Leu	Ser
		115					120					125			
Phe	Ala	Val	Pro	Asp	Gln	Arg	Ser	Gly	Lys	Gly					
	130					135									

(2) INFORMATION FOR SEQ ID NO:4267:

(A) LENGTH: 106 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..106

(D) OTHER INFORMATION: / Ceres Seq. ID 1580090

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4267:

Met	Val	Gly	Pro	Gly	Leu	Tyr	Thr	Glu	Ile	Gly	Lys	Lys	Thr	Arg	Asp
1				5					10					15	
Leu	Leu	Tyr	Lys	Asp	Tyr	Gln	Thr	Asp	His	Lys	Phe	Thr	Leu	Thr	Thr
		20						25					30		
Tyr	Thr	Ser	Asn	Gly	Val	Ala	Val	Thr	Ala	Ser	Ser	Thr	Lys	Lys	Ala
		35					40					45			
Asp	Leu	Ile	Leu	Gly	Glu	Ile	Gln	Ser	Gln	Ile	Lys	Asn	Lys	Asn	Met
	50					55					60				
Thr	Ile	Asp	Val	Lys	Ala	Asn	Ser	Glu	Ser	Asn	Ile	Ile	Thr	Thr	Ile
65				70						75				80	
Thr	Val	Asp	Glu	Ile	Ala	Thr	Pro	Gly	Leu	Lys	Thr	Ile	Leu	Ser	Phe
				85					90					95	

Ala Val Pro Asp Gln Arg Ser Gly Lys Gly  
100 105

(2) INFORMATION FOR SEQ ID NO:4268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 488 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..488
- (D) OTHER INFORMATION: / Ceres Seq. ID 1580112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4268:

acaagcacaa agagaggccc cgaccgcat ggatcgtcag cgacagaccg accgtgacac	60
agccaacaac taacacgcac gcgcgcgaga gagaaagaga gctgcccggg agagagagag	120
agaggaaatc aaacgaaggc gacgacgtac ggagacggca tggccgatca ccaccaccac	180
caccaccacg ggcacccgcc ggacggggccc ggcggcgcgg gggaccagct ggaggtaatc	240
aaggagcagg accggctgct gcccatcgcc aacgtcggcc gcatcatgaa gcagatcctg	300
ccgcccaacg ccaagatctc caaggaggcc aaggagacga tgcaggagtg cgtgtccgag	360
ttcatcagct tcgtcacggg cgaggcctcc gacaagtgcc acaaggagaa gcgcaagacc	420
gtcaacggcg acgacgtctg ctgcgccttc ggcgcgctcg gcttcgacga ctacgtcgac	480
cccatgcg	

(2) INFORMATION FOR SEQ ID NO:4269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..162
- (D) OTHER INFORMATION: / Ceres Seq. ID 1580113

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4269:

Lys His Lys Glu Arg Pro Arg Pro Arg Trp Ile Val Ser Asp Arg Pro	
1 5 10 15	
Thr Val Thr Gln Pro Thr Thr Asn Thr His Ala Arg Glu Arg Glu Arg	
20 25 30	
Glu Leu Pro Gly Arg Glu Arg Glu Arg Lys Ser Asn Glu Gly Asp Asp	
35 40 45	
Val Arg Arg Arg His Gly Arg Ser Pro Pro Pro Pro Pro Arg Ala	
50 55 60	
Ser Ala Gly Arg Ala Arg Arg Arg Gly Gly Pro Ala Gly Gly Asn Gln	
65 70 75 80	
Gly Ala Gly Pro Ala Ala Ala His Arg Gln Arg Arg Pro His His Glu	
85 90 95	
Ala Asp Pro Ala Ala Gln Arg Gln Asp Leu Gln Gly Gly Gln Gly Asp	
100 105 110	
Asp Ala Gly Val Arg Val Arg Val His Gln Leu Arg His Gly Arg Gly	
115 120 125	
Leu Arg Gln Val Pro Gln Gly Glu Ala Gln Asp Arg Gln Arg Arg Arg	
130 135 140	
Arg Leu Leu Arg Leu Arg Arg Ala Arg Leu Arg Arg Leu Arg Arg Pro	
145 150 155 160	
His Ala	

(2) INFORMATION FOR SEQ ID NO:4270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..109  
(D) OTHER INFORMATION: / Ceres Seq. ID 1580114  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4270:

Met Ala Asp His His His His His His His Gly His Pro Pro Asp Gly  
1 5 10 15  
Pro Gly Gly Ala Gly Asp Gln Leu Glu Val Ile Lys Glu Gln Asp Arg  
20 25 30  
Leu Leu Pro Ile Ala Asn Val Gly Arg Ile Met Lys Gln Ile Leu Pro  
35 40 45  
Pro Asn Ala Lys Ile Ser Lys Glu Ala Lys Glu Thr Met Gln Glu Cys  
50 55 60  
Val Ser Glu Phe Ile Ser Phe Val Thr Gly Glu Ala Ser Asp Lys Cys  
65 70 75 80  
His Lys Glu Lys Arg Lys Thr Val Asn Gly Asp Asp Val Cys Cys Ala  
85 90 95  
Phe Gly Ala Leu Gly Phe Asp Asp Tyr Val Asp Pro Met  
100 105

(2) INFORMATION FOR SEQ ID NO:4271:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 435 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..435  
(D) OTHER INFORMATION: / Ceres Seq. ID 1580115  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4271:

gacaagcaga gtcgcggcgg ccgaaccgcc acctcccttt gcgcctcact catcagtcac 60  
ggcgctcgctg ccgcctggac ctccggcggtg gtcggtgacc ctgagcctaa ggcaccgtgg 120  
cgggctggag atccgtgccc ccgcggagaa cttgctccca gggtagggcc gcggcgggga 180  
gcgcattgcc ctctgtctcc gcctccgcgc ctgctctctc ctctccgtca catccaattg 240  
cggcggtcgt ccgcggcgga ccacacagcc cgggcgcgc ccgcgcggca gcagggtcgt 300  
ccgcttcctg cggagcaggt gggcgcggt gccgcgggca cctccatttg gaggcgcaag 360  
aaacagcccc cggcgcgcg gcgcgtgcc cgggactgcc gggaccagcg gattcgaacg 420  
ctggcgcggc ctgtc

(2) INFORMATION FOR SEQ ID NO:4272:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 145 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..145  
(D) OTHER INFORMATION: / Ceres Seq. ID 1580116  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4272:

Asp Lys Gln Ser Arg Gly Gly Arg Thr Ala Thr Ser Leu Cys Ala Ser  
1 5 10 15  
Leu Ile Ser His Gly Val Ala Ala Ala Trp Thr Ser Gly Val Val Gly  
20 25 30  
Asp Pro Glu Pro Lys Ala Pro Trp Arg Ala Gly Asp Pro Cys Arg Arg  
35 40 45  
Gly Glu Leu Ala Pro Arg Val Gly Pro Arg Arg Gly Ala His Val Pro

50 55 60  
Pro Ala Pro Pro Pro Pro Leu Pro Pro Pro Leu Arg His Ile Gln Leu  
65 70 75 80  
Arg Arg Ser Ser Arg Gly Asp His Thr Ala Arg Ala Ala Ala Arg  
85 90 95  
Gln Gln Gly Arg Pro Leu Pro Ala Glu Gln Val Gly Ala Ala Ala Ala  
100 105 110  
Gly Thr Ser Ile Trp Arg Arg Lys Lys Gln Pro Pro Ala Arg Ala Ala  
115 120 125  
Val Pro Pro Asp Cys Arg Asp Gln Arg Ser Arg Thr Leu Ala Arg Pro  
130 135 140  
Val  
145

(2) INFORMATION FOR SEQ ID NO:4273:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 144 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..144

(D) OTHER INFORMATION: / Ceres Seq. ID 1580117

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4273:

Thr Ser Arg Val Ala Ala Ala Glu Pro Pro Pro Pro Phe Ala Pro His  
1 5 10 15  
Ser Ser Val Met Ala Ser Leu Pro Pro Gly Pro Pro Ala Trp Ser Val  
20 25 30  
Thr Leu Ser Leu Arg His Arg Gly Leu Glu Ile Arg Ala Ala Ala  
35 40 45  
Glu Asn Leu Leu Pro Gly Trp Gly Arg Gly Gly Glu Arg Met Ser Leu  
50 55 60  
Leu Leu Arg Leu Arg Arg Cys Leu Leu Leu Ser Val Thr Ser Asn Cys  
65 70 75 80  
Gly Gly Arg Pro Ala Thr Thr Gln Pro Gly Pro Pro Pro Arg Gly  
85 90 95  
Ser Arg Val Val Arg Phe Leu Arg Ser Arg Trp Ala Arg Leu Pro Arg  
100 105 110  
Ala Pro Pro Phe Gly Gly Ala Arg Asn Ser Pro Arg Arg Ala Pro Pro  
115 120 125  
Cys Arg Arg Thr Ala Gly Thr Ser Gly Val Glu Arg Trp Arg Gly Leu  
130 135 140

(2) INFORMATION FOR SEQ ID NO:4274:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..125

(D) OTHER INFORMATION: / Ceres Seq. ID 1580118

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4274:

Met Ala Ser Leu Pro Pro Gly Pro Pro Ala Trp Ser Val Thr Leu Ser  
1 5 10 15  
Leu Arg His Arg Gly Gly Leu Glu Ile Arg Ala Ala Ala Glu Asn Leu  
20 25 30

Leu Pro Gly Trp Gly Arg Gly Gly Glu Arg Met Ser Leu Leu Leu Arg  
35 40 45  
Leu Arg Arg Cys Leu Leu Leu Ser Val Thr Ser Asn Cys Gly Gly Arg  
50 55 60  
Pro Ala Ala Thr Thr Gln Pro Gly Pro Pro Pro Arg Gly Ser Arg Val  
65 70 75 80  
Val Arg Phe Leu Arg Ser Arg Trp Ala Arg Leu Pro Arg Ala Pro Pro  
85 90 95  
Phe Gly Gly Ala Arg Asn Ser Pro Arg Arg Ala Pro Pro Cys Arg Arg  
100 105 110  
Thr Ala Gly Thr Ser Gly Val Glu Arg Trp Arg Gly Leu  
115 120 125

(2) INFORMATION FOR SEQ ID NO:4275:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..379
- (D) OTHER INFORMATION: / Ceres Seq. ID 1580119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4275:

aaggagcgcc tgatagtcta cgattacatg ccgaacctga gcatacactc tcagctccat	60
gggcagcacg cggcggagtg caacctcagc tgggagagga ggatgaggat cgctgtggac	120
tccgcggaag ggatcgcta cctgcaccac agcgcgacgc cgcacatcat ccacagagac	180
gtgaaggcga gcaacgtgct cctggacgcc gacttccagg cgcggtcgc cgacttcggc	240
ttcgccaagc tgggtcccgga cggcgcgacg caggtcacca caaggtgaaa ggcacgctgg	300
ggtacctggc gccggagtac gcgatgctcg ggaaggcctc cgagagctgc gacgtcttca	360
gcttcggggg cagctgct	

(2) INFORMATION FOR SEQ ID NO:4276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..95
- (D) OTHER INFORMATION: / Ceres Seq. ID 1580120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4276:

Lys Glu Arg Leu Ile Val Tyr Asp Tyr Met Pro Asn Leu Ser Ile His  
1 5 10 15  
Ser Gln Leu His Gly Gln His Ala Ala Glu Cys Asn Leu Ser Trp Glu  
20 25 30  
Arg Arg Met Arg Ile Ala Val Asp Ser Ala Glu Gly Ile Ala Tyr Leu  
35 40 45  
His His Ser Ala Thr Pro His Ile Ile His Arg Asp Val Lys Ala Ser  
50 55 60  
Asn Val Leu Leu Asp Ala Asp Phe Gln Ala Arg Val Ala Asp Phe Gly  
65 70 75 80  
Phe Ala Lys Leu Val Pro Asp Gly Ala Thr His Val Thr Thr Arg  
85 90 95

(2) INFORMATION FOR SEQ ID NO:4277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

00000000-00000000



aatgcagagc	tcgcgttgac	ggcacaggaa	gcagcagcag	agcaggccag	gaacaagaac	60
agcaatgaac	tcgcgcgcgg	gcgacgacgg	cggcggcagc	gcgcacggct	tattcgggtc	120
ggcgcgcac	cgcgggttcg	gctacggcgt	cgcggtgtcc	atcggcaccc	tcctggtggc	180

caccaccatc ggcgtcgcca tctacttctg cacgcgcacc tccatgcccg tgtccgcgcg 240  
cgcgccagcg ccgcccgggc agggcgggcga cgccggggcg ggcacgcacg aggccacgct 300  
cgaggcggtc ccggcggtgg cctacgcgga ggcgaggaag gcggcggcga accaggcggtg 360  
ctgctgcccc gtctgcctcg agtgctacgg cgacggcgac gtggt

(2) INFORMATION FOR SEQ ID NO:4280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..135
- (D) OTHER INFORMATION: / Ceres Seq. ID 1580128

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4280:

Asn Ala Glu Val Ala Leu Thr Ala Gln Glu Ala Ala Ala Glu Gln Ala  
1 5 10 15  
Arg Asn Lys Asn Ser Asn Glu Leu Ala Ala Gly Arg Arg Arg Arg Arg  
20 25 30  
Gln Arg Ala Arg Leu Ile Arg Val Gly Arg His Pro Arg Val Arg Leu  
35 40 45  
Arg Arg Arg Arg Val His Arg His Pro Pro Gly Gly His His His Arg  
50 55 60  
Ala Arg His Leu Leu Leu His Ala His Leu His Ala Arg Val Arg Arg  
65 70 75 80  
Arg Ala Ser Ala Ala Ala Ala Gly Arg Arg Arg Arg Ala Gly His Arg  
85 90 95  
Arg Gly His Ala Arg Gly Val Pro Gly Gly Gly Leu Arg Gly Gly Glu  
100 105 110  
Glu Gly Gly Gly Glu Pro Gly Val Leu Leu Pro Arg Leu Pro Arg Val  
115 120 125  
Leu Arg Arg Arg Arg Arg Gly  
130 135

(2) INFORMATION FOR SEQ ID NO:4281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..113
- (D) OTHER INFORMATION: / Ceres Seq. ID 1580129

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4281:

Met Asn Ser Pro Gly Asp Asp Gly Gly Gly Ser Ala His Gly Leu  
1 5 10 15  
Phe Gly Ser Gly Gly Ile Arg Gly Phe Gly Tyr Gly Val Gly Val Ser  
20 25 30  
Ile Gly Ile Leu Leu Val Ala Thr Thr Ile Ala Leu Ala Ile Tyr Phe  
35 40 45  
Cys Thr Arg Thr Ser Met Pro Val Ser Ala Ala Ala Pro Ala Pro Pro  
50 55 60  
Arg Gln Gly Gly Asp Ala Gly Arg Gly Ile Asp Glu Ala Thr Leu Glu  
65 70 75 80  
Ala Phe Pro Ala Val Ala Tyr Ala Glu Ala Arg Lys Ala Ala Ala Asn  
85 90 95  
Gln Ala Cys Cys Cys Pro Val Cys Leu Glu Cys Tyr Gly Asp Gly Asp  
100 105 110  
Val